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(54) Title: *ENTEROCOCCUS FAECALIS* POLYNUCLEOTIDES AND POLYPEPTIDES

(57) Abstract

The present invention relates to novel genes from *Enterococcus faecalis* and the polypeptides they encode. Also provided are vectors, host cells, antibodies and methods for producing the same. The invention additionally relates to diagnostic methods for detecting *Enterococcus* nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by *Enterococcus*.

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Enterococcus faecalis polynucleotides and polypeptides

Field of the Invention

The present invention relates to novel *Enterococcus faecalis* genes (*E. faecalis*)
5 nucleic acids and polypeptides. Also provided are vectors, host cells and recombinant
methods for producing the same. Further provided are diagnostic methods for
detecting *Enterococcus faecalis* using probes, primers, and antibodies to the *E. faecalis*
nucleic acids and polypeptides of the present invention. The invention further relates
to screening methods for identifying agonists and antagonists of *E. faecalis*
10 polypeptide activity and to vaccines using *E. faecalis* nucleic acids and polypeptides.

Background of the Invention

Enterococci have been recognized as being pathogenic for humans since the
turn of the century when they were first described by Thiercelin in 1988 as
15 microscopic organisms. The genus *Enterococcus* includes the species *Enterococcus*
faecalis or *E. faecalis* which is the most common pathogen in the group, accounting for
80 - 90 percent of all enterococcal infections. See Lewis et al. (1990) Eur J. Clin
Microbiol Infect Dis.9:111-117.

The incidence of enterococcal infections has increased in recent years and
20 enterococci are now the second most frequently reported nosocomial pathogens.
Enterococcal infection is of particular concern because of its resistance to antibiotics.
Recent attention has focused on enterococci not only because of their increasing role in
nosocomial infections, but also because of their remarkable and increasing resistance to
antimicrobial agents. These factors are mutually reinforcing since resistance allows
25 enterococci to survive in an environment in which antimicrobial agents are heavily
used; the hospital setting provides the antibiotics which eliminate or suppress
susceptible bacteria, thereby providing a selective advantage for resistant organisms,
and the hospital also provides the potential for dissemination of resistant enterococci
via the usual routes of hand and environmental contamination.

Antimicrobial resistance can be divided into two general types: inherent or intrinsic property, and that which is acquired. Examples for intrinsic resistance, like other species characteristics, appear to reside on the chromosome. Acquired resistance results from either a mutation or the uptake of DNA or acquisition of new DNA. The various inherent traits expressed by enterococci include resistance to semisynthetic penicillinase-resistant penicillins, cephalosporins, low levels of aminoglycosides, and low levels of clindamycin. Examples of acquired resistance include resistance to chloramphenicol, erythromycin, high levels of clindamycin, tetracycline, high levels of aminoglycosides, resistance to penicillin by means of penicillinase, fluoroquinolones, and vancomycin. Resistance to high levels of penicillin without penicillinase and resistance to fluoroquinolones are not known to be plasmid or transposon mediated and presumably are due to mutation(s).

Although the main reservoir for enterococci in humans is the gastrointestinal tract, the bacteria can also reside in the gall bladder, urethra and vagina.

E. faecalis has emerged as an important pathogen in endocarditis, bacteremia, urinary tract infections (UTIs), intraabdominal infections, soft tissue infections, and neonatal sepsis. See Lewis et al. (1990). In the 1970s and 1980s enterococci became firmly established as major nosocomial pathogens. They are now the fourth leading cause of hospital-acquired infection and the third leading cause of bacteremia in the United States. Fatality ratios for enterococcal bacteremia range from 12% to 68%, with death due to enterococcal sepsis in 50% of these cases. See T.G. Emori (1993) Clin. Microbiol. Rev. 6:428-442.

The ability of enterococci to colonize the gastrointestinal tract, plus the many intrinsic and acquired resistance traits, make these organisms, which usually seem to have relatively low intrinsic virulence, given an excellent opportunity to become secondary invaders. Since nosocomial isolates of enterococci have displayed resistance to essentially every useful antimicrobial agent, it will likely become increasingly difficult to successfully treat and cure enterococcal infections.

Particularly when the various resistance genes are together in a single strain, an event almost certain to occur at some time in the future.

The etiology of diseases mediated or exacerbated by *Enterococcus faecalis*, involves the programmed expression of *E. faecalis* genes, and that characterizing these
5 genes and their patterns of expression would dramatically add to our understanding of the organism and its host interactions. Knowledge of the *E. faecalis* gene and genomic organization would improve our understanding of disease etiology and lead to improved and new ways of preventing, treating and diagnosing diseases. Thus, there is a need to characterize the genome of *E. faecalis* and for polynucleotides of this
10 organism.

Summary of the Invention

The present invention provides for isolated *E. faecalis* polynucleotides and polypeptides shown in Table 1 and SEQ ID NO:1 through SEQ ID NO:496
15 (polynucleotide sequences having odd SEQ ID NOs and polypeptide sequences having even SEQ ID NOs). One aspect of the invention provides isolated nucleic acid molecules comprising polynucleotides having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence shown in Table 1; (b) a nucleotide sequence encoding any of the amino acid sequences of the polypeptides shown in
20 Table 1; and (c) a nucleotide sequence complementary to any of the nucleotide sequences in (a) or (b). The invention further provides for fragments of the nucleic acid molecules of (a), (b) & (c) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise a polynucleotide having a nucleotide sequence at least 90% identical,
25 and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b) or (c) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b) or (c) above. Additional nucleic acid embodiments of the invention relate to isolated nucleic acid molecules comprising polynucleotides which encode the amino acid sequences of

epitope-bearing portions of a *E. faecalis* polypeptide having an amino acid sequence in (a) above.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention and to host cells containing the recombinant vectors, as well as to methods of using such vectors and host cells. The present invention further relates to the use of the vectors in the production of *E. faecalis* polypeptides or peptides by recombinant techniques.

The invention further provides isolated *E. faecalis* polypeptides having an amino acid sequence selected from the group consisting of an amino acid sequence of any of the polypeptides described in Table 1 or fragments thereof.

The polypeptides of the present invention include polypeptides having an amino acid sequence with at least 70% identity, and more preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity to those described in Table 1, as well as polypeptides having an amino acid sequence at least 70% identical, more preferably at least 75% identical, and still more preferably 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to those shown, as well as isolated nucleic acid molecules encoding such polypeptides.

The present invention further provides a one or multi-component vaccine comprising one or more of the *E. faecalis* polypeptides or polypeptides described in Table 1, or fragments thereof, together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the *E. faecalis* polypeptide(s) are present in an amount effective to elicit an immune response to members of the *Enterococcus* genus, or at least *E. faecalis*, in an animal. The *E. faecalis* polypeptides of the present invention may further be combined with one or more immunogens of one or more other Enterococcal or non-Enterococcal organisms to produce a multi-component vaccine intended to elicit an immunological response against members of the *Enterococcus* genus and, optionally, one or more non-Enterococcal organisms.

The vaccines of the present invention can be administered in a DNA form, e.g., "naked" DNA, wherein the DNA encodes one or more Enterococcal polypeptides

and, optionally, one or more polypeptides of an *Enterococcal* organism. The DNA encoding one or more polypeptides may be constructed such that these polypeptides are expressed as fusion proteins.

The vaccines of the present invention may also be administered as a
5 component of a genetically engineered organism or host cell. Thus, a genetically engineered organism or host cell which expresses one or more *E. faecalis* polypeptides may be administered to an animal. For example, such a genetically engineered organism or host cell may contain one or more *E. faecalis* polypeptides of the present invention intracellularly, on its cell surface, or in its periplasmic space. Further, such
10 a genetically engineered organism or host cell may secrete one or more *E. faecalis* polypeptides. The vaccines of the present invention may also be co-administered to an animal with an immune system modulator (e.g., GDS6 and GM-CSF).

The invention also provides a method of inducing an immunological response in an animal to one or more members of the *Enterococcus* genus, preferably one or
15 more isolates of the *E. faecalis* species, comprising administering to the animal a vaccine as described above.

The invention further provides a method of inducing a protective immune response in an animal, sufficient to prevent, attenuate, or control an infection by members of the *Enterococcus* genus, preferably at least *E. faecalis* species,
20 comprising administering to the animal a composition comprising one or more of the polynucleotides or polypeptides described in Table I, or fragments thereof. Further, these polypeptides, or fragments thereof, may be conjugated to another immunogen and/or administered in admixture with an adjuvant.

The invention further relates to antibodies elicited in an animal by the
25 administration of one or more *E. faecalis* polypeptides of the present invention and to methods for producing such antibodies and fragments thereof. The invention further relates to recombinant antibodies and fragments thereof and to methods for producing such antibodies and fragments thereof.

The invention also provides diagnostic methods for detecting the expression of

the polynucleotides of Table 1 by members of the *Enterococcus* genus in an animal. One such method involves assaying for the presence of a polynucleotide encoding *E. faecalis* polypeptide in a sample from an animal. This expression may be assayed either directly (e.g., by assaying polypeptides using antibodies elicited in response to amino acid sequences described in Table 1) or indirectly (e.g., by assaying for antibodies having specificity for amino acid sequences described in Table 1). The expression of polynucleotides can also be assayed by detecting the nucleic acids of Table 1. An example of such a method involves the use of the polymerase chain reaction (PCR) to amplify and detect *Enterococcus* nucleic acid sequences.

The present invention also relates to nucleic acid probes having all or part of a nucleotide sequence described in Table 1 (e.g., SEQ ID NOs) which are capable of hybridizing under stringent conditions to polynucleotide nucleic acids. The invention further relates to a method of detecting one or more *Enterococcus* nucleic acids in a biological sample obtained from an animal, comprising: (a) hybridizing the sample with one or more *Enterococcus* polypeptides, comprising: (i) hybridizing the sample with one or more of the above-described nucleic acid probes under conditions such that hybridization occurs, and (b) detecting hybridization of one or more probes to the *Enterococcus* nucleic acid present in the biological sample.

Other uses of the polypeptides of the present invention include: *inter alia*, to detect *E. faecalis* in immunoassays, as epitopes, as molecular weight markers on SDS-PAGE gels, as molecular weight markers for molecular sieve gel filtration columns, to generate antibodies that specifically bind *E. faecalis* polypeptides of the present invention for the detection *E. faecalis* in immunoassays, to generate an immune response against *E. faecalis* and other *Enterococcus* species, and as vaccines against *E. faecalis*, other *Enterococcus* species and other bacteria genera.

Isolated nucleic acid molecules of the present invention, particularly DNA molecules, are useful as probes for gene mapping and/or identifying *E. faecalis* in a biological sample, for instance, by Southern and Northern blot analysis. Polynucleotides of the present invention are also useful in detecting *E. faecalis* by

PCR using primers for a particular *E. faecalis* polynucleotide. Isolated polynucleotides of the present invention are also useful in making the polypeptides of the present invention.

5 Detailed Description

The present invention relates to recombinant *E. faecalis* nucleic acids and fragments thereof. The present invention further relates to recombinant *E. faecalis* polypeptides and fragments thereof. The invention also relates to methods for using these polypeptides to produce immunological responses and to confer immunological
10 protection to disease caused by members of the genus *Enterococcus*, at least isolates of the *E. faecalis* genus. The invention further relates to nucleic acid sequences which encode antigenic *E. faecalis* polypeptides and to methods for detecting *E. faecalis* nucleic acids and polypeptides in biological samples. The invention also relates to antibodies specific for the polypeptides and peptides of the present invention and
15 methods for detecting such antibodies produced in a host animal.

Definitions

The following definitions are provided to clarify the subject matter which the inventors consider to be the present invention.

20 As used herein, the phrase "pathogenic agent" means an agent which causes a disease state or affliction in an animal. Included within this definition, for examples, are bacteria, protozoans, fungi, viruses and metazoan parasites which either produce a disease state or render an animal infected with such an organism susceptible to a disease state (e.g., a secondary infection). Further included are species and strains of
25 the genus *Enterococcus* which produce disease states in animals.

As used herein, the term "organism" means any living biological system, including viruses, regardless of whether it is a pathogenic agent.

As used herein, the term "*Enterococcus*" means any species or strain of bacteria which is members of the genus *Enterococcus*. Such species and strains are

known to those of skill in the art, and include those that are pathogenic and those that are not.

As used herein, the phrase "one or more *E. faecalis* polypeptides of the present invention" means polypeptides comprising an amino acid sequence of one or more of the *E. faecalis* polypeptides described in Table 1 (even SEQ ID NOs). These polypeptides may be expressed as fusion proteins wherein the *E. faecalis* polypeptides of the present invention are fused to additional amino acid sequences which may be of Enterococcal or non-Enterococcal origin. This phrase further includes polypeptide comprising fragments of the *E. faecalis* polypeptides of the present invention. Additional definitions are provided throughout the specification.

Explanation of Table 1

Table 1, below, provides information concerning genes which encode polypeptides of *E. faecalis*. The table lists the gene identifier which consists of the letters EF, which denote *E. faecalis*, followed immediately by a three digit numeric code, which arbitrarily number the *E. faecalis* genes of the present invention. A number from 1 through 4 follows the three digit number. A number 1 represents the full length open reading frame of the gene identified by the preceding three digit number. A number 2 represents the full length polypeptide encoded by the gene specified the preceding three digit number. A number 3 represents a polynucleotide fragment, of the gene represented by the preceding three digit number, used to produce an antigenic polypeptide. A number 4 represents an antigenic polypeptide fragment, of the gene represented by the preceding three digit number, used to stimulate an immune response or as a vaccine. The nucleotide and amino acid sequences of each gene and fragment are all shown in the Sequence Listing under the SEQ ID NO listed in Table 1.

Explanation of Table 2

Table 2 lists accession numbers for nucleotide matching sequences between

the polypeptides of the present invention are those available through GenBank and Derwent databases. These reference numbers are the database entry numbers commonly used by those of skill in the art who will be familiar with their denominations. The descriptions of the numbers relating to GenBank are available from the National Center for Biotechnology Information. Column 1 lists the gene or ORF of the present invention. Column 2 lists the accession number of a "match" gene sequence in GenBank or Derwent databases. Column 3 lists the description of the "match" gene sequence. Columns 4 and 5 are the high score and smallest sum probability, respectively, calculated by BLAST. Polypeptides of the present invention that do not share significant identity/similarity with any polypeptide sequences of GenBank and Derwent are not represented in Table 2. Polypeptides of the present invention that share significant identity/similarity with more than one of the polypeptides of GenBank and Derwent are represented more than once.

15 ***Explanation of Table 3.***

The *E. faecalis* polypeptides of the present invention may include one or more conservative amino acid substitutions from natural mutations or human manipulation as indicated in Table 3. Changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein. Residues from the following groups, as indicated in Table 3, may be substituted for one another: Aromatic, Hydrophobic, Polar, Basic, Acidic, and Small,

Explanation of Table 4

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in each of the full-length *E. faecalis* polypeptides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power Macintosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). *E. faecalis*

polypeptide shown in Table 1 may one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown described in Table 4 correspond to the amino acid sequences for each full length gene sequence shown in Table 1 and in the Sequence Listing. Polypeptides of the present invention that do not have antigenic epitopes recognized by the Jameson-Wolf algorithm are not represented in Table 2.

10 *Selection of Nucleic Acid Sequences Encoding Antigenic E. faecalis Polypeptides*

Sequenced *E. faecalis* genomic DNA was obtained from the *E. faecalis* strain V586. The *E. faecalis* strain V586 was deposited 2 May 1997 at the ATCC, 10801 University Blvd, Manassas, VA 20110-2209, and given accession number 55969.

Some ORFs contained in the subset of fragments of the *E. faecalis* genome disclosed herein were derived through the use of a number of screening criteria detailed below. The ORFs are bounded at the amino terminus by a methionine or valine residue and usually at the carboxy terminus by a stop codon.

Most of the selected sequences consist of complete ORFs. The polypeptides that do not comprise a complete ORF can be determined by determining whether the corresponding polynucleotide sequence comprises a stop codon after the codon for the last amino acid residue in the polypeptide sequence. It is not always preferred to express a complete ORF in a heterologous system. It may be challenging to express and purify a highly hydrophobic protein by common laboratory methods. Some of the polypeptide vaccine candidates described herein have been modified slightly to simplify the production of recombinant protein. For example, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, have been excluded from some constructs used for expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus have also been excluded from the recombinant expression

constructs. Thus, in one embodiment, a polypeptide which represents a truncated or modified ORF may be used as an antigen.

While numerous methods are known in the art for selecting potentially immunogenic polypeptides, many of the ORFs disclosed herein were selected on the basis of screening *Enterococcus faecalis* ORFs for several aspects of potential immunogenicity. One set of selection criteria are as follows:

1. *Type I signal sequence:* An amino terminal type I signal sequence generally directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Experimental evidence obtained from studies with *Escherichia coli* suggests that the typical type I signal sequence consists of the following biochemical and physical attributes (Izard, J. W. and Kendall, D. A. *Mol. Microbiol.* 13:765-773 (1994)). The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus. In addition, the central region of the signal sequence adopts an alpha-helical conformation in a hydrophobic environment. Finally, the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

2. *Type IV signal sequence:* The type IV signal sequence is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed above. Although functionally related, the type IV signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory, S., *J. Bacteriol.* 174:7345-7351 (1992)). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, type IV signal sequences generally contain a phenylalanine residue at the +1 site relative to the cleavage site.

3. *Lipoproteins:* Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence

for lipoprotein cleavage. Nearly three-quarters of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hirohashi, S. and Watanabe, T., *J. Bioenerg. Biomembr.*, 22:451-471 (1990)).

5 4. *LP-anchored proteins*. It has been experimentally determined that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes*, *S. maritimus*, *E. faecalis*, *S. pneumoniae*, and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V.
10 A., *ASM News*, 62:405-411 (1996)). The conserved region consists of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins examined. The amino acid sequence of this region is -P-X-T-G-X, where X is any
15 amino acid.

An algorithm for selecting antigenic and immunogenic *Enterococcus faecalis* polypeptides including the foregoing criteria was developed. The algorithm is similar to that described in U.S. patent application #8/781,986, filed January 3, 1997, which is fully incorporated by reference herein. Use of the algorithm by the inventors to
20 select immunologically useful *Enterococcus faecalis* polypeptides resulted in the selection of a number of the disclosed ORFs. Polypeptides comprising the polypeptides identified in this group may be produced by techniques standard in the art and as further described herein.

25 *Nucleic Acid Molecules*

Sequenced *E. faecalis* genomic DNA was obtained from the *E. faecalis* strain V586. As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining libraries and for sequencing are

provided below, for instance. A wide variety of *Enterococcus faecalis* strains that can be used to prepare *E. faecalis* genomic DNA for cloning and for obtaining polynucleotides and polypeptides of the present invention. A wide variety of *Enterococcus faecalis* strains are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). It is recognized that minor variation in the nucleic acid and amino acid sequence may be expected from *E. faecalis* strain to strain. The present invention provides for genes, including both polynucleotides and polypeptides, of the or the present invention from all the *Enterococcus faecalis* strains.

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc., Foster City, CA), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion. In case of conflict between Table 1 and either the nucleic acid sequence of the clones listed in Table 1 or the amino acid sequence of the protein expressed by the clones listed in Table 1, the clones listed in Table 1 are controlling. By "nucleotide sequence" of a nucleic acid molecule or

polynucleotide sequence may mean either a DNA or an RNA sequence. Using the information provided herein, such as the amino acid sequence in Table 1, a nucleic acid molecule of the present invention encoding an *E. faecalis* polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning DNAs using genomic DNA as starting material (e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). Illustrative of the invention, the nucleic acid molecule described in Table 1 was discovered in a DNA library derived from a *E.*

5
10 *faecalis* genomic DNA.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, DNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

15

By "isolated" nucleic acid molecule, is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. This includes segments of DNA comprising the *E. faecalis* polynucleotides of the present invention isolated from the native chromosome. These fragments include both isolated fragments consisting only of *E. faecalis* DNA and fragments comprising heterologous sequences such as vector sequences or other foreign DNA. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant

20
25 DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode a *E. faecalis* polypeptides and peptide of the present invention (e.g. polypeptides of Table 1).
5 That is, all possible DNA sequences that encode the *E. faecalis* polypeptides of the present invention. This includes the genetic code and species-specific codon preferences known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above, for instance, to optimize codon expression for a particular host (e.g., change codons in the bacteria mRNA to those
10 preferred by a mammalian or other bacterial host such as *E. coli*).

The invention further provides isolated nucleic acid molecules having the nucleotide sequence shown in Table 1 or a nucleic acid molecule having a sequence complementary to one of the above sequences. Such isolated molecules, particularly DNA molecules, are useful as probes for gene mapping and for identifying *E. faecalis*
15 in a biological sample, for instance, by PCR, Southern blot, Northern blot, or other form of hybridization analysis.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1, or the *E. faecalis* nucleotide
20 sequences contained in the plasmid clones listed in Table 1, at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in Table 1 is position 1. That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10
25 contiguous nucleotides in length could occupy is included in the invention. At least means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of Table 1 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of Table 1 wherein the

contiguous fragments, an integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, or by position by nucleotide positions. The invention includes
5 any fragment of a contiguous nucleotide sequence, selected from integers between 10 and the length of an entire nucleotide sequence minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in
10 length which include, as discussed above, fragments representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in Table 1 or of the *E. faecalis* nucleotide sequences of the plasmid clones listed in Table 1. The preferred sizes are, of course, meant to exemplify not limit the present invention as all
15 size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, are included in the invention. Additional preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of *E. faecalis* polypeptides identified in Table 4.

The present invention also provides for the exclusion of any fragment,
20 specified by 5' and 3' base positions or by size in nucleotide bases as described above for any nucleotide sequence of Table 1 or the plasmid clones listed in Table 1. Any number of fragments of nucleotide sequences in Table 1 or the plasmid clones listed in Table 1, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

25 In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of a polynucleotide or a nucleic acid molecules of the invention described above, for instance, nucleotide sequences of Table 1 or the *E. faecalis* sequences of the plasmid clones listed in Table 1, by stringent hybridization

conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (15 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides bases, and more preferably at least about 20 nucleotides bases, still more preferably at least about 30 nucleotides bases, and even more preferably about 30-70 (e.g., 50) nucleotides bases of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above. By a portion of a polynucleotide of "at least 20 nucleotides bases in length," for example, is intended 20 or more contiguous nucleotides bases nucleotides from the nucleotide sequence of the reference polynucleotide (e.g., the nucleotide sequence as shown in Table 1). Portions of a polynucleotide which hybridizes to a nucleotide sequence in Table 1, which can be used as probes and primers, may also be precisely specified by 5' and 3' base positions or by size in nucleotide bases as described above or precisely excluded in the same manner.

The nucleic acid molecules of the present invention include those encoding the full length *E. faecalis* polypeptides of Table 1 and portions of the *E. faecalis* polypeptides of Table 1. Also included in the present invention are nucleic acids encoding the above full length sequences and further comprise additional sequences, such as those encoding an added secretory leader sequence, such as a pre-, or pro- or prepro- protein sequence. Further included in the present invention are nucleic acids encoding the above full length sequences and portions thereof and further comprise additional heterologous amino acid sequences encoded by nucleic acid sequences from a different source.

Also included in the present invention are nucleic acids encoding the above protein sequences together with additional, non-coding sequences, including for

example, but not limited to, including functional sequences. These sequences include transcribed, non-transcribed sequences that may play a role in transcription, and mRNA processing, for example, ribosome binding and stability of mRNA. Also included in the present invention are additional coding sequences which provide additional functionality.

Thus, a nucleic acid sequence encoding a polypeptide may be fused to a marker sequence, such as a sequence encoding a peptide which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Evo Avenue, Crawfordsville, IN, 47931), among others, many of which are commercially available. For instance, hexa-histidine provides for convenient purification of the fusion protein. See Gentz et al. (1989) Proc. Natl. Acad. Sci. 86:821-24. The "HIS" tag is another peptide useful for purification which corresponds to an epitope derived from the influenza hemagglutinin protein. See Wilson et al. (1984) Cell 37:75-77. As discussed below, other such fusion proteins include the *E. faecalis* polypeptides of the present invention fused to Fc at the N- or C-terminus.

Variant and Mutant Polynucleotides

The present invention further relates to variants of the nucleic acid molecules which encode portions, analogs or derivatives of a *E. faecalis* polypeptides of Table 1 and variant polypeptides thereof including portions, analogs, and derivatives of the *E. faecalis* polypeptides. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. See, e.g., B. Lewin, Genes IV (1990). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such nucleic acid variants include those produced by nucleotide substitutions, deletions, or additions. The substitutions, deletions, or additions may involve one or

more nucleotide. The variants may be located in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of a *E. faecalis* protein of the present invention or portions thereof. Also especially preferred in this regard are conservative substitutions.

Such polypeptide variants include those produced by amino acid substitutions, deletions or additions. The substitutions, deletions, or additions may involve one or more residues. Alterations may produce conservative or non-conservative amino acid substitutions, deletions, or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of a *E. faecalis* protein of the present invention or portions thereof. Also especially preferred in this regard are conservative substitutions.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using them for production of *E. faecalis* polypeptides or peptides by recombinant techniques.

The present application is directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in Table 1. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *E. faecalis* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *E. faecalis* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *E. faecalis* activity include, *inter alia*, isolating an *E. faecalis* gene or allelic variants thereof from a DNA library, and detecting *E. faecalis*

mRNA expression of the *E. faecalis* gene *hlyEF* is expected of containing *E. faecalis* by the *E. faecalis* sequence.

Preferred nucleic acid sequences encoding polypeptides having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences shown in Table 1, which do, in fact, encode polypeptides having *E. faecalis* protein activity. By "a polypeptide having *E. faecalis* protein activity" is intended a polypeptide exhibiting activity, but not necessarily identical, to an activity of *E. faecalis* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in Table 1 will encode polypeptides having *E. faecalis* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assays. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *E. faecalis* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly affect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity. Table 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank and Derwent databases. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genera, species, or strains listed in Table 2.

mRNA expression samples, environmental samples, suspected of containing *E. faecalis* by Northern Blot analysis.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in Table 1, which do, in fact, encode a polypeptide having *E. faecalis* protein activity. By "a polypeptide having *E. faecalis* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *E. faecalis* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in Table 1 will encode a polypeptide having *E. faecalis* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *E. faecalis* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank and Derwent databases. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genuses, species, or strains listed in Table 2.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *E. faecalis* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. See Brutlag et al. (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=1, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3'

truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

Vectors and Host Cell

The present invention also relates to vectors which include the isolated DNA molecules of the present invention, host cells comprising the recombinant vectors, and the production of *E. faecalis* polypeptides and peptides of the present invention expressed by the host cells.

5 Recombinant constructs may be introduced into host cells using well known techniques such as infection, transduction, transfection, transvection, electroporation and transformation. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, full propagation generally will occur only in
10 complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged *in vitro* using an appropriate packaging cell line
15 and then transduced into host cells.

Preferred are vectors comprising *cis*-acting control regions to the polynucleotide of interest. Appropriate *trans*-acting factors may be supplied by the host, supplied by a complementing vector or supplied by the vector itself upon introduction into the host.

20 In certain preferred embodiments in this regard, the vectors provide for specific expression, which may be inducible and/or cell type-specific. Particularly preferred among such vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

Expression vectors useful in the present invention include chromosomal-,
25 episomal- and virus-derived vectors, *e.g.*, vectors derived from bacterial plasmids, bacteriophage, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli lac*, *trp* and *tac* promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating site at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin, or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera Sf9* cells; animal cells such as CHO, COS and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE9, pQE10 available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH146A available from Stratagene; pEF series of vectors available from Novagen; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the *E. coli lacI* and *lacZ* promoters, the T3, T5 and T7 promoters, the *gpt* promoter, the lambda PR and PL promoters and the *trp* promoter. Suitable eukaryotic

promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus (RSV), and metallothionein promoters, such as the mouse metallothionein-I promoter.

5 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals (for example, Davis, *et al.*, *Basic Methods In Molecular Biology* (1986)).

10 Transcription of DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are *cis*-acting elements of DNA, usually about from 10 to 300 nucleotides that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of
15 the replication origin at nucleotides 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated polypeptide into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment,
20 appropriate secretion signals may be incorporated into the expressed polypeptide, for example, the amino acid sequence KDEL. The signals may be endogenous to the polypeptide or they may be heterologous signals.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals, but also additional heterologous
25 functional regions. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the

polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability and to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize proteins. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is thoroughly advantageous for use in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified in the advantageous manner described. This is the case when Fc portion proves to be a hindrance to use in therapy and diagnosis, for example when the fusion protein is to be used as antigen for immunizations. In drug discovery, for example, human proteins, such as, hIL5-receptor has been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See Bennett, D. et al. (1995) J. Molec. Recogn. 8:52-58 and Johanson, K. et al. (1995) J. Biol. Chem. 270 (16):9459-9471.

The *E. faecalis* polypeptides can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography and high performance liquid chromatography ("HPLC") is employed for purification. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells.

Polypeptides and Fragments

The invention further provides an isolated *E. faecalis* polypeptide having an amino acid sequence in Table 1, or a peptide or polypeptide comprising a portion of the above polypeptides.

5

Variant and Mutant Polypeptides

To improve or alter the characteristics of *E. faecalis* polypeptides of the present invention, protein engineering may be employed. Recombinant DNA technology known to those skilled in the art can be used to create novel mutant
10 proteins or muteins including single or multiple amino acid substitutions, deletions, additions, or fusion proteins. Such modified polypeptides can show, e.g., enhanced activity or increased stability. In addition, they may be purified in higher yields and show better solubility than the corresponding natural polypeptide, at least under certain purification and storage conditions.

15

N-Terminal and C-Terminal Deletion Mutants

It is known in the art that one or more amino acids may be deleted from the N-terminus or C-terminus without substantial loss of biological function. For instance, Ron et al. J. Biol. Chem., 268:2984-2988 (1993), reported modified KGF
20 proteins that had heparin binding activity even if 3, 8, or 27 N-terminal amino acid residues were missing. Accordingly, the present invention provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of the *E. faecalis* polypeptides shown in Table 1, and polynucleotides encoding such polypeptides.

25

Similarly, many examples of biologically functional C-terminal deletion muteins are known. For instance, Interferon gamma shows up to ten times higher activities by deleting 8-10 amino acid residues from the carboxy terminus of the protein. See, e.g., Dobeli, et al. (1988) J. Biotechnology 7:199-216. Accordingly, the present invention provides polypeptides having one or more residues from the

carboxy terminus of the amino acid sequence of the *E. faecalis* polypeptides shown in Table 1. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini as described below.

The present invention is further directed to polynucleotide encoding portions
5 or fragments of the amino acid sequences described herein as well as to portions or
fragments of the isolated amino acid sequences described herein. Fragments include
portions of the amino acid sequences of Table 1, are at least 5 contiguous amino acid
in length, are selected from any two integers, one of which representing a N-terminal
position. The initiation codon of the polypeptides of the present inventions position
10 1. Every combination of a N-terminal and C-terminal position that a fragment at least
5 contiguous amino acid residues in length could occupy, on any given amino acid
sequence of Table 1 is included in the invention. At least means a fragment may be 5
contiguous amino acid residues in length or any integer between 5 and the number of
residues in a full length amino acid sequence minus 1. Therefore, included in the
15 invention are contiguous fragments specified by any N-terminal and C-terminal
positions of amino acid sequence set forth in Table 1 wherein the contiguous fragment
is any integer between 5 and the number of residues in a full length sequence minus 1.

Further, the invention includes polypeptides comprising fragments specified
by size, in amino acid residues, rather than by N-terminal and C-terminal positions.
20 The invention includes any fragment size, in contiguous amino acid residues, selected
from integers between 5 and the number of residues in a full length sequence minus 1.
Preferred sizes of contiguous polypeptide fragments include about 5 amino acid
residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino
acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100
25 amino acid residues, about 200 amino acid residues, about 300 amino acid residues,
and about 400 amino acid residues. The preferred sizes are, of course, meant to
exemplify, not limit, the present invention as all size fragments representing any
integer between 5 and the number of residues in a full length sequence minus 1 are
included in the invention. The present invention also provides for the exclusion of any

fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

- 5 The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

10 *Other Mutants*

- In addition to N- and C-terminal deletion forms of the protein discussed above, it also will be recognized by one of ordinary skill in the art that some amino acid sequences of the *E. faecalis* polypeptide can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated,
15 it should be remembered that there will be critical areas on the protein which determine activity.

- Thus, the invention further includes variations of the *E. faecalis* polypeptides which show substantial *E. faecalis* polypeptide activity or which include regions of *E. faecalis* protein such as the protein portions discussed below. Such mutants include
20 deletions, insertions, inversions, repeats, and type substitutions selected according to general rules known in the art so as to have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided. There are two main approaches for studying the tolerance of an amino acid sequence to change. See, Bowie, J. U. *et al.* (1990), Science 247:1306-1310. The first
25 method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality.

 These studies have revealed that proteins are surprisingly tolerant of amino

acid substitutions. The studies indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described by

5 Bowie et al. (*supra*) and the references cited therein. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic

10 residues Phe, Tyr.

Thus, the fragment, derivative, analog, or homolog of the polypeptide of Table 1, or that encoded by the plaimds listed in Table 1, may be: (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted

15 amino acid residue may or may not be one encoded by the genetic code; or (ii) one in which one or more of the amino acid residues includes a substituent group; or (iii) one in which the *E. faecalis* polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol); or (iv) one in which the additional amino acids are fused to the above form of

20 the polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the above form of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Thus, the *E. faecalis* polypeptides of the present invention may include one or

25 more amino acid substitutions, deletions, or additions, either from natural mutations or human manipulation. As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 3).

Amino acids in the *E. faecalis* proteins of the present invention that are

essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis. See, e.g., Cunningham et al. (1989) Science 244:1081-1085. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then
5 tested for biological activity using assays appropriate for measuring the function of the particular protein.

Of special interest are substitutions of charged amino acids with other charged or neutral amino acids which may produce proteins with highly desirable improved characteristics, such as less aggregation. Aggregation may not only reduce activity but
10 also be problematic when preparing pharmaceutical formulations, because aggregates can be immunogenic. See, e.g., Pinckard et al., (1967) Clin. Exp. Immunol. 2:331-340; Robbins, et al., (1987) Diabetes 36:838-845; Cleland, et al., (1993) Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377.

The polypeptides of the present invention are preferably provided in an
15 isolated form, and preferably are substantially purified. A recombinantly produced version of the *E. faecalis* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in
20 the art of protein purification.

The invention further provides for isolated *E. faecalis* polypeptides comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of a full-length *E. faecalis* polypeptide having the complete amino acid sequence shown in Table 1; (b) the amino acid sequence of a full-length *E.*
25 *faecalis* polypeptide having the complete amino acid sequence shown in Table 1 excepting the N-terminal methionine; (c) the complete amino acid sequence encoded by the plasmids listed in Table 1; and (d) the complete amino acid sequence excepting the N-terminal methionine encoded by the plasmids listed in Table 1. The polypeptides of the present invention also include polypeptides having an amino acid

sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a), (b), (c), and (d) above.

Further polypeptides of the present invention include polypeptides which
5 have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *E. faecalis* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not
10 more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *E. faecalis* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino
15 acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid
20 alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy
25 terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences

shown in Table 1 or to the amino acid sequence encoded by the plasmids listed in Table 1 can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) *Comp. App. Biosci.* 6:237-245. In a sequence alignment the query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10 residues at the N-terminus. The 10 unpaired residues
5 represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query
10 sequence. This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned
15 with the query sequence are manually corrected. No other manual corrections are to be made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would
20 still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present invention that do not have *E. faecalis* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

25 As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *E. faecalis* protein expression or as agonists and antagonists capable of enhancing or inhibiting *E. faecalis* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *E. faecalis* protein binding proteins

which are also candidate agonists and antagonists according to the present invention. See, e.g., Fields et al. (1989) Nature 340:245-246.

Epitope-Bearing Portions

5 In another aspect, the invention provides peptides and polypeptides comprising epitope-bearing portions of the *E. faecalis* polypeptides of the present invention. These epitopes are immunogenic or antigenic epitopes of the polypeptides of the present invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein or polypeptide is the
10 immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic determinant" or "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, e.g., Geysen, et al. (1983) Proc. Natl. Acad. Sci. USA 81:3998- 4002.
15 Predicted antigenic epitopes are shown in Table 4, below. It is pointed out that Table 4 only lists amino acid residues comprising epitopes predicted to have the highest degree of antigenicity. The polypeptides not listed in Table 4 and portions of polypeptides not listed in Table 4 are not considered non-antigenic. This is because they may still be antigenic *in vivo* but merely not recognized as such by the particular
20 algorithm used. Thus, Table 4 lists the amino acid residues comprising preferred antigenic epitopes but not a complete list. Amino acid residues comprising other antigenic epitopes may be determined by algorithms similar to the Jameson-Wolf analysis or by *in vivo* testing for an antigenic response using the methods described herein or those known in the art.

25 As to the selection of peptides or polypeptides bearing an antigenic epitope (*i.e.*, that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, e.g., Sutcliffe, et al., (1983) Science 219:660-666.

Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (*i.e.*, immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are
5 extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. *See*, Sutcliffe, et al., *supra*, p. 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1
10 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind
15 specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. *See* Sutcliffe, et al., *supra*, p. 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to
20 different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (*e.g.*, about 9 amino acids) can bind and displace the larger
25 peptides in immunoprecipitation assays. *See, e.g.*, Wilson, et al., (1984) *Cell* 37:767-778. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention

designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 50 to about 100 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (*i.e.*, the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

Non-limiting examples of antigenic polypeptides or peptides that can be used to generate an enterococcal-specific immune response or antibodies include portions of the amino acid sequences identified in Table 1. More specifically, Table 4 discloses a list of non-limiting residues that are involved in the antigenicity of the epitope-bearing fragments of the present invention. Therefore, the present invention provides for isolated and purified antigenic epitope-bearing fragments of the polypeptides of the present invention comprising a peptide sequences of Table 4. The antigenic epitope-bearing fragments comprising a peptide sequence of Table 4 preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) of a polypeptide of the present invention. That is, included in the present invention are antigenic polypeptides between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4. Therefore, in most cases, the polypeptides of Table 4 make up only a portion of the antigenic polypeptide. All combinations of sequences between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4 are included. The antigenic epitope-bearing

fragments may be specified by either the number of contiguous amino acid residues or by specific N-terminal and C-terminal positions as described above for the polypeptide fragments of the present invention, wherein the initiation codon is residue 1. Any number of the described antigenic epitope-bearing fragments of the present invention may also be excluded from the present invention in the same manner.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, an epitope-bearing amino acid sequence of the present invention may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks (Houghten, R. A. Proc. Natl. Acad. Sci. USA **82**:5131-5135 (1985)). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten and coworkers (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously (Houghten et al. (1985) Proc. Natl. Acad. Sci. **82**:5131-5135 at 5134).

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. *See, e.g.,* Sutcliffe, et al., *supra*; Wilson, et al., *supra*; and Bittle, et al. (1985) J. Gen. Virol. **66**:2347-2354. Generally, animals may be immunized with free peptide; however, anti-peptide

antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may
5 be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two
10 weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known
15 in the art.

Immunogenic epitope-bearing peptides of the invention, *i.e.*, those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen, *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of
20 peptides of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease
25 virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the

reaction with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

5 Further still, U.S. Patent No. 5,194,392, to Geysen (1990), describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (*i.e.*, a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092, also to Geysen (1989),
10 describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) discloses linear C₁-C₇-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and
15 libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods. The entire disclosure of each document cited in this section on "Polypeptides and Fragments" is hereby incorporated herein by reference.

20 As one of skill in the art will appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, *e.g.*, for chimeric proteins consisting of the
25 first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EPA 0,394,827; Trauncker *et al.* (1988) *Nature* 331:84-86. Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than a monomeric *E. faecalis* polypeptide or

fragment thereof alone. See Fountoulakis et al. (1995) J. Biochem. 270:3958-3964. Nucleic acids encoding the above epitopes of *E. faecalis* polypeptides can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

5

Antibodies

E. faecalis protein-specific antibodies for use in the present invention can be raised against the intact *E. faecalis* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to
10 an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')₂ and
15 other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present
20 invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *E. faecalis* polypeptide or fragment thereof is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific
25 activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988);

Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')₂ fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, *E. faecalis* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *E. faecalis* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *E. faecalis* polypeptide-specific antibody can be blocked by the *E. faecalis* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *E. faecalis* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *E. faecalis* polypeptide-specific antibodies.

Antibodies and fragments thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragments of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragments discussed above, i.e., by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies the specifically bind a particularly described fragment of a polypeptide of the present

invention and allows for the exclusion of the same.

Antibodies and fragments thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragments that do not bind polypeptides of any other species of *Enterococcus* other than *E. faecalis* are included in the present invention. Likewise, antibodies and fragments that bind only species of *Enterococcus*, i.e. antibodies and fragments that do not bind bacteria from any genus other than *Enterococcus*, are included in the present invention.

10 *Diagnostic Assays*

The present invention further relates to methods for assaying *staphylococcal* infection in an animal by detecting the expression of genes encoding *staphylococcal* polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Enterococcus*-specific antibodies, nucleic acids, or
15 proteins. Analysis of nucleic acid specific to *Enterococcus* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. See, e.g., Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Ereemeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing
20 differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids via PCR).

Where diagnosis of a disease state related to infection with *Enterococcus* has already been made, the present invention is useful for monitoring progression or
25 regression of the disease state whereby patients exhibiting enhanced *Enterococcus* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Enterococcus*

polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Enterococcus* polypeptides or nucleic acids. Methods for obtaining biological samples such as
5 tissue are well known in the art.

The present invention is useful for detecting diseases related to *Enterococcus* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable
10 technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Enterococcus* polypeptides having sufficient homology to the nucleic acid sequences identified in Table 1 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1
15 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described
20 above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium
25 phosphate buffer. A *E. faecalis* polynucleotide sequence shown in Table 1 labeled according to any appropriate method (such as the ³²P-multiprimered DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides

in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *E. faecalis* DNA sequence of the present invention is used as a
5 template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (i.e., mRNA encoding *Enterococcus* polypeptides).

10 Levels of mRNA encoding *Enterococcus* polypeptides are assayed, for e.g., using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction
15 mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers.

Alternatively, rather than labeling the primers, a labeled dNTP can be included in the
20 PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate bands (corresponding to the mRNA encoding the *Enterococcus* polypeptides of the present invention) are
25 quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold

Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or Enterococcal species including *E. faecalis* using bio chip technology. The present invention
5 includes both high density chip arrays (>1000 oligonucleotides per cm^2) and low density chip arrays (<1000 oligonucleotides per cm^2). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. The bio
10 chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips can also be used to monitor an *E. faecalis* or other Enterococcal infections and to monitor the genetic
15 changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in
20 the same manner as for the fragments, i.e, by their 5' and 3' positions or length in contiguous base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681,
25 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *E. faecalis* or other Enterococcal species and

infections thereof. Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using biosensors include those known in the art and those of: U.S. Patent Nos 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Enterococcus* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Enterococcus* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, e.g., with urea and neutral detergent, for the liberation of *Enterococcus* polypeptides for Western-blot or dot/slot assay. See, e.g., Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Enterococcus* polypeptide can be accomplished using an isolated *Enterococcus* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Enterococcus* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Enterococcus* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and

quantify a *Enterococcus* polypeptide. The amount of a *Enterococcus* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In
5 another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Enterococcus* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Enterococcus*
10 polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be
15 brought into contact with the component and readily removed from the sample. Variations of the above and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group,
20 which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable labels include
25 radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulphur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Enterococcus* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include

malate dehydrogenase, Enterococcal nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and
5 acetylcholine esterase.

Examples of suitable radioisotopic labels include ^3H , ^{111}In , ^{125}I , ^{131}I , ^{32}P , ^{35}S , ^{14}C , ^{51}Cr , ^{57}To , ^{58}Co , ^{59}Fe , ^{75}Se , ^{152}Eu , ^{90}Y , ^{67}Cu , ^{217}Ci , ^{211}At , ^{212}Pb , ^{47}Sc , ^{109}Pd , etc. ^{111}In is a preferred isotope where *in vivo* imaging is used since it avoids the problem of dehalogenation of the ^{125}I or ^{131}I -labeled monoclonal antibody by the liver. In
10 addition, this radionuclide has a more favorable gamma emission energy for imaging. See, e.g., Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumors tissues, particularly the liver, and therefore enhances specificity of tumor
15 localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Tr , and ^{56}Fe .

Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin
20 label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an
25 oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977)

Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

5 In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *E. faecalis* infection. Such a kit may include an isolated *E. faecalis* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*E. faecalis* antibody. Such a kit also includes means for detecting the binding of said antibody to the antigen. In specific
10 embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached.
15 Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *E. faecalis* antigen can be detected by binding of the reporter labeled antibody to the anti-*E. faecalis* polypeptide antibody.

In a related aspect, the invention includes a method of detecting *E. faecalis* infection in a subject. This detection method includes reacting a body fluid, preferably
20 serum, from the subject with an isolated *E. faecalis* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of reporter-labeled
25 antibody.

The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or

covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

5 The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect Enterococcal species including *E. faecalis* using bio chip and biosensor technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize Enterococcal species, including *E. faecalis*. Bio chip and
10 biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect Enterococcal species, including *E. faecalis* or specific polypeptides of the present invention. Bio chips or biosensors comprising polypeptides or antibodies of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and
15 environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

 The bio chips of the present invention may further comprise polypeptide
20 sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragments thereof specific for other pathogens including bacteria, viral, parasitic, and fungal polypeptide
25 sequences, in addition to the antibodies or fragments thereof of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *E. faecalis* or other Enterococcal infection and to monitor the genetic changes (amino acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug

development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention
5 may be specified in the same manner as for the fragments, i.e. by their N-terminal and C-terminal positions or length in contiguous amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect Enterococcal species, including *E. faecalis*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos.
10 and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

15 ***Treatment:***

Agonists and Antagonists - Assays and Molecules

The invention also provides a method of screening compounds to identify those which enhance or block the biological activity of the *E. faecalis* polypeptides of the present invention. The present invention further provides where the compounds
20 kill or slow the growth of *E. faecalis*. The ability of *E. faecalis* antagonists, including *E. faecalis* ligands, to prophylactically or therapeutically block antibiotic resistance may be easily tested by the skilled artisan. See, e.g., Straden et al. (1997) J Bacteriol. 179(1):9-16.

An agonist is a compound which increases the natural biological function or
25 which functions in a manner similar to the polypeptides of the present invention, while antagonists decrease or eliminate such functions. Potential antagonists include small organic molecules, peptides, polypeptides, and antibodies that bind to a polypeptide of the invention and thereby inhibit or extinguish its activity.

The antagonists may be employed for instance to inhibit peptidoglycan cross

bridge formation. Antibodies against *E. faecalis* may be employed to bind to and inhibit *E. faecalis* activity to treat antibiotic resistance. Any of the above antagonists may be employed in a composition with a pharmaceutically acceptable carrier.

5 *Vaccines*

The present invention also provides vaccines comprising one or more polypeptides of the present invention. Heterogeneity in the composition of a vaccine may be provided by combining *E. faecalis* polypeptides of the present invention. Multi-component vaccines of this type are desirable because they are likely to be
10 more effective in eliciting protective immune responses against multiple species and strains of the *Enterococcus* genus than single polypeptide vaccines.

Multi-component vaccines are known in the art to elicit antibody production to numerous immunogenic components. See, e.g., Decker et al. (1996) J. Infect. Dis. 174:S270-275. In addition, a hepatitis B, diphtheria, tetanus, pertussis tetravalent
15 vaccine has recently been demonstrated to elicit protective levels of antibodies in human infants against all four pathogenic agents. See, e.g., Aristegui, J. et al. (1997) Vaccine 15:7-9.

The present invention in addition to single-component vaccines includes multi-component vaccines. These vaccines comprise more than one polypeptide,
20 immunogen or antigen. Thus, a multi-component vaccine would be a vaccine comprising more than one of the *E. faecalis* polypeptides of the present invention.

Further within the scope of the invention are whole cell and whole viral vaccines. Such vaccines may be produced recombinantly and involve the expression of one or more of the *E. faecalis* polypeptides described in Table 1. For example, the
25 *E. faecalis* polypeptides of the present invention may be either secreted or localized intracellular, on the cell surface, or in the periplasmic space. Further, when a recombinant virus is used, the *E. faecalis* polypeptides of the present invention may, for example, be localized in the viral envelope, on the surface of the capsid, or internally within the capsid. Whole cells vaccines which employ cells expressing

heterologous proteins are known in the art. *See, e.g.,* Robinson, K. et al. (1997) Nature Biotech. 15:653-657; Sirard, J. et al. (1997) Infect. Immun. 65:2029-2033; Chabalgoity, J. et al. (1997) Infect. Immun. 65:2402-2412. These cells may be administered live or may be killed prior to administration. Chabalgoity, J. et al., *supra*,
5 for example, report the successful use in mice of a live attenuated *Salmonella* vaccine strain which expresses a portion of a platyhelminth fatty acid-binding protein as a fusion protein on its cells surface.

A multi-component vaccine can also be prepared using techniques known in the art by combining one or more *E. faecalis* polypeptides of the present invention, or
10 fragments thereof, with additional non-Enterococcal components (*e.g.,* diphtheria toxin or tetanus toxin, and/or other compounds known to elicit an immune response). Such vaccines are useful for eliciting protective immune responses to both members of the *Enterococcus* genus and non-Enterococcal pathogenic agents.

The vaccines of the present invention also include DNA vaccines. DNA
15 vaccines are currently being developed for a number of infectious diseases. *See, et al.,* Boyer, et al. (1997) Nat. Med. 3:526-532; reviewed in Spier, R. (1996) Vaccine 14:1285-1288. Such DNA vaccines contain a nucleotide sequence encoding one or more *E. faecalis* polypeptides of the present invention oriented in a manner that allows for expression of the subject polypeptide. For example, the direct
20 administration of plasmid DNA encoding *B. burgdorgeri* OspA has been shown to elicit protective immunity in mice against borrelial challenge. *See, Luke et al. (1997) J. Infect. Dis. 175:91-97.*

The present invention also relates to the administration of a vaccine which is co-administered with a molecule capable of modulating immune responses. Kim et al.
25 (1997) Nature Biotech. 15:641-646, for example, report the enhancement of immune responses produced by DNA immunizations when DNA sequences encoding molecules which stimulate the immune response are co-administered. In a similar fashion, the vaccines of the present invention may be co-administered with either nucleic acids encoding immune modulators or the immune modulators themselves.

These immune modulators include granulocyte macrophage colony stimulating factor (GM-CSF) and CD86.

The vaccines of the present invention may be used to confer resistance to Enterococcal infection by either passive or active immunization. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through active immunization, a vaccine of the present invention is administered to an animal to elicit a protective immune response which either prevents or attenuates a Enterococcal infection. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through passive immunization, the vaccine is provided to a host animal (*e.g.*, human, dog, or mouse), and the antisera elicited by this antisera is recovered and directly provided to a recipient suspected of having an infection caused by a member of the *Enterococcus* genus.

The ability to label antibodies, or fragments of antibodies, with toxin molecules provides an additional method for treating Enterococcal infections when passive immunization is conducted. In this embodiment, antibodies, or fragments of antibodies, capable of recognizing the *E. faecalis* polypeptides disclosed herein, or fragments thereof, as well as other *Enterococcus* proteins, are labeled with toxin molecules prior to their administration to the patient. When such toxin derivatized antibodies bind to *Enterococcus* cells, toxin moieties will be localized to these cells and will cause their death.

The present invention thus concerns and provides a means for preventing or attenuating a Enterococcal infection resulting from organisms which have antigens that are recognized and bound by antisera produced in response to the polypeptides of the present invention. As used herein, a vaccine is said to prevent or attenuate a disease if its administration to an animal results either in the total or partial attenuation (*i.e.*, suppression) of a symptom or condition of the disease, or in the total or partial immunity of the animal to the disease.

The administration of the vaccine (or the antisera which it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically,

the compound(s) are provided in advance of any symptoms of Enterococcal infection. The prophylactic administration of the compound(s) serves to prevent or attenuate any subsequent infection. When provided therapeutically, the compound(s) is provided upon or after the detection of symptoms which indicate that an animal may be infected with a member of the *Enterococcus* genus. The therapeutic administration of the compound(s) serves to attenuate any actual infection. Thus, the *E. faecalis* polypeptides, and fragments thereof, of the present invention may be provided either prior to the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

The polypeptides of the invention, whether encoding a portion of a native protein or a functional derivative thereof, may be administered in pure form or may be coupled to a macromolecular carrier. Example of such carriers are proteins and carbohydrates. Suitable proteins which may act as macromolecular carrier for enhancing the immunogenicity of the polypeptides of the present invention include keyhole limpet hemacyanin (KLH) tetanus toxoid, pertussis toxin, bovine serum albumin, and ovalbumin. Methods for coupling the polypeptides of the present invention to such macromolecular carriers are disclosed in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

A composition is said to be "pharmacologically or physiologically acceptable" if its administration can be tolerated by a recipient animal and is otherwise suitable for administration to that animal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

While in all instances the vaccine of the present invention is administered as a pharmacologically acceptable compound, one skilled in the art would recognize that the composition of a pharmacologically acceptable compound varies with the animal to which it is administered. For example, a vaccine intended for human use will

generally not be co-administered with Freund's adjuvant. Further, the level of purity of the *E. faecalis* polypeptides of the present invention will normally be higher when administered to a human than when administered to a non-human animal.

As would be understood by one of ordinary skill in the art, when the vaccine
5 of the present invention is provided to an animal, it may be in a composition which may contain salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants are substances that can be used to specifically augment a specific immune response. These substances generally perform two functions: (1) they protect the antigen(s) from being rapidly catabolized
10 after administration and (2) they nonspecifically stimulate immune responses.

Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the animal being immunized. Adjuvants can be loosely divided into several groups based upon their composition. These groups include oil adjuvants (for example, Freund's complete and
15 incomplete), mineral salts (for example, $AlK(SO_4)_2$, $AlNa(SO_4)_2$, $AlNH_4(SO_4)$, silica, kaolin, and carbon), polynucleotides (for example, poly IC and poly AU acids), and certain natural substances (for example, wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, or *Bordetella pertussis*, and members of the genus *Brucella*). Other substances useful as adjuvants are the saponins
20 such as, for example, Quil A. (Superfos A/S, Denmark). Preferred adjuvants for use in the present invention include aluminum salts, such as $AlK(SO_4)_2$, $AlNa(SO_4)_2$, and $AlNH_4(SO_4)$. Examples of materials suitable for use in vaccine compositions are provided in REMINGTON'S PHARMACEUTICAL SCIENCES 1324-1341 (A. Osol, ed, Mack Publishing Co, Easton, PA, (1980) (incorporated herein by reference).

25 The therapeutic compositions of the present invention can be administered parenterally by injection, rapid infusion, nasopharyngeal absorption (intranasopharyngeally), dermoabsorption, or orally. The compositions may alternatively be administered intramuscularly, or intravenously. Compositions for parenteral administration include sterile aqueous or non-aqueous solutions,

suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral
5 administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening,
10 flavoring, or perfuming agents.

Therapeutic compositions of the present invention can also be administered in encapsulated form. For example, intranasal immunization using vaccines encapsulated in biodegradable microsphere composed of poly(DL-lactide-co-glycolide). *See*, Shahin, R. et al. (1995) *Infect. Immun.* 63:1195-1200. Similarly, orally administered
15 encapsulated *Salmonella typhimurium* antigens can also be used. Allaoui-Attarki, K. et al. (1997) *Infect. Immun.* 65:853-857. Encapsulated vaccines of the present invention can be administered by a variety of routes including those involving contacting the vaccine with mucous membranes (*e.g.*, intranasally, intracolonicly, intraduodenally).

20 Many different techniques exist for the timing of the immunizations when a multiple administration regimen is utilized. It is possible to use the compositions of the invention more than once to increase the levels and diversities of expression of the immunoglobulin repertoire expressed by the immunized animal. Typically, if multiple immunizations are given, they will be given one to two months apart.

25 According to the present invention, an "effective amount" of a therapeutic composition is one which is sufficient to achieve a desired biological effect. Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the animal's or human's age, condition, sex, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in

the art.

The antigenic preparations of the invention can be administered by either single or multiple dosages of an effective amount. Effective amounts of the compositions of the invention can vary from 0.01-1,000 µg/ml per dose, more
5 preferably 0.1-500 µg/ml per dose, and most preferably 10-300 µg/ml per dose.

Examples

Example 1: Isolation of a Selected DNA Clone From the Deposited Sample of E. faecalis

10 Three approaches can be used to isolate a *E. faecalis* clone comprising a polynucleotide of the present invention from any *E. faecalis* genomic DNA library. The *E. faecalis* strain V586 has been deposited as a convenient source for obtaining a *E. faecalis* strain although a wide variety of strains *E. faecalis* strains can be used which are known in the art.

15 *E. faecalis* genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, washed two times with TES (30mM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the
20 mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear).
25 A CsCl gradient is then set up in SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and

precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *E. faecalis* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with
5 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (See, e.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable
10 host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the
15 appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR
20 BIOLOGY (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of Table 1 are synthesized and used to amplify the desired DNA by PCR using a *E. faecalis* genomic DNA prep as a template. PCR is carried out
25 under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 μg of the above DNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a

Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

- 5 Finally, overlapping oligos of the DNA sequences of Table 1 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

Example 2(a): Expression and Purification Enterococcal polypeptides in E. coli

- 10 The bacterial expression vector pQE60 was used for bacterial expression of some of the polypeptide fragments used in the soft tissue and systemic infection models discussed below. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding
15 site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl
20 terminus of that polypeptide.

- The DNA sequence encoding the desired portion of a *E. faecalis* protein of the present invention was amplified from *E. faecalis* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *E. faecalis* polynucleotide shown in Table 1. Additional nucleotides
25 containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

 For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *E. faecalis* polynucleotide sequence in Table 1. One of

ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form.

The 3' primer has a sequence containing an appropriate restriction site followed by
5 nucleotides complementary to the 3' end of the polypeptide coding sequence of Table 1, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *E. faecalis* DNA fragment and the vector pQE60 were digested with restriction enzymes which recognize the sites in the primers and the digested
10 DNAs were then ligated together. The *E. faecalis* DNA was inserted into the restricted pQE60 vector in a manner which places the *E. faecalis* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture was transformed into competent *E. coli* cells using
15 standard procedures such as those described by Sambrook et al., *supra*. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), was used in carrying out the illustrative example described herein. This strain, which was only one of many that are suitable for expressing a *E. faecalis* polypeptide, is available commercially
20 (QIAGEN, Inc., *supra*). Transformants were identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA was isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs were grown overnight ("O/N") in
25 liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture was used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells were grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") was then added to a final concentration of 1 mM to induce transcription

from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently were incubated further for 3 to 4 hours. Cells then were harvested by centrifugation.

The cells were then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8.

- 5 The cell debris was removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide was loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity were purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the
- 10 supernatant was loaded onto the column in 6 M guanidine-HCl, pH 8, the column was first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *E. faecalis* polypeptide was eluted with 6 M guanidine-HCl, pH 5.

- The purified protein was then renatured by dialyzing it against
- 15 phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of
- 20 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM imidazole. Imidazole was removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein was stored at 4° C or frozen at -80° C.

- Some of the polypeptide of the present invention were prepared using a non-
- 25 denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture was resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm was

approximately 10-20 O.D. ml. The suspension was then put through three freeze thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells were lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample was then centrifuged at
5 15,000 RPM for 30 minutes at 4°C. The supernatant was passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction was collected.

The pre-cleared flow-through was applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag
10 bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant was loaded onto the column in Lysis Buffer A at 4°C, the column was first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column was washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-
15 Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein was eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations were used: 3 volumes of 75 mM Imidazole, 3 volumes of 150 mM Imidazole, 5 volumes of 500 mM
20 Imidazole. The fractions containing the purified protein were analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein was then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein was stored at 4°C or frozen at -80°.

The following alternative method may be used to purify *E. faecalis* expressed
25 in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per

unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

5 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

10 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

 Following high speed centrifugation (30,000 x g) to remove insoluble particles, 15 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

 To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared 20 tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same 25 buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

 Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive

Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A₂₈₀ monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 2(b): Alternative Expression and Purification Enterococcal polypeptides in E. coli

The vector pQE10 was alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example. The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of Table 1 were amplified using PCR oligonucleotide primers from genomic *E. faecalis* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid

sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were
5 selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain
10 its reading frame with that of *E. faecalis* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences encoding the amino acid sequences of Table 1 may also be cloned and expressed as fusion proteins by a protocol similar to that described
15 directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

The above methods are not limited to the polypeptide fragments actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragments thereof.

20

Example 2(c): Alternative Expression and Purification of Enterococcal polypeptides in E. coli

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in
25 this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

The DNA sequence encoding the desired portion of the *E. faecalis* amino acid sequence is amplified from an *E. faecalis* genomic DNA prep the deposited DNA

clones using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *E. faecalis* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

5 For cloning a *E. faecalis* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers
10 contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

 The amplified *E. faecalis* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs
15 are then ligated together. Insertion of the *E. faecalis* DNA into the restricted pQE60 vector places the *E. faecalis* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

20 The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for
25 expressing *E. faecalis* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the *lacI* repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *E. faecalis* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. faecalis* polypeptide. The purified protein is stored at 4°C or frozen at -80°C.

The following alternative method may be used to purify *E. faecalis* polypeptides expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells were then lysed by passing the solution through a microfluidizer

(Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

5 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x g) to remove insoluble particles,
10 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared
15 tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same
20 buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive
25 Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5.

Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after
5 the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

10 *Example 2(d): Cloning and Expression of E. faecalis in Other Bacteria*

E. faecalis polypeptides can also be produced in: *E. faecalis* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr. Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods
15 Chang et al., U.S. Patent No. 4,952,508.

Example 3: Cloning and Expression in COS Cells

A *E. faecalis* expression plasmid is made by cloning a portion of the DNA encoding a *E. faecalis* polypeptide into the expression vector pDNAI/Amp or
20 pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several
25 codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived

from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

5 A DNA fragment encoding a *E. faecalis* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *E. faecalis* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of
10 *E. faecalis* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *E. faecalis* DNA, a stop codon, and a convenient restriction site.

 The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested
15 with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis
20 or other means for the presence of the fragment encoding the *E. faecalis* polypeptide

 For expression of a recombinant *E. faecalis* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *E. faecalis* by the vector.

25 Expression of the *E. faecalis*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing ³⁵S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM

NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression
5 product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 4: Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *E. faecalis* polypeptide in this
10 example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the
15 chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.,* Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target
20 enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one
25 or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rousc Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell

41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718.

Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the
5 expression, e.g., the human β -actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV1. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. faecalis* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551. For the polyadenylation of the mRNA
10 other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as *gpt*, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

15 The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphatase by procedures known in the art. The vector is then isolated from a 1% agarose gel. The DNA sequence encoding the *E. faecalis* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a
20 restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *E. faecalis* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified
25 again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for

transfection. Five μg of the expression plasmid pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE.™ (LifeTechnologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme
5 that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well
10 petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM , 2 μM , 5 μM , 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of
15 100-200 μM . Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 5: Quantitative Murine Soft Tissue Infection Model for E. faecalis

Compositions of the present invention, including polypeptides and peptides,
20 are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following quantitative murine soft tissue infection model. Mice (e.g., NIH Swiss female mice, approximately 7 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present
25 invention using methods known in the art, such as those discussed above. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5×10^8 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 with sterilized Cytodex 3 microcarrier beads preswollen in sterile PBS (3g/100ml). Mice are anesthetized briefly until docile, but still mobile and injected with 0.2 ml of the Cytodex 3 bead/bacterial mixture into each animal subcutaneously in the inguinal region. After four days, counting the day of injection as day one, mice are sacrificed and the contents of the abscess is excised and placed in a 15 ml conical tube containing 1.0ml of sterile PBS. The contents of the abscess is then enzymatically treated and plated as follows.

The abscess is first disrupted by vortexing with sterilized glass beads placed in the tubes. 3.0mls of prepared enzyme mixture (1.0ml Collagenase D (4.0 mg/ml), 1.0ml Trypsin (6.0 mg/ml) and 8.0 mls PBS) is then added to each tube followed by a 20 min. incubation at 37C. The solution is then centrifuged and the supernatant drawn off. 0.5 ml dH2O is then added and the tubes are vortexed and then incubated for 10 min. at room temperature. 0.5 ml media is then added and samples are serially diluted and plated onto agar plates, and grown overnight at 37C. Plates with distinct and separate colonies are then counted, compared to positive and negative control samples, and quantified. The method can be used to identify composition and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

Example 6: Murine Systemic Neutropenic Model for E. faecalis Infection

Compositions of the present invention, including polypeptides and peptides, are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following qualitative murine systemic neutropenic model. Mice (e.g., NIH Swiss female mice, approximately 7
5 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present invention using methods known in the art, such as those discussed above. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.
10 Mice are then injected with 250 - 300 mg/kg cyclophosphamide intraperitoneally. Counting the day of C.P. injection as day one, the mice are left untreated for 5 days to begin recovery of PMNL'S.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5×10^8
15 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 in 4% Brewer's yeast in media. Mice are injected with the bacteria/brewer's yeast challenge intraperitoneally. The Brewer's yeast solution alone is used as a control. The mice are then monitored twice
20 daily for the first week following challenge, and once a day for the next week to ascertain morbidity and mortality. Mice remaining at the end of the experiment are sacrificed. The method can be used to identify compositions and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in
25 the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific
5 embodiments described herein, which are intended as single illustrations of individual
aspects of the invention. Functionally equivalent methods and components are within
the scope of the invention, in addition to those shown and described herein and will
become apparant to those skilled in the art from the foregoing description and
accompanying drawings. Such modifications are intended to fall within the scope of
10 the appended claims.

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF001-1 (SEQ ID NO:1)

TGAAAGAATA TTGCCAGAAC GTGGCGAGCA AATTGTTTTA TAAATTTTTT TAAGGGAGAG
 AAAAAAATGA AGTTCAAAAC TCTAGCAACA ACAGTGTTAG CAACCGCAGC TATTTTCGCA
 TTGGGGGGCTT GTGGTAACGG TAATGGGGCC AAAGAATCAA ACGATATTGT GAAAGAAGTG
 AAGGAAGATA CGACAATCAC TTTCTGGCAT GCAATGAATG GGGTTCAAGA AGAAGCGTTA
 ACAAATTAAT CGAAAGACTT CATGAAAGAA AATCCAAAAA TTAAAGTGGA ATTACAAAAT
 CAATCTGCTT ACCCTGATTT ACAAGCCAAA ATCAATTCTGA CTTTAACTTC ACCAAAAGAT
 TTACCAACAA TTACGCAAGC GTACCCAGGC TGGTTATGGA ATGCTGCACA AGATGAAATG
 TTAGTGGAAT TAAAACCAT TATGGATGAT GACACAATCG GCTGGAAAGA TGCAGAGCCA
 ATTCGTGAAG TATTGTTAGA CGGCGCCAAA ATCGACGGCA AACAAATACGG CATTCATT
 AATAAATCGA CAGAAATGTT ATTCTATAAT GCTGATTGTT TGAAAGAATA TGGTGTGAA
 GTACCGAAAA CATTAGAGGA ATTAAGAGAA GCTTCTAAAA CAATTACGA AAAATCCAAC
 AAAGAAGTCG TTGGTGCTGG TTTTGACTCG TTAAATAACT ATTACGCAAT TGGAAATGAAA
 AACAAAGGCG TTGATTTTAA TAAAGACTTA GATTTAACAA GCAAAGATTG ACAAGAAGTC
 GTGGACTATT ACCGTGATGG TATCGAAGCA GGTACTTCC GCACAGCTGG TTCAGATAAA
 TATTTATCTG GCCCATTTGC AAACAAAAAG GTAGCAATGT TTGTCGGTAG TATTGCTGGT
 GCTGGTTTTG TTCAAAAAGA TGCTGAAGCT GGTGGCTATG AATACGGTGT TGCACCACGT
 CCTGAAAAAA TCAACTTACA ACAAGGAACA GATATTTATA TGTTTCGATAG TGCTACGCCA
 GAACAACGGA CAGCGGCAT TGAATTCATG AAATTCCTAG CTACTCCTGA TTCACAATTG
 TACTGGGCAC AACAAACAGG TTATATGCCA ATTTTAGAAT CTGTTTTACA CAGTGATGAG
 TACAAAAAAT CTAAGACAAC CAAAGTACCT GCACAACTTG AAAACGCAGT AAAAGATTTA
 TTCGCTATCC CAGTAGAAGA AAATGCTGAT TCAGCCTATA ATGAAATGCG GACAATTATG
 GAAAGTATTT TTGCTTCATC AAATAAAGAC ACGAGAAAAT TATTGAAAGA TGCAACATCA
 CAATTTGAAC AAGCATGGAA CCAATAA

EF001-2 (SEQ ID NO:2)

MKFKTLATTT VLATAAIFAL GACGNGNGAK ESNDIVKEVK
 EDTTITFWHA MNGVQEEALT KLTKDFMKEN PKIKVELQNO SAYPDLQAKI NSTLTSFKDL
 PTITQAYPGW LWNAAQDEML VDLKPYMDDD TIGWKDAEPI REVLLDGAKI DGKQYGIPFN
 KSTEMLFYNA DLLKEYGVEV PKTLEELKEA SKTIYEKSNK EVVGAGFDSL NNYAIGMKN
 KGVDNFNKDL LSKDSQEVV DYRDGIEAG YFRTAGSDKY LSGPFANKKV AMFVGSIAGA
 GFVQKDAEAG GYEVGVAPRP EKINLQQGTD IYMFDSATPE QRTAAFEFMK FLATPDSQLY
 WAQQTGYMPI LESVLHSDEY KNSKTTKVPA QLENAVKDLF AIPVEENADS AYNEMRTIME
 SIFASSNKDT RKLLKDATSQ FEQAWNQ

EF001-3 (SEQ ID NO:3)

TT GTGGTAACGG TAATGGGGCC AAAGAATCAA ACGATATTGT GAAAGAAGTG
 AAGGAAGATA CGACAATCAC TTTCTGGCAT GCAATGAATG GGGTTCAAGA AGAAGCGTTA
 ACAAATTAAT CGAAAGACTT CATGAAAGAA AATCCAAAAA TTAAAGTGGA ATTACAAAAT
 CAATCTGCTT ACCCTGATTT ACAAGCCAAA ATCAATTCTGA CTTTAACTTC ACCAAAAGAT
 TTACCAACAA TTACGCAAGC GTACCCAGGC TGGTTATGGA ATGCTGCACA AGATGAAATG
 TTAGTGGAAT TAAAACCAT TATGGATGAT GACACAATCG GCTGGAAAGA TGCAGAGCCA
 ATTCGTGAAG TATTGTTAGA CGGCGCCAAA ATCGACGGCA AACAAATACGG CATTCATT
 AATAAATCGA CAGAAATGTT ATTCTATAAT GCTGATTGTT TGAAAGAATA TGGTGTGAA
 GTACCGAAAA CATTAGAGGA ATTAAGAGAA GCTTCTAAAA CAATTACGA AAAATCCAAC
 AAAGAAGTCG TTGGTGCTGG TTTTGACTCG TTAAATAACT ATTACGCAAT TGGAAATGAAA
 AACAAAGGCG TTGATTTTAA TAAAGACTTA GATTTAACAA GCAAAGATTG ACAAGAAGTC
 GTGGACTATT ACCGTGATGG TATCGAAGCA GGTACTTCC GCACAGCTGG TTCAGATAAA
 TATTTATCTG GCCCATTTGC AAACAAAAAG GTAGCAATGT TTGTCGGTAG TATTGCTGGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCTGTTTTT TTTCAAAAAGA TCTGAAGCT GGTGGCTATG AATACGGTGT TGCACCACGT
 CCTSAAAAA TCAACTTACA ACAAGGAACA GATATTTATA TGTTGATAG TGCTACGCCA
 GAADAACGGA CAGCGGCATT TGAATTCATG AAATTCTTAG CTACTCCTGA TTCACAATTG
 TACTGGGCAC AACAAACAGG TTATATGCCA ATTTTAGAAT CTGTTTTACA CAGTGATGAG
 TACAAAAATT CTAAGACAAC CAAASTACCT GTACAACTTG AAAACGCAGT AAAAGATTTA
 TTCGTATCC CAGTAGAAGA AAATCTGTAT TCAGCCTATA ATGAAATGCG GACAATTATG
 GAAATATTT TTCCTTCATC AAATAAAGAC ACGAGAAAAT TATTGAAAGA TGCAACATCA
 CAATTTGAAC AAGCATGGAA CCAA

EF001-4 (SEQ ID NO:4)

CGNGNGAK ESNLIVKEVK
 EDTTITFWHA MNGVQEEALT KLTKDFMKEN PKIKVELQNG SAYPDLQAKI NSTLTSPKDL
 PTITQAYPGW LWNAAQDEML VILKPYMDDD TIGWKDAEPI REVLLDGAKI DGKQYGI PFN
 KSTEMLFYNA DLLKEYGVEV PFTLEELKEA SKTIYEKSNK EVVGAGFDSL NNYIAIGMKN
 KGVDFNKDLD LTSKDSQEVV IYYRDGIEAG YFRTAGSDKY LSGPFANKKV AMFVGSIAAG
 GFVQKDAEAG GYEYGVAPRP EKINLQCGTD IYMFDSATPE QRTAAFEFMK FLATPDSQLY
 WAQQTGYMPI LESVLHSDEY KNSKTKKVA QLENAVKDLF AIPVEENADS AYNEMRTIME
 SIFASSNKDT RKLLKDATSQ FEQAWNQ

EF002-1 (SEQ ID NO:5)

TAAATAGCGG AGGTAGTACA AATGAAATTT TGGAAAAAAG GCTTAACAGC GGCAGCGCTG
 TTAGCAGTGG CGGCAGTAAC TTTAACAGCA TGTGGTGGTT CAAGTGA AAAAGCAACT
 GAAAAGAGTG AAGATGGCAA AACAAAATTA ACAGTAACTA CTTGGAATTA TGACACGACC
 CCAGAATTTG AGAAATTATT CAGAGCTTTT GAAGCGGAAA ATCCTGATAT CACTATTGAA
 CCGGTGGACA TTGCTTCAGA TGATTATGAC ACAAAGTAA CAACGATGCT TTCATCAGGA
 GATACGACGG ATATTTTAAC CATGAAAAAC TTACTTTTAT ATTCTAATTA CGCGCTACGC
 AATCAATTGG TGGATTTAAC CGATCACGTT AAAGATTTAG ATATCGAACC TGCCAAAGCA
 ACTTACGAGA TGTATGAAAT CGATGGTAAA ACCTATGCTC AGCCTTACCG TACAGATTTT
 TGGGTATTGT ATTACAATAA AAAAATGTTT GATGAAGCCG GAATTGCTTA TCCCGATAAC
 TTAACCTGGG ATGAATATGA AGCGTTAGCG AAAAAATTAT CTAAACCAGA AGAACAGTA
 TATGGTGCCT ATCAACATAC TTGGCGCTCA ACCGTTCAAG CGATTGCTGC TGCTCAAAAC
 AATGCCAATT TGATTGAACC AAAATACAAT TATATGGAAA CTTATTATGA TCGCGCATTG
 AGAATGCAAA AAGATCAATC ACAAATGGAT TTTGGAACAG CAAAATCAAC AAAAGTAACG
 TATCAATCAC AATTTGAAAA TTCAAAAGCG GCGATGATGT ACATGGGTAG CTGGTACATG
 GGGACTTTAT TAACAAACAT TGATGATGGC AAAACAAATG TCGAATGGGG GATTGCCGAA
 ATACCACAAC AAGAAAAAGG CAAAGCAACT ACCTTTGGCT CACCGACAAG TTTTGCAATT
 AATAAAAAACA GTAAAAACA AAAAGCTGCT CAAAAATTCT TAGACTTTGC TTCAGGTAAA
 GAAGGTGCAA AACTTTTAGC AGAAGTAGGG GTGGTTCCCT CTTATAAAAC AGATGAAATT
 GATAAAATCT ACTTTGCAAG AAAAGGAATG CCTTCAGACG AGTCTCACAA AAAGCCTTTA
 ACCCAGATAC AATTAATTTA G

EF002-2 (SEQ ID NO:6)

MKFW KKGLTAAALL AVAAVTLTAC GGSSEKKATE KSEDGKTKLT VTTWNYDTP
 EFEKLFRAFE AENPDITIEP VDIASDDYDT KVTMLSSGD TTDILTMKNL LSYSNYALRN
 QLVLDLTHVK LLDIEPAKAS YEMYEIDGKT YQPYRTDFW VLYYNKKMFD EAGIAYPDNL
 TWDEYEALAK KLSKPEEQVY GAYQHTWRST VQAIAAAQNN ANLIEPKYNY METYYDRALR
 MQKQSQMDMF GTAKSTKVTY QSQFENSKAA MMYMGSWYMG TLLTNIDDGK TNVEWGIAEI
 PQQEKGKATT FGSPTSFAIN KNSKKQKAAQ KFLDFASGKE GAKLLAEVGV VPSYKTDEID

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KIYFARKGMP SDESHKKPLT QIQLI

EF002-3 (SEQ ID NO:7)

A TGTGGTGGTT CAAGTGAAAA GAAAGCAACT
 GAAAAGAGTG AAGATGGCAA AACAAAATTA ACAGTAACTA CTTGGAATTA TGACACGACC
 CCAGAATTTG AGAAATTATT CAGAGCTTTT GAAGCGGAAA ATCCTGATAT CACTATTGAA
 CCGGTGGACA TTGCTTCAGA TGATTATGAC ACAAAGTAA CAACGATGCT TTCATCAGGA
 GATACGACGG ATATTTTAAC CATGAAAAAC TTACTTTCAT ATTCTAATTA CGCGCTACGC
 AATCAATTGG TGGATTTAAC CGATCACGTT AAAGATTTAG ATATCGAACC TGCCAAAGCA
 AGTTACGAGA TGTATGAAAT CGATGGTAAA ACCTATGCTC AGCCTTACCG TACAGATTTC
 TGGGTATTGT ATTACAATAA AAAAATGTTT GATGAAGCCG GAATTGCCTA TCCCGATAAC
 TTAAGTTGGG ATGAATATGA AGCGTTAGCG AAAAAATTAT CTAAACCAGA AGAACAAGTA
 TATGGTGCCT ATCAACATAC TTGGCGCTCA ACCGTTCAAG CGATTGCTGC TGCTCAAAAC
 AATGCCAATT TGATTGAACC AAAATACAAT TATATGGAAA CTTATTATGA TCGCGCATTG
 AGAATGCAAA AAGATCAATC ACAAATGGAT TTTGGAACAG CAAAATCAAC AAAAGTAACG
 TATCAATCAC AATTTGAAAA TTCAAAAGCG GCGATGATGT ACATGGGTAG CTGGTACATG
 GGGACTTTAT TAACAAACAT TGATGATGGC AAAACAAATG TCGAATGGGG GATTGCCGAA
 ATACCACAAC AAGAAAAAGG CAAAGCAACT ACCTTTGGCT CACCGACAAG TTTTGCAATT
 AATAAAAAACA GTAAAAAACA AAAAGCTGCT CAAAAATTCT TAGACTTTGC TTCAGGTAAA
 GAAGGTGCAA AACTTTTAGC AGAAGTAGGG GTGGTTCCTT CTTATAAAAC AGATGAAATT
 GATAAAATCT ACTTTGCAAG AAAAGGAATG CCTTCAGACG AGTCTCACA AAAGCCTTTA
 ACCCAGATAC AATTAATT

EF002-4 (SEQ ID NO:8)

C GGSSEKKATE KSEDGKTKLT VTWNYDTP
 EFEKLFRAFE AENPDITIEP VDIASDDYDT KVTMLSSGD TTDILTMKNL LSYSNYALRN
 QLVDLTDHVK DLDIEPAKAS YEMYEIDGKT YAQPYRTDFW VLYYNKKMFD EAGIAYPDNL
 TWDEYEALAK KLSKPEEQVY GAYQHTWRST VQAIAAAQNN ANLIEPKYNY METYYDRALR
 MQKDQSQMDF GTAKSTKVY QSQFENSkaa MMYGMSWYMG TLLTNIDDGK TNVEWGIAEI
 PQQEKGKATT FGSPTSFAIN KNSKKQKAAQ KFLDFASGKE GAKLLAEVGV VPSYKTDEID
 KIYFARKGMP SDESHKKPLT QIQLI

EF003-1 (SEQ ID NO:9)

TAGGAGGACA AAAGAATGAA GAAGTTTAT TTAGCNACAT TCGCTGTTAT TGCAACAGTT
 ATTTTAGCTG CCTGTGGGGG AAATAAACAA GCAGACCAGA AAGAAGACAA GGAGATTACC
 GTTGCCGTGC AATTGGAATC TTCAAAAGAT ATCTTGAGA TTGCCAAGAA AGAAGCTGAG
 AAAAAAGGGT ACAAATTAAT CATTTATGGA GTGAGCGACA ATGTTGCCTA CAACGATGCC
 GTGCAACATG ACGAAGCGGA TGCTAATTTT GCGCAACATC AACCCTTCAT GGAAATGTTT
 AACAAAGAGA AAAAGCTGA TTTAGTGGCT GTGCAACCGA TTTATTATTT TGCTGGTGGT
 TTCTATTCAA AAGAATACCA AGATGCGAAA GATTACCTG AAAATGCCAA AGTGGGGATT
 CCTAGCGATC CAACCAATGA AGGTCGTGCT TTAGCAATTT TAAATGCAAA CGGCGTGATT
 AAATTAAAAG AAGGTGTCGG CTTTAACGGC ACGGTGGCAG ATGTCGTGGA AAATCCTAAA
 AACATCACTT TTGAAAGCAT TGATTACTG AATTAGCTA AAGCCTATGA TGAAAAAGAC
 ATCGCTATGG TGTTCGTGTA CCCAGCCTAC TTAGAACCTG CTGGTTTAAAC AACGAAAGAT
 GCGATCTTGT TAGAAGATAA AGAAGCAAGT AAACATTACG CATTGCAAGT TGTGACACGC
 AAAGGCGAAA AAGATAGCGA AAAAATCAAG GTTTTAAAAG AAGCGATGAC AACAAAAGAA
 GTTGCTGAAT ACATCAAGAA AAATTCTAAA GCGCCAATA TTCTGCGTT TTA

EF003-2 (SEQ ID NO:10)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

MKKFYLL ATFVIAITVI LAACGGNKA DQKEDKEITV AVQLESSKDI LEIAKKEAEK
 RGYKINIMEV SDNVAYNDV QHDEADANFA QHQPFFMEMFN KEKKADLVAV QPIYYFAGGF
 YSKEYQDAKD LPENAKVGIP SDPTNEGRAL AILNANGVIK LKEGVGFNGT VADVVENPKN
 ITFESIDLLN LAKAYDEKDI AMVFCYPAYL EPAGLTTKDA ILLEDKEASK HYALQVVTRK
 GEKDSEKIKV LKEAMTTKEV AEYIKKNSKG ANIPAF

EF003-3 (SEQ ID NO:11)

CTGTGGGGG AAATAAACAA GCAGACCAGA AAGAAGACAA GGAGATTACC
 GTTGCCGTGC AATTGGAATC TTCAAAAGAT ATCTTGGAGA TTGCCAAGAA AGAAGCTGAG
 AAAAAAGGGT ACAAAATTA CATTATGGAA GTGAGCGACA ATGTTGCCTA CAACGATGCC
 GTGCAACATG ACGAAGCGGA TGCTAATTTT GCGCAACATC AACCCCTTCAT G3AAATGTTT
 AACAAAGAGA AAAAAGCTGA TTTAGTGGCT GTGCAACCGA TTTATTATTT TGCTGGTGGT
 TTCTATTCAA AAGAATACCA AGATGCGAAA GATTTACCTG AAAATGCCAA AGTGGGGATT
 CCTAGCGATC CAACCAATGA AGGTCGTGCT TTAGCAATTT TAAATGCAA C3GCGTGATT
 AAATTAAAAG AAGGTGTCGG CTTTAACGGC ACGGTGGCAG ATGTCGTGGA AAATCCTAAA
 AACATCACTT TTGAAAGCAT TGATTTACTG AATTTAGCTA AAGCCTATGA T3AAAAAGAC
 ATCGCTATGG TGTTCGCTA CCCAGCCTAC TTAGAACCTG CTGGTTTAAAC AACGAAAGAT
 GCGATCTTGT TAGAAGATAA AGAAGCAAGT AAACATTACG CATTGCAAGT TGTGACACGC
 AAAGGCGAAA AAGATAGCGA AAAAATCAAG GTTTTAAAAG AAGCGATGAC AACAAAAGAA
 GTTGCTGAAT ACATCAAGAA AAATTCTAAA GGCGCCAATA TTCTGCGTT T

EF003-4 (SEQ ID NO:12)

CGGNKQA DQKEDKEITV AVQLESSKDI LEIAKKEAEK
 RGYKINIMEV SDNVAYNDV QHDEADANFA QHQPFFMEMFN KEKKADLVAV QPIYYFAGGF
 YSKEYQDAKD LPENAKVGIP SDPTNEGRAL AILNANGVIK LKEGVGFNGT VADVVENPKN
 ITFESIDLLN LAKAYDEKDI AMVFCYPAYL EPAGLTTKDA ILLEDKEASK HYALQVVTRK
 GEKDSEKIKV LKEAMTTKEV AEYIKKNSKG ANIPAF

EF004-1 (SEQ ID NO:13)

TAAATCGAAA GAAGGATGAT AGAAATGAAA AAAATGATTA AATTTGCAGG CATTGCTCTT
 ATTTTTCAG CTCTTCTCTC TGCCTGTAGC AACGCAAAA ATAATACACA AAAGAAAGCC
 GAAACTGCTG CCCAGTCAAG CACTATTGAA GCTTCAGACA GTAACGAAA CGAGCCTAAT
 ACAGAAAACA TAACCCAAGC AGTTAAACAG TTAGAAGAAA AATTTAACTC TGACGAGAAA
 TTAGTAAAAA TAGATGTTAA AAATAATGTT AAAGATGACA CATCAGATAA CCCTCACGCT
 GTCATTACCG TTAAGGTAAT TAATGATGAA GCAAAAAAA ATATGGAAGA AATGCAGACT
 GCGATAGATT CCAACTCAGG TACAGAGGCA CAAAAGACTG CCATATACGG AATTCAATTA
 AATGTTGAAG AAGTAGCCAA AACATTAGAA AATGATAACG ATGTTATTTT TTTTCATCACA
 CCTTACACGA ATGGGAACGA CAGAACATA GCAAAATCAA CTA AAAATGA AAATATTATT
 CCGTTAGTAA AATAA

EF004-2 (SEQ ID NO:14)

MKK MIKFIAGIALI FAALLSACSN AKNNTQKKAE TAAQSSTIEA SDSNENEPNT
 ENITQAVKQL EEKFNSDEKL VKIDVKNVVK DDTSDNPHAV ITVKVINDEA KKNMEEMQTA
 IDSNSGTEAQ KTAIYGIQLN VEEVAKTLEN DNDVISFITP YTNGNDRTIA KSTKNENIIP
 LVK

EF004-3 (SEQ ID NO:15)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CTGTAGC AACGCAAAAA ATAATACACA AAAGAAAGCC
 GAAACTGCTG CCCAGTCAAG CACTATTGAA GCTTCAGACA GTAACGAAAA CGAGCCTAAT
 ACAGAAAAACA TAACCCAAGC AGTTAAACAG TTAGAAGAAA AATTTAACTC TGACGAGAAA
 TTAGTAAAAA TAGATGTTAA AAATAATGTT AAAGATGACA CATCAGATAA CCCTCACGCT
 GTCATTACGG TTAAGGTAAT TAATGATGAA GCAAAAAAAA ATATGGAAGA AATGCAGACT
 GCGATAGATT CCAACTCAGG TACAGAGGCA CAAAAGACTG CCATATACGG AATTCAATTA
 AATGTTGAAG AAGTAGCCAA AACATTAGAA AATGATAACG ATGTTATTTC TTTCATCACA
 CCTTACACGA ATGGGAACGA CAGAACCATA GCAAAATCAA CTAAAAATGA AAATATTATT
 CCGTTAGTAA AA

EF004-4 (SEQ ID NO:16)

CSN AKNNTQKKAE TAAQSSTIEA SDSNENEPNT
 ENITQAVKQL EEKFNSDEKL VKIDVKNNVK DDTSDNPHAV ITVKVINDEA KKNMEEMQTA
 IDNSNGTEAQ KTAIYGIQLN VEEVAKTLEN DNDVISFITP YTNGNDRTIA KSTKNENIIP
 LVK

EF005-1 (SEQ ID NO:17)

TAAAAAATGA AAAAACGATT GACGATTGTG GGGATGCTTT TTCTGGCCAT TTTAGTAATG
 GTTGGTTGTG GTAAAAATCA GCAAGCAACG ACAAAGAAAA AAGAGACAAA ACCTGAAGAA
 CTAACCTCTTT ACATTGTGCG CCACGGAAAA ACCATGTTAA ATACGACGGA CCGCGTACAA
 GGATGGTCAG ATGCGGTCTT AACACCAGAA GGTGAAAAAG TTGTGACAGC AACTGGGATT
 GGACTGAAAG ATGTTGCCTT TCAAAATGCA TATAGTAGTG ATAGTGGCCG CGCCTTGCAA
 ACTGCTCAAC TTATTTTAGA TCAAAATAAA GCAGGCAAAG ACCTTGAAGT CGTGCGTGAC
 CCAGATTTAC GTGAATTTAA TTTTGGTAGC TATGAAGGGG ATTTAAATAA GACAATGTGG
 CAGGATATTG CTGATGATCA AGGTGTTTCC TTAGAAGAAT TTATGAAAAA CATGACTCCT
 GAATCCTTTT CCAATAGTGT AGCTAACTG GATCAACAGC GCGAGGAAAG CAAGAATAAC
 TGGCCTGCAG AAGACTATGC TACAATTACT AAACGTTTGA AAAAAGGCTT AGATAAAATT
 GTTGCCACAG AATCAGCCAA TTCTGGGAAT GGCAATGTTT TAGTGGTCTC TCATGGCTTG
 AGTATTTTCAG CGTTGTTAGC AACTTTATTT GATGATTTTA AAGTCCCAGA AGGCGGTTTG
 AAGAATGCTA GTGTCACAAC AATTCATTAC AAAAATGGCG AATATACTTT GGATAAAGTC
 AATGATGTCA GCTACTTAGA AGCAGGCGAA AAAGAATCAA AATAA

EF005-2 (SEQ ID NO:18)

MKKRLTIVG MLFLAILVMV GCGKNQQATT KEKETKPEEL TLYIVRHGKT MLNTTDRVQG
 WSDAVLTPEG EKVVATGIG LKDVAFQNAV SSDSGRALQT AQLILDQNK A GKDLEVVRDP
 DLREFNFGSY EGDNLKTMWQ DIADDQGVSL EEFMKNMTPE SFANSVAKLD QQREESKNW
 PAEDYATITK RLKGLDKIV ATESANSNGN NVLVVSHGLS ISALLATLFD DFKVPEGGLK
 NASVTTIHYK NGEYTLDKVN DVSYLEAGEK ESK

EF005-3 (SEQ ID NO:19)

TTGTG GTAAAAATCA GCAAGCAACG ACAAAGAAAA AAGAGACAAA ACCTGAAGAA
 CTAACCTCTTT ACATTGTGCG CCACGGAAAA ACCATGTTAA ATACGACGGA CCGCGTACAA
 GGATGGTCAG ATGCGGTCTT AACACCAGAA GGTGAAAAAG TTGTGACAGC AACTGGGATT
 GGACTGAAAG ATGTTGCCTT TCAAAATGCA TATAGTAGTG ATAGTGGCCG CGCCTTGCAA
 ACTGCTCAAC TTATTTTAGA TCAAAATAAA GCAGGCAAAG ACCTTGAAGT CGTGCGTGAC
 CCAGATTTAC GTGAATTTAA TTTTGGTAGC TATGAAGGGG ATTTAAATAA GACAATGTGG
 CAGGATATTG CTGATGATCA AGGTGTTTCC TTAGAAGAAT TTATGAAAAA CATGACTCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAATCCTTTG DCAATAGTGT AGCTAAACTG GATCAACAGC GCGAGGAAAG CAAGAATAAC
 TGGCCTGCA3 AAGACTATGC TACAATTACT AAACGTTTGA AAAAAGGCTT AGATAAAATT
 GTTGCCADAB AATCAGCCAA TTCTGGGAAT GGCAATGTTT TAGTGGTCTC TCATGGCTTG
 AGTATTCAG3 CGTTGTTAGC AACTTTATTT GATGATTTTA AAGTCCCAGA AGGCGGTTTG
 AAGAATGCTA GTGTGACAAC AATTCATTAC AAAAATG3CG AATATACTTT GSATAAAGTC
 AATGATGTCA GCTACTTAGA AGCAGGCGAA AAAGAATCAA AA

EF005-4 (SEQ ID NO:20)

CGKNQQATT KEKETKPEEL TLYIVRHGKT MLNNTDRVQG
 WSDAVLTPEG EKVVTTATGIG LKDVAFQNAV SSDSGRALQT AQLILDQNK A GKDLEVVVRDP
 DLREFNFGSY EGDLNKTMWQ DIADDQGVSL EEFMKNMTPF SFANSVAKLD QQREESKNNW
 PAEDYATITK RLKKGDKIV ATESANSNGN NVLVVSHGLS ISALLATLFD DFKVPEGGLK
 NASVTTIHYK NGEYTLDKVN DVSYLEAGEK ESK

EF006-1 (SEQ ID NO:21)

TAAACGATAA ATGGAGGGAA TAAGATGAAA AAACGTACAT TATGGTCAGT AATTACTGTA
 GCAGTAGCTG TCTTAGTTTT AGGGGCTTGC GGCAATAAAA AGAGTGATGA CTCGGTCTTG
 AAAGTTGGAG CTTCAACAGT TCCACATGCA GAGATTTTAG AACATGTAAA ACCTTTATTA
 GAAAAAGAAG CGGTAAAATT AGAAGTGACG ACTTATACAG ATTACGTGCT ACCTAACAAG
 CGCTTGGAAA GTGGCGATAT CGATGCCAAC TATTTCCAAC ATGTGCCGTT CTTTAATGAA
 GCGGTAAAG AAAATGATTA TGACTTTGTG AATGCAGGTG CGATTCATTT AGAACCAGTT
 GGGCTTTACT CGAAAAATA CAAATCGTTA CAAGAAATTC CTGATGGTTC AACGATTTAC
 GTTAGCTCTT CCGTTTCAGA TTGGCCACGC GTATTAAC TA TCTTAGAAGA TGCTGGTTTA
 ATCAGCTGA AAGAAGGGGT AGACCGGACA ACTGCTACTT TCGATGATAT TGATAAAAAAT
 ACTAAAAAGT TGAATTCAGT TCATGAAAGT GATCCAGCAA TCATGACCAC TCTTTATGAC
 AATGAAGAAG GGGCTGCGGT TTTAATTAAC TCAAACCTTG CCGTGGATCA AGGATTAAAT
 CCGAAAAAAG ATCCGATTGC CTTAGAAAAA GAAAGTTCAC CTTATGCCAA TATTATTGCG
 GTTCGTAAAG AAGACGAAAA CAACGAAAAAT GTAAAAAAT TAGTCAAAGT GTTACGTAGC
 AAAGAAGTCC AAGATTGGAT TACGAAAAAA TGGAACGGCG CTATTGTTCC AGTCAATGAA
 TAA

EF006-2 (SEQ ID NO:22)

MKK RTLWSVITVA VAVLVLGACG NKSDDSVLK VGASPVPHAE ILEHVKPLLE
 KEGVKLEVTT YTDYVLPNKA LESGDIDANY FQHVPPFNEA VKENDYDFVN AGAIHLEPVG
 LYSKKYKSLQ EIPDGSTIYV SSSVSDWPRV LTILEDAGLI TLKEGVDRRT ATFDIDKNT
 KKLKFNHESD PAIMTTLYDN EEGAAVLINS NFAVDQGLNP KKDAIALEKE SSPYANIIAV
 RKEDENNENV KKLKVLRSK EVQDWITKKW NGAIVPVNE

EF006-3 (SEQ ID NO:23)

TTGC GGCAATAAAA AGAGTGATGA CTCGGTCTTG
 AAAGTTGGAG CTTCAACAGT TCCACATGCA GAGATTTTAG AACATGTAAA ACCTTTATTA
 GAAAAAGAAG CGGTAAAATT AGAAGTGACG ACTTATACAG ATTACGTGCT ACCTAACAAG
 CGCTTGGAAA GTGGCGATAT CGATGCCAAC TATTTCCAAC ATGTGCCGTT CTTTAATGAA
 GCGGTAAAG AAAATGATTA TGACTTTGTG AATGCAGGTG CGATTCATTT AGAACCAGTT
 GGGCTTTACT CGAAAAATA CAAATCGTTA CAAGAAATTC CTGATGGTTC AACGATTTAC
 GTTAGCTCTT CCGTTTCAGA TTGGCCACGC GTATTAAC TA TCTTAGAAGA TGCTGGTTTA
 ATCAGCTGA AAGAAGGGGT AGACCGGACA ACTGCTACTT TCGATGATAT TGATAAAAAAT
 ACTAAAAAGT TGAATTCAGT TCATGAAAGT GATCCAGCAA TCATGACCAC TCTTTATGAC
 AATGAAGAAG GGGCTGCGGT TTTAATTAAC TCAAACCTTG CCGTGGATCA AGGATTAAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCGAAAAAAG ATGCGATTGC CTTAGAAAAA GAAAGTTCAC CTTATGCCAA TATTATTGCG
 GTTCGTAAAG AAGACGAAAA CAACGAAAAAT GTAAAAAAT TAGTCAAAGT GTTACGTAGC
 AAAGAAGTCC AAGATTGGAT TACGAAAAAA TGAACGGCG CTATTGTTCC AGTCAATGAA

EF006-4 (SEQ ID NO:24)

CG NKKSDDSVLK VGASPVPHAE ILEHVKPLLE
 KEGVKLEVTT YTDYVLPNKA LESGDIDANY FQHPVFFNEA VKENDYDFVN AGAIHLEPVG
 LYSKKYKSLQ EIPDGSTIYV SSSVSDWPRV LTILEDAGLI TLKEGVDRIT ATFDDIDKNT
 KKLKFNHESD PAIMTTLYDN EEGAAVLINS NFAVDQGLNP KKDAIALEKE SSPYANIIAV
 RKEDENNENV KKLVLVLRK EVQDWITKKW NGAIVPVNE

EF008-1 (SEQ ID NO:25)

TAAACCGTGA GAAAGAAATG GAGGAATCAA CGAATGAAAA AATTTAGTTT ATTTTITTTA
 AACTTTTGTAG CAGGGTTAAC GTTAGCTGCT TCGGGGAATC AAGCCGCTGA AAAGAAAGAA
 AAATTAGCAA TTGTGACAAC GAACTCGATC CTATCTGATT TAGTGAAAAA TGTTGGGCAA
 GACAAAATTG AGCTGCATAG TATTGTGCCA ATTGGGACAG ACCCTCACGA ATATGAACCG
 TTACCAGAAG ACATTGCGAA AGCTTCTGAA GCGGACATTT TATTCTTTAA CGGCTTGAAC
 TTAGAAACAG GCGGAAATGG CTGGTTTAAAC AAATTAATGA AAACGGCCAA AAAAGTTGAG
 AATAAAGATT ACTTTTCTAC AAGCAAAAAT GTTACGCCAC AATATTTAAC AAGTGCCGGT
 CAAGAACAAA CAGAAGATCC ACATGCTTGG TTAGACATTG AAAATGGCAT TAAATATGTA
 GAAAACATTC GTGACGTGTT AGTAGAAAAA GATCCAAAAA ATAAAGATTT CTATACAGAA
 AACGCGAAAA ATTATACCGA AAAACTTAGC AAACCTACATG AGGAAGCCAA AGCTAAATTT
 GCTGATATTC CTGATGATAA AAAATTATTA GTTACAAGTG AAGGTGCCTT TAAATATTTT
 TCCAAAGCTT ATGATTTAAA TGCCGCTTAT ATTTGGGAAA TTAACACAGA AAGTCAAGGN
 ACACCTGAAC AAATGACCAC GATTATTGAT ACCATTAAGA AATCAAAAGC ACCTGTGTTA
 TTTGTTGAAA CCAGTGTGCGA TAAACGTAGT ATGGAACGGG TCTCAAAGA AGTGAAACGA
 CCAATTTACG ATACACTTTT CACAGACTCT CTGCGCAAAG AAGGAACAGA AGGCGATACG
 TACTACAGCA TGATGAACATG GAATTTAACA AAAATCCATG ATGGCTTAAT GAGTAAATAA

EF008-2 (SEQ ID NO:26)

MKKFSLFFLT LLAGLTLAAC GNQAAEKKEK LAIVTNSIL SDLVKNVQD
 KIELHSIVPI GTDPHEYEPL PEDIAKASEA DILFNGLNL ETGNGWFNK LMKTAKKVEN
 KDYFSTSKNV TPQYLTSAGQ EQTEDPHAWL DIENGIKYVE NIRDVLVEKD PKNKDFYTN
 AKNYTEKLSK LHEEAKAKFA DIPDDKLLV TSEGAFKYFS KAYDLNAAI WEINTESQGT
 PEQMTTIIDT IKKSKAPVLF VETSVDKRSM ERVSKEVKRP IYDTLFTDSL AKEGTEGDTY
 YSMNNWNLTK IHDGLMSK

EF008-3 (SEQ ID NO:27)

T TCGGGGAATC AAGCCGCTGA AAAGAAAGAA
 AAATTAGCAA TTGTGACAAC GAACTCGATC CTATCTGATT TAGTGAAAAA TGTTGGGCAA
 GACAAAATTG AGCTGCATAG TATTGTGCCA ATTGGGACAG ACCCTCACGA ATATGAACCG
 TTACCAGAAG ACATTGCGAA AGCTTCTGAA GCGGACATTT TATTCTTTAA CGGCTTGAAC
 TTAGAAACAG GCGGAAATGG CTGGTTTAAAC AAATTAATGA AAACGGCCAA AAAAGTTGAG
 AATAAAGATT ACTTTTCTAC AAGCAAAAAT GTTACGCCAC AATATTTAAC AAGTGCCGGT
 CAAGAACAAA CAGAAGATCC ACATGCTTGG TTAGACATTG AAAATGGCAT TAAATATGTA
 GAAAACATTC GTGACGTGTT AGTAGAAAAA GATCCAAAAA ATAAAGATTT CTATACAGAA
 AACGCGAAAA ATTATACCGA AAAACTTAGC AAACCTACATG AGGAAGCCAA AGCTAAATTT
 GCTGATATTC CTGATGATAA AAAATTATTA GTTACAAGTG AAGGTGCCTT TAAATATTTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCDAAGCCTT ATGATTATAA TGCCGCTTAT ATTTGGGAAA TTAACACAGA AAGTCAAGGN
 ACACCTGAAC AAATGACCAC GATTATTGAT ACCATTAAGA AATCAAAAGC ACCTGTGTTA
 TTTGTTGAAA CCAAGTGTGA TAAACCTAGT ATGGAACGGG TCTCAAAAGA ASTGAAACGA
 CCAATTTACG ATACACTTTT CACAGACTCT CTTGCCAAAG AAGGAACAGA AGGCGATACG
 TACTACAGCA TGATGAACTG GAATTTAACA AAAATCCATG ATGGCTTAAT GAGTAAA

EF008-4 (SEQ ID NO:28)

C GNQAAEKKEK LAIVTTNSIL SDLVKNVQGD
 KIELHSIVPI GTDPHEYEPL PEDIAKASEA DILFFNSLNL ETGNGWPNK LMKTAKKVEN
 KDYFSTSKNV TPQYLTSAGQ EQTECFHAWL DIENGIKYVE NIRDVLVEKD PKNKDFYTEN
 AKNYTEKLSK LHEEAFKAKFA DIPDDKLLV TSEGAFKYFS KAYDLNAAI WEINTESQGT
 PEQMTTIIDT IKKSKAPVLF VETSVEKRSM ERVSKEVKRP IYDTLFTDSL AKEGTEGDTY
 YSMNWNLTG 1HDGLMSK

EF009-1 (SEQ ID NO:29)

TGACAAATGA AAAAATTTAG TAAATTAATT GGACTTATTG GGGTATTAGC TTTTACGATT
 GCAGGTTGTG CATCGGGGTC TGTGAAGGAT ACTAAGACAG AAACCGTTAA ACTAGGGGTT
 GTAGGAACAA AAAATGATGA ATGGGAATCG GTCAAAGACC GTTTGAAAAA GAAAAATATT
 GATTTACAAT TGGTAGAATT TACAGACTAT ACGCAACCAA ACGCAGCATT AGCAGAAAAA
 GAAATTGATT TAAATGCCTT TCAGCATCAA ATCTTTTATG ACAATTACAA TAAAGAGCAT
 GGAACGAAAT TAGTATCAAT TGGCAATACA GTCAATGCAC CATTGGGAAT TTACGCTAAT
 AAATTGAAAG ATATCACGAA AATTAAAGAC GGCGGAGAAA TTGCTATTCC TAATGACCCA
 ACGAATGGCG GGCGGGCGTT AATTTTATTA CAAACTGCAG GACTGATAAA AGTAGATCCT
 GCGAAACAGC AACTACCGAC TGTCAGTGAT ATTACTGAAA ATAAACGCCA ATTGAAAATA
 ACTGAATTAG ATGCTACGCA AACAGCGCGC GCTTTACAAG ATGTCGATGC TTCAGTGATT
 AATAGCGGCA TGGCTGTCTG TGCTGGGTAT ACACCAGATA AAGATGCTAT TTTCTTAGAA
 CCTGTAAACG AAAAAGCGAA ACCTTATGTG AACATTGTCT TGGCCCCGAGA AGAAGATCAA
 GAGAATAAAC TTTATCAAAA AGTTGTAGAA GAATATCAAC AAGAAGAAAC GAAAAAGGTC
 ATTGCAGAAA CATCAAAAGG CGCCAATGTT CCAGCCTGGG AAACATTGTTG TAAAAAATAA

EF009-2 (SEQ ID NO:30)

MEKFSKLIG LIGVLAFTIA GCASGSVKDT KTETVKLGTV GTKNDEWESV KDRLKKKNID
 LQLVEFTDYT QPNAALAEKE IDLNAFQHQI FLDNYNKEHG TKLVSGNTV NAPLGIYANK
 LKIDITKIDG GEIAIPNDPT NGGRALILLQ TAGLIKVDPA KQQLPTVSDI TENKRQLKIT
 ELDATQTARA LQDVDASVIN SGMAVDAGYT PDKDAIFLEP VNEKAKPYVN IVVAREEDQE
 NKLYQKVVEE YQQEETKKVI AETSKGANVP AWETFGKK

EF009-3 (SEQ ID NO:31)

TTGTG CATCGGGGTC TGTGAAGGAT ACTAAGACAG AAACCGTTAA ACTAGGGGTT
 GTAGGAACAA AAAATGATGA ATGGGAATCG GTCAAAGACC GTTTGAAAAA GAAAAATATT
 GATTTACAAT TGGTAGAATT TACAGACTAT ACGCAACCAA ACGCAGCATT AGCAGAAAAA
 GAAATTGATT TAAATGCCTT TCAGCATCAA ATCTTTTATG ACAATTACAA TAAAGAGCAT
 GGAACGAAAT TAGTATCAAT TGGCAATACA GTCAATGCAC CATTGGGAAT TTACGCTAAT
 AAATTGAAAG ATATCACGAA AATTAAAGAC GGCGGAGAAA TTGCTATTCC TAATGACCCA
 ACGAATGGCG GGCGGGCGTT AATTTTATTA CAAACTGCAG GACTGATAAA AGTAGATCCT
 GCGAAACAGC AACTACCGAC TGTCAGTGAT ATTACTGAAA ATAAACGCCA ATTGAAAATA
 ACTGAATTAG ATGCTACGCA AACAGCGCGC GCTTTACAAG ATGTCGATGC TTCAGTGATT
 AATAGCGGCA TGGCTGTCTG TGCTGGGTAT ACACCAGATA AAGATGCTAT TTTCTTAGAA
 CCTGTAAACG AAAAAGCGAA ACCTTATGTG AACATTGTCT TGGCCCCGAGA AGAAGATCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAGAATAAAC TTTATCAAAA AGTTGTAGAA GAATATCAAC AAGAAGAAAC GAAAAAGGTC
ATTGCAGAAA CATCAAAAGG CGCCAATGTT CCAGCCTGGG AACATTTGG TAAAAAA

EF009-4 (SEQ ID NO:32)

CASGSVKDT KTETVKLGVV GTKNDEWESV KDRLKKKNID
LQLVEFTDYT QPNAALAEKE IDLNAFQHQI FLDNYNKEHG TKLVSIGNTV NAPLGIYANK
LKDITKIKDG GEIAIPNDPT NGGRALILLQ TAGLIKVDPA KQQLPTVSDI TENKRQLKIT
ELDATQTARA LQVDASVIN SGMAVDAGYT PDKDAIFLEP VNEKAKPYVN IVVAREEDQE
NKLYQKVVEE YQQEETKKVI AETSKGANVP AWETFGKK

EF010-1 (SEQ ID NO:33)

TGAAAGAATA AAATTGTACA GGAGGAAATA AGGAATGAAA AAATGGCAAA AAGGATTAGC
CGTAGCTGGC GCACAGCTTT AGCTGTAGGA CTAAGCGCGT GCGGTAAATC TTCAAAAGAT
GCAGCGTCAA AAGGTGATGA TAGTACACCA ACGTTATTAA TGTATCGTGT TGGGGACAAA
CCAGATAATT ATGACCAATT AATCGATAAT GCGAATAAAA TTATCGAGAA AAAAATTGGG
GCAAAATTAA AAATGGAATT TGTGGTTGG GCGGATTGGG ACCAAAAAAT GTCAACAATC
GTTGCTTCTG GTGAAAGCTA TGATATTTCA TTAGCACAAA ATTATGCAAC GAATGCACAA
AAAGGCGCCT ATGCTGATTT AACTGATTTA GCACCTAAAT ATGCCAAAGA AGCCTATGAT
CAATTGCCAG ATAAGTATAT TAAAGGAAAT ACGATTAATG GAAAAGTGTG TCGCTTCCCA
ATTTTAGGTA ACTCTTACGG TCAACAAGTT TTAACCTTTA ATAAAGAATA TGTCGATAAA
TACAATTTAG ATATTAGTAA AGTCGATGGT AGTTATGAAA GTGCAACGGA AGTTCTAAAA
GAATTCNTA AAAANGANCC AAATATTGCT GCTTTTGCTA TCGGCCAAAC ATTCTTTGCA
ACAGGTAATT ATGACTTCCC TATTGGTAAC CAATATCCAT TTGCAGTAAA AACAACTGAT
ACTGGCTCAC CAAAAATTAT TAACCAATAT GCCGACAAAG ACATGATTAA TAACTTAAAA
GTCTTGATC AATGGTATAA AGATGGCTTG ATTCCAACAG ATGCTGCTAC AAGTACAACA
CCATATGACT TAAATACCAA TACTTGGTTT ATGCGTCAAG AAACACAAGG ACCTATGGAT
TATGGTGATA CAATCTTAAC ACAAGCTGCT GGCAAACCAC TTGTTTCTCG TCCACTAACA
GAACCATTA AAACAACAGC TCAAGCGCAA ATGGCTAACT ATGTGTTGTC AAACACGTCT
AAAAACAAAG AAAAATCTGT TGAATTGTTA GGTTTATTAA ACAGCAATCC AGAATTGTTA
AACGGACTTG TTTATGGTGA AGAAGGCAAA CAATATGAAA AAGTTGGCGA TGATCGTGTG
AAATTGTTGA AAGATTACAC ACCAACAACT CATTTGAGTG CTTGGAACAC AGGAAAACAC
TTAATCATT GGCCAGAAGA ATCTGTCCT GAAGAAATGG TTAAAGAACG TGATAAGAGC
ATCGAAGAAG CAAAAGATTC ACCAATTCTT GGTTTTACTT TTGTAAATGA TAAAGTGAAA
ACTGAAATCA CTAACGTTGC TACAGTTATG AACCGTTACG CAGCAAGCTT AAATACAGGA
ACTGTTGATC CAGAAGAAAC ACTTCAAAA TTAATGGATG ACCTAAAAAC AGCTGGCTGG
GATAAAGTTC AAAAAGAAAT GCAAACACAA TTAGACGAAT ATATCCAATC TCAAAAATAA

EF010-2 (SEQ ID NO:34)

MAKRISR SWRTALAVGL SACGKSSKDA ASKGDDSTPT LLMYRVGDKP
DNYDQLIDNA NKIEKKIGA KLKMEFVGWG DWDQKMSTIV ASGESYDISL AQNYATNAQK
GAYADLTDLA PKYAKEAYDQ LPDNYIKGNT INGKLYAFPI LGNSYGQQVL TFNKEYVDKY
NLDISKVDGS YESATEVLKE FXKXPNIAA FAIGQTFAT GNYDFPIGNQ YPFAVKTDT
GSPKIINQYA DKDMINNLKV LHQWYKDGLI PTDAATSTTP YDLNNTWFM RQETQGPMDY
GDTILTQAAG KPLVSRPLTE PLKTTAQAQM ANYVVANTSK NKEKSVELLG LLNSNPELLN
GLVYGEEGKQ YEKVGDDRK LKDYTPPTH LSAWNTGNNL IIWPEESVTE EMVKERDKSI
EEAKDSPILG FTFVNDKVK EITNVATVMN RYAASLNTGT VDPEETLPKL MDDLKTAGWD
KVQKEMQTQL DEYIQSQK

EF010-3 (SEQ ID NO:35)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GT GCGGTAAATC TTCAAAAGAT

GCAGGCTCAA	AAGGTGATGA	TAGTACACCA	AGGTTATTAA	TGTATCGTGT	TGGGGACAAA
GCAGATAATT	ATGACCAATT	AATCGATAAT	GCBAATAAAA	TTATCGAGAA	AAAAATTGGG
GCAGAAATTAA	AAATGGAATT	TGTTGTTTGG	GGGATTGGG	ACCAAAAAAT	GTCAACAATC
GTGCTTCTG	GTGAAAGCTA	TGATATTTCA	TTAGCACAAA	ATTATGCAAC	GAATGCACAA
AAAGGCGCCT	ATGCTGATTT	AACTGATTTA	GCAGCTAAAT	ATGCCAAAGA	AGCCTATGAT
CAATTGCCAG	ATAACTATAT	TAAAGGAAAT	AGGATTAATG	GAAAACGTGA	TGCGTTCCCA
ATTTTAGGTA	ACTGTTACGG	TCAACAAGTT	TTAACTTTTA	ATAAAGAATA	TGTCGATAAA
TACAAATTA	ATATTAGTAA	AGTCGATGCT	AGTTATGAAA	GTGCAACGGA	AGTTCTAAAA
GAATTCNTA	AAAANGANCC	AAATATTGCT	GGTTTTGCTA	TCGGCCAAAC	ATTCTTTGCA
ACAGGTAATT	ATGACTTCCC	TATTTGTAAC	CAATATCCAT	TTGCAGTAAA	AACAACGTAT
ACTGGCTCAC	CAAAAATTAT	TAACCAATAT	GGGACAAAAG	ACATGATTAA	TAACTTAAAA
GTCTTGCATC	AATGCTATTA	AGATGCTTGG	ATTGCAACAG	ATGCTGCTAC	AAGTACAACA
CCATATGACT	TAAATACCAA	TACTTGGTTT	ATGCGTCAAG	AAACACAAGG	ACCTATGGAT
TATGCTGATA	CAATCTTAAC	ACAAGCTGCT	GGCAAACCCAC	TTGTTTCTCG	TCCACTAACA
GAACCATTA	AAACAACAGC	TCAAGCGCAA	ATGGCTAACT	ATGTTGTTGC	AAACACGTCT
AAAAACAAAG	AAAAATCTGT	TGAATTGTTA	GGTTTATTAA	ACAGCAATCC	AGAATTGTTA
AACGGACTTG	TTTATGCTGA	AGAAGGCAAA	CAATATGAAA	AAGTTGGCGA	TGATCGTGTG
AAATTGTTGA	AAGATTACAC	ACCAACAAC	CATTTGAGTG	CTTGGAACAC	AGGAAACAAC
TTAATCATTT	GGCCAGAAGA	ATCTGCTACT	GAAGAAATGG	TTAAAGAACG	TGATAAGAGC
ATCGAAGAAG	CAAAAGATTG	ACCAATTCCT	GGTTTACTT	TTGTAAATGA	TAAAGTGAAG
ACTGAAATCA	CTAACGTTGC	TACAGTTATG	AACCGTTACG	CAGCAAGCTT	AAATACAGGA
ACTGTTGATC	CAGAAGAAAC	ACTTCCAAAA	TTAATGGATG	ACCTAAAAAC	AGCTGGCTGG
GATAAAGTTC	AAAAAGAAAT	GCAAAACAAA	TTAGACGAAT	ATATCCAATC	TCAAAAA

EF010-4 (SEQ ID NO:36)

CGKSSKDA ASKGDDSTPT LLMYRVGDKF

DNYDQLIDNA	NKIIIEKKIGA	KLKMEFVGWG	DWDQKMSTIV	ASGESYDISL	AQNYATNAQK
GAYADLTDLA	PKYAKEAYDQ	LPDNYIKGNT	INGKLYAFPI	LGNSYGGQVL	TFNKEYVDKY
NLDISKVDGS	YESATEVLKE	FXKXXPNIAA	FAIGQTFPAT	GNYDFPIGNQ	YPFAVKTTDT
GSPKIINQYA	DKDMINNLKV	LHQWYKDGLI	PTDAATSTTP	YDLNNTNWFN	RQETQGPMDY
GDTILTQAAG	KPLVSRPLTE	PLKTTAQAQM	ANYVVANTSK	NKEKSVELLG	LLNSNPELLN
GLVYGEEGKQ	YEKVGDDRVK	LLKDYTPPTH	LSAUNTGNL	IIWPEESVTE	EMVKERDKSI
EEAKDSPILG	FTFVNDKVK	EITNVATVMN	RYAASLNTGT	VDPEETLPKL	MDDLKTAGWD
KVQKEMQTQL	DEYIQSQK				

EF011-1 (SEQ ID NO:37)

TAACGTTTTT	GGAGGAAAAG	AATGAAAAG	AAATTTTTAG	CAATGATGGC	AGTTTCAATG
ATGGGACTGT	TAATGTTAAG	TGCTTGTCAG	ACAAATAAAA	AAACAGCAGA	TTCTGCAACA
ACAGAAACAA	CAGCTAAAAC	GGAAGTCACA	GTCAAAGACA	CCAATGGTCA	ATTAACCGTT
CCCAAAAATC	CTAAGAAAGT	CGTTGTTTTT	GATAATGGTT	CCTTGGATAC	AATGGATGCA
CTAGGTGTG	GTGACCGCGT	GGTAGGTGCG	CCAACATAAA	ATATCCCTGC	GTATTTGAAA
AAATACCAAA	AAGTTGAATC	AGCAGGCGGC	ATTAAAGAAC	CAGATTTAGA	AAAAATCAAT
CAACTAAAAC	CAGACTTAAT	TATTATTCT	GGTCGTCAAC	AAGATTATCA	AGAACAATTA
AAAGCCATTG	CGCCAACCAT	TTACTTAGCT	GATAGTGCCA	AAAATCCTTG	GGCATCAACG
AAACAAAATA	TCGAAACGTT	AGGCACTATT	TTTGATAAAG	AAGAGGTAGC	TAAAGAAAAA
ATAACTGGCT	TAGAAAAAGA	AATTGCTGAC	GTGAAAAAAC	AAGCAGAAGC	TAGCGCGAAT
AATGCGCTTG	TTGTGTTAGT	TAACGAAGGA	CAACTTCCG	CTTACGGAAA	AGGCTCTCGT
TTGCGTTTTA	TTCATGATAC	ATTGCGCTTC	AAAGCAGCAG	ACGATAAGAT	TGAAGCTTCC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACTCATGGGC AAAGTGTTTC TTACGAATAT GTTTTAGAAA AAAATCCTGG GATTCTCTTT
 GTGGTAGATC GCACCAAAGC AATTGGTGGC GACGATTCAA AAGATAACGT CGCTGCAAAC
 GAATTGATTC AAAAAACCGA TGCTGGTAAA AATGATAAAG TCATTATGCT TCAACCAGAT
 GTTTGGTATC TAAGCGGTGG TGGATTAGAA TCAATGCATT TGATGATAGA AGATGTTAAA
 AAAGGATTAG AGTAA

EF011-2 (SEQ ID NO:38)

MKKK FLAMMAVSM GLLMLSACQT NKKTADSATT ETTAKTEVTV KDTNGQLTVP
 KNPKKVVFVD NGS�DTMDAL GVGDRVVGAP TKNIPAYLKK YQKVESAGGI KEPDLEKINQ
 LKPDLIISG RQQDYQEQLK AIAPTIYLAV DAKNPWASTK QNIETLGTIF DKEEVAKEKI
 TGLEKEIADV KKQAEASANN ALVVLVNEGQ LSAYGKGSRF GLIHDTFGFK AADDKIEAST
 HGQSVSYEYV LEKNPGILFV VDRTKAIGGD DSKDNVAANE LIQKTDAGKN DKVIMLQPDV
 WYLSGGGLES MHLMIEDVKK GLE

EF011-3 (SEQ ID NO:39)

TTGTCAA ACAAATAAAA AAACAGCAGA TTCTGCAACA
 ACAGAAACAA CAGCTAAAAC GGAAGTCACA GTCAAAGACA CCAATGGTCA ATTAACCGTT
 CCCCCAAATC CTAAGAAAGT CGTTGTTTTT GATAATGGTT CCTTGGATAC AATGGATGCA
 CTAGGTGTGG GTGACCGCGT GGTAGGTGCG CCAACTAAAA ATATCCCTGC GTATTTGAAA
 AAATACCAAA AAGTTGAATC AGCAGGCGGC ATTAAAGAAC CAGATTTAGA AAAAATCAAT
 CAACTAAAAC CAGACTTAAT TATTATTTCT GGTGCTCAAC AAGATTATCA AGAACAATTA
 AAAGCCATTG CGCCAACCAT TTACTTAGCT GTAGATGCCA AAAATCCTTG GGCATCAACG
 AAACAAAATA TCGAAACGTT AGGCATATT TTTGATAAAG AAGAGGTAGC TAAAGAAAAA
 ATAAGTGCTG TAGAAAAAGA AATTGCTGAC GTGAAAAAAC AAGCAGAAGC TAGCGCGAAT
 AATGCGCTTG TTGTGTTAGT TAACGAAGGA CAACTTTCCG CTTACGGAAA AGGCTCTCGT
 TTCGGTTTAA TTCATGATAC ATTTGGCTTC AAAGCAGCAG ACGATAAGAT TGAAGCTTCC
 ACTCATGGGC AAAGTGTTTC TTACGAATAT GTTTTAGAAA AAAATCCTGG GATTCTCTTT
 GTGGTAGATC GCACCAAAGC AATTGGTGGC GACGATTCAA AAGATAACGT CGCTGCAAAC
 GAATTGATTC AAAAAACCGA TGCTGGTAAA AATGATAAAG TCATTATGCT TCAACCAGAT
 GTTTGGTATC TAAGCGGTGG TGGATTAGAA TCAATGCATT TGATGATAGA AGATGTTAAA
 AAAGGATTAG AG

EF011-4 (SEQ ID NO:40)

CQT NKKTADSATT ETTAKTEVTV KDTNGQLTVP
 KNPKKVVFVD NGS�DTMDAL GVGDRVVGAP TKNIPAYLKK YQKVESAGGI KEPDLEKINQ
 LKPDLIISG RQQDYQEQLK AIAPTIYLAV DAKNPWASTK QNIETLGTIF DKEEVAKEKI
 TGLEKEIADV KKQAEASANN ALVVLVNEGQ LSAYGKGSRF GLIHDTFGFK AADDKIEAST
 HGQSVSYEYV LEKNPGILFV VDRTKAIGGD DSKDNVAANE LIQKTDAGKN DKVIMLQPDV
 WYLSGGGLES MHLMIEDVKK GLE

EF012-1 (SEQ ID NO:41)

TGAGGGGGCA ACAACATGAA ATTGGGGAAA AAAGTAGTAG GTTTGATTGC AACAGGGTTT
 CTTTTAGCCG CATGTGGCGG AACCAGAGAA GCGGCAGAGA AAGTAGATTC GGGAAATTTA
 GCAGCTGAAC AAAAAATCAG TATTAGTTCA CCTGCACCAA TCTCAACATT GGATACAACA
 CAAACAACAG ATAAAAATAC CTTTACAATG GCACAACATT TATTGAAGG CCTTTATCGG
 TTTGATGATG ATAGTGCCAC GGTGCCAGCT CTAGCTAAAG ATGTCAAGAT TAGTGACGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GGGCGCAAGT ACCACTTTAC CTTGGGGGAG GGGATTAAGT GGAGCAACGG CGAGCCAATC
ACGGCCCAAG ATTTTGTGTTA TTCTTGGAAG AAAGTGGTGA CAGCAGCGAC GATTGGACCG
AATGCCTATT TACTAGACAG TGTTAAAAAT AGTTTGTGAA TACGCAACGG TGAAGAGTCA
GTGGATGAAT TAGGGATTTC AGCCCCGAAT GACAAAGAAT TCATTGTTGA ATTAAAAACAG
GGCCAACTTT CCTTCTTAGC AGTCGTTTCG ATTGCTTGST TAGCGCCACA AAATCAAAAA
TTTGTGGAAG CGCAAGGCAA AGATTACGGC TTGGATAGTG AACATTTACT TTATAGCGGG
CGATTTACGG TAGCCAATTG GATGCGGACT TCAGATACTT CGACATTGAA AAAAAATCCA
GAATACTATG ATGCGGATCA AGTGAAAGTG GAAGAAGTTG CGGTTAGCAC AATCAAGAA
GATAATACTG GGATTAAGTT ATATCAAGTG AATGAAGTAG ACTTAGTTGC CATTAACGGA
CAATATGTTT AACAATATCA AGATGATCCA GCTATGTCA GTCATCCAGA TGTGGCCAAC
TACTTCTTAG ATTTCAACAA AAAAGAAGGA AGGCCATTAG CGAATGTTCA TTTACGAAAA
GGGATTTGGC AAGCAATTGA TAAAGAAGCC TTAACACAAA GTGTCTTAAA CGATGGGTCA
AAACCCCTTA ACGGATTGAT TCCAAGTAAA CTTTATGCGA ATCCAGAAAC GGATGAAGAT
TTCCGAGCTT ACASTGGGCA ATATTTGAAA AATGACGTCA AAAAAGCTCA AGGTGAATGG
ACGAAAGCCC AAGCGGATGT CGSTAAAAAA GTGAACTTT CATTGCTGGC GGCAGACACA
GATCAAGGAA AAGCAATTGC TGAATATGTT CAAAGTCAGT TGCAAGAAAA TCTGCCAGGT
TTAGAAATTA CCATTTTCATC GCAACCAAGT AATAATGTGA ACCAATCGCG ACGTGAAAAA
AATTATGAGT TGTCTCTTTC AGGATGGATT GCCGGCAGTA GTGAATTAGA CTCTTACTTT
AACTTATATG CAGGAGAATC AAGTTACAAT TACGGCAATT ATCATAATGC CAAATACGAC
CAATTGGTAG AAGAGGCACG AACGATTAAT GCCAATAATC CAGAGAAACA GTTTGCAGAA
TACAAAGAAG CGGAAGACAT CTGTTGAAC CAAGATGCTG CCCAAGTACC GCTGTATCAA
AGTGCCCTCA ATTATCTAAT CAATCCTAAA TTGAAAGGCA TTAGTTATCA CTTGTATGGG
GATTATTTCC ACTTGCGCAA TGCTATTATA ACAGAATGA

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EF012-2 (SEQ ID NO:42)

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MKLGKK VVGLIATGFL LAACGGTKEA AEKVDSGNLA AEQKISISSP APISTLDTTQ
TTDKNTFTMA QHLEGLYRF EDDSATVPAL AKDVKISDDG RKYHFTLREG IKWSNGEPIT
AQDFVYSWKK LVTPATIGPN AYLLDSVKNS FEIRNGEKSV DELGISAPND KEFIVELKQA
QPSFLAVVSI AWLAPQNKQF VEAQGKDIAL DSEHLLYSGP FTLANWDATS DTWTLKKNP
YYEADQVKLE EVAVSTIKED NTGINLYQVN ELDLVRINGQ YVQYQDDPG YVSHPDVANY
FLDFNKKEGT PLANVHLRKA IGQAIKKEAL TQSVLNDGSK PLNGLIPSKL YANPETDEDF
RAYSGEYLKN DVKKAQAEWT KAQADVGGKV KLSLLAADTD QGKRIAEYVQ SQLQENLPGL
EITISSQPSN NVNQSRREKN YELSLSGWIA GSSELDYFYN LYAGESSYNY GNYHNAKYDQ
LVEEARTINA NNPEKQFAEY KEAEDILLNQ DAAQVPLYQS ASNYLINPKL KGISYHLYGD
YFHLRNAYLT E

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EF012-3 (SEQ ID NO:43)

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ATGTGGCGG AACCAAGAA GCGGCAGAGA AAGTAGATTC GGGAAATTTA
GCAGCTGAAC AAAAAATCAG TATTAGTTCA CCTGCACCAA TCTCAACATT GGATACAACA
CAAACAACAG AAAAAATAC CTTTACAATG GCACAACATT TATTTGAAGG CCTTTATCGG
TTTGATGATG ATAGTGCCAC GGTGCCAGCT CTAGCTAAAG ATGTCAAGAT TAGTGACGAT
GGGCGCAAGT ACCACTTTAC CTTGGGGGAG GGGATTAAGT GGAGCAACGG CGAGCCAATC
ACGGCCCAAG ATTTTGTGTTA TTCTTGGAAG AAAGTGGTGA CACCAGCGAC GATTGGACCG
AATGCCTATT TACTAGACAG TGTTAAAAAT AGTTTGTGAA TACGCAACGG TGAAGAGTCA
GTGGATGAAT TAGGGATTTC AGCCCCGAAT GACAAAGAAT TCATTGTTGA ATTAAAAACAG
GCCCCAACCTT CCTTCTTAGC AGTCGTTTCG ATTGCTTGGT TAGCGCCACA AAATCAAAAA
TTTGTGGAAG CGCAAGGCAA AGATTACGCC TTGGATAGTG AACATTTACT TTATAGCGGG
CCATTTACGC TAGCCAATTG GATGCGACT TCAGATACTT GGACATTGAA AAAAAATCCA
GAATACTATG ATGCGGATCA AGTGAAAGTG GAAGAAGTTG CGGTTAGCAC AATCAAGAA
GATAATACTG GGATTAAGTT ATATCAAGTG AATGAAGTAG ACTTAGTTGC CATTAACGGA
CAATATGTTT AACAATATCA AGATGATCCA GGCTATGTCA GTCATCCAGA TGTGGCCAAC

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TACTTCTTAG ATTTCAACAA AAAAGAAGGA ACGCCATTAG CGAATGTTCA TTTACGAAAA
 GCGATTGGCC AAGCAATTGA TAAAGAAGCC TTAACACAAA GTGTCTTAAA CGATGGGTCA
 AAACCCCTTA ACGGATTGAT TCCAAGTAAA CTTTATGCGA ATCCAGAAAC GGATGAAGAT
 TTCCGAGCTT ACAGTGGCGA ATATTTGAAA AATGACGTCA AAAAAGCTCA AGCTGAATGG
 ACGAAAGCCC AAGCGGATGT CGGTAAAAAA GTGAAACTTT CATTGCTGGC GGCAGACACA
 GATCAAGGAA AACGAATTGC TGAATATGTT CAAAGTCAGT TGCAAGAAAA TCTGCCAGGT
 TTAGAAATTA CCATTTTCATC GCAACCAAGT AATAATGTGA ACCAATCGCG ACGTGAAAAA
 AATTATGAGT TGTCTCTTTC AGGATGGATT GCCGGCAGTA GTGAATTAGA CTCTTACTTT
 AACTTATATG CAGGAGAATC AAGTTACAAT TACGGCAATT ATCATAATGC CAAATACGAC
 CAATTGGTAG AAGAGGCACG AACGATTAAT GCCAATAATC CAGAGAAACA GTTTGCAGAA
 TACAAAGAAG CGGAAGACAT CTGTGTTGAAC CAAGATGCTG CCCAAGTACC GCTGTATCAA
 AGTGCCCTCAA ATTATCTAAT CAATCCTAAA TTGAAAGGCA TTAGTTATCA CTTGTATGGG
 GATTATTTCC ACTTGCGCAA TGCCTATTTA ACAGAA

EF012-4 (SEQ ID NO:44)

CGGTKEA AEKVDSGNLA AEQKISSP APISTLDTTQ
 TTDKNTFTMA QHLFEGLYRF DDDSATVPAL AKDVKISDDG RKYHFTLREG IKWSNGEPIT
 AQDFVYSWKK LVTPATIGPN AYLLDSVKNS FEIRNGEKSV DELGISAPND KEFIVELKQA
 QPSFLAVVSI AWLAPQNQKF VEAQGKDYL DSEHLLYSGP FTLANWDATS DTWTLKKNPE
 YYDADQVKLE EVAVSTIKED NTGINLYQVN ELDLVRINGQ YVQYQDDPG YVSHPDVANY
 FLDNFNKEGT PLANVHLRKA IGQAIDKEAL TQSVLNDGSK PLNGLIPSKL YANPETDEDF
 RAYSGEYLKN DVKKAQAEWT KAQADVGGKV KLSLLAADTD QGKRIAQVQ SQLQENLPLGL
 EITISSQPSN NVNQSRREKN YELSLSGWIA GSSELDYFN LYAGESSYNY GNYHNAKYDQ
 LVEEARTINA NNEPKQFAEY KEAEDILLNQ DAAQVPLYQS ASNYLINPKL KGISYHLYGD
 YFHLRNAYLT E

EF013-1 (SEQ ID NO:45)

TAACGAAAAA TGAAAAAAT TGCTTTGTTC AGTATGTTAA CGTTCAGTGT ATTGTCTTTA
 AGTCTAGCAG GATGTGGAAC CAAAAAACA GCAAGCACAA ATGATTCTAA GCCAAAGCAA
 GAAACAAAGA AAGCCACGCA GAAATCCTCT AGCCAACAAG AAATGAAAAG TAGTCATTCTG
 TCTGTACACG GTCAAAATTC TAATGTGACA GGGGAAAATC CGTCAGAAAA TGCCACGCAG
 CCTTCTGCAG GAACTGATGA AACGAATGAA GTCCCTCAAA ACCAAGCACC TGATACAAAC
 ATTACAATTA CCAATGTTGT TTTCAATCCT GAAAGAAATG AAATTAATGG TACTACATTA
 CCTAATGCAA CCATTACAGC AACGGTAGTC GGTGATGCTT CTGCACAAGC AGGTGTTTTT
 TATGCGGATG CCAATGGCAA TTTTACAGTA ATTAGTCCCA GAGCGGGAGC GACTACTCAA
 TTAATCGCAA CCGTTGATCA ACGGAATAGT GCACCTGTCC AAATTGATAT TCCAAGTTCA
 GGACAAGAAG CAGCGCTTTC TTTTAGCAAT ATTACGATTG ATCCGAAACA AGGGACAATT
 TCTGGTAAAA CAGCACCGAA TGCAACTATT TTAGTGTCAC GTGCAGATGA TGCGCGGGTG
 ATTTTAGCAA GTTTTACTGC GGATGCCCAA GGGAATTTCA CAGCCAGTAA TTTAGTTCCC
 GGCACAAAAA ATCGCTTAGA TGTTACGTTA AATGGAGAAA TAGGGACACC TTAGTTGTTT
 GATTTACCAA ATTAA

EF013-2 (SEQ ID NO:46)

MKKIALFS MLTFSVLSLS LAGCGNKKTA STNDSKPKQE TKKATQKSSS QQEMKSSHSS
 VTGQNSNVTG ENPSENATQP SAGTDETEV PQNQAPDTNI TITNVVFNPE RNEINGTTLP
 NATITATVVG DASAQAGVYF ADANGNFTVI SPRAGATTQL IATVDQRNSA PVQIDIPSSG
 QEAAALFSNI TIDPKQGTIS GKTAPNATIL VSRADDARVI LASFTADAQG NFTASNLVPG
 TKNRLDVTLN GEIGTPYLFDP LPN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF013-3 (SEQ ID NO:47)

ATGTGGAAA CAAAAAACA GCAAGCACAA ATGATTCTAA GCCAAAGCAA
 GAAACAAAGA AAGCCACGCA GAAATCCTCT AGCCAACAAG AAATGAAAAG TAGTCATTCCG
 TCTGTACCGG GTCAAAATTC TAATGTGACA GGSBAAAATC CGTCAGAAAA TGCCACGCAG
 CCTTCTGCAG GAACTGATGA AACBAATGAA GTCCCTCAA ACCAAGCACCG TGATACAAAC
 ATTACAATTA CCAATGTTGT TTTTAATCCT GAAAGAAATG AAATTAATGG TACTACATTA
 CCTAATGCAA CCATTACAGC AACBGTAGTC GGTGATGCTT CTGCACAAGC AGGTGTTTTT
 TATGCGGATG CCAATGGCAA TTTTACAGTA ATTAGTCCCA GAGCGGGAGC GACTACTCAA
 TTAATCGCAA CCGTTGATCA ACGSAATAGT GCACCTGTCC AAATTGATAT TCCAAGTTCA
 GGACAAGAAG CAGCGCTTTC TTTTAGCAAT ATTACGATTG ATCCGAAACA AGGGACAATT
 TCTGGTAAAA CAGCACCAGG TGCAACTATT TTASTGTCAO GTGCAGATGA TGCGCGGGTG
 ATTTTAGCAA GTTTTACTGC GGATGCCCAA GGGAAATTCA CAGCCAGTAA TTTAGTTCCC
 GGCACAAAAA ATCGCTTAGA TGTTACGTTA AATGGAGAAA TAGGGACACC TTACTTGTTT
 GATTTACCAA AT

EF013-4 (SEQ ID NO:48)

CGNKKTA STNDSKPKQE TKKATQKSSS QQEMKSSHSS
 VTGQNSNVFG ENPSENATQP SAGTDETNV PQNQAPDTNI TITNVVFNP RNEINGTTLP
 NATITATVVG DASAQGVFY ADANGNFTVI SPRAGATTQL IATVDQRNSA PVQIDIPSSG
 QEAALSFNSI TIDPKQGTIS GKTAPNATIL VSRADDARVI LASFTADAQG NFTASNLVPG
 TKNRLDVTLN GEIGTPYLFDP LPN

EF014-1 (SEQ ID NO:49)

TGATGGTGGA GACTTTTTTAA GAGAGAGGAA GTACAGCCAA TGAGTAGGAA GCGAAAAATC
 AGCTTAATTA GTTTAGTCAT CATTTTGGTT TTTGTACAG TCGGCTCAGC ATACTTTGCT
 GTAGCGGGTA GCTATTTTAA GAAAACAATT GATAAAGGCT ATGTTCCCAT AAAAAATGAT
 TATAATGAAG CGCAAAATAA AGATAGTCAA TCGTTTTTGA TTATGGGGCT AGACAATACA
 ATTGAACGGA AATTAGGCAC AACTAGGACT GATGCTATGA TGGTGATTAC CGTGAATAAC
 AAGACGAAGA AAATAACCTA TTTAAGTTTG CCACGGGATA GTTTTGTTC AATTGATGCG
 AAAAATTACC AAGGGATGCA GCGAATTGAA GCCGCCTATA CCTACGATGG ACCAACAGCT
 TCTGTTAACA CAGTTGAGAA ATTATTGAAT ATTCCAATCA ATCATTACGT TGTGTTTAAC
 TTTTATCTT TTATTAAGTT AATTGATGCG GTTGGCGGCA TAGATGTCAA TGTCAAGCAG
 GCGTTTGATG GTGTCACCAA AGACGGGCCA GGATCCATTC ATTTTGATGC AGGGAACAG
 CATTTAGATG GTACGAAAGC TTTATCTTAT GCCCGTGAAA GACATAGCGA TAACGATATT
 ATGCGTGGAT TCCGACAACA AGAAATTATT CAAGCAGTTG AAGACAAGTT GAAATCTGGT
 CAATCAATCA TGAAAATAAT GGACATTATT GATTCGTTAA ATGGAAACAT TCAAACATGAT
 GTGGATTCCA ATGAATTGAC TCATTTAGTC AAAGAAGGTT TGAATTGGAC CAATTATGAT
 AAACAACAGC TTTCTTTTGA CTGGCGCACT TTTAGTAATG AAGGGCGCAG TATGTTTGAA
 CTATACCCAG ATAGTATTGA AAATGTCCGT CATCAATTAC GTGTGTCTTT AAATTTAGAA
 AAGCCAGATG AACGAGATCA AGACGGCTAT GTCTTCCATA CGAACGGTGA ATTTTATAT
 CAAAGTGATT ATACCGTTCA AGATGAAGCA GCTGAGGAAA ACGAAATGAC TTCCATCAAC
 GGCAATACGT ATATTGGTGT TCCTGGTAAT ACACAGACCG GCCCGTTGCC ATCAGTTAAA
 ACGGAAAATG GCTTTATAAA ATAA

EF014-2 (SEQ ID NO:50)

MSRKRKIS LISLVIILVF VTVGSAYFAV AGSYLKKTID KGYVPIKNDY
 NEAQNKDSQS FLIMGLDNTI ERKLGTTTRD AMMVITVNNK TKKITYLSLP RDSFVQIDAK
 NYQGMQRIEA AYTYDGPTAS VNTVEKLLNI PINHYVVFNF LSFIKLIDAV GGIDVNVKQA
 FDGVTKDGP SIHFDAGKQH LDGTKALSIA RERHSDNDIM RGFRQOEIIQ AVEDKLKSGQ
 SIMKIMDIID SLNGNIQTDV DSNELTHLVK EGLTWTNYDK QQLSFDWRTF SNEGRSMVEL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YPDSIENVRH QLRVSLNLEK PDERDQDGYV FHTNGEFLYQ SDYTVQDEAA EENEMTSING
NTYIGVPGNT QTGPLPSVKT ENGFIK

EF014-3 (SEQ ID NO:51)

TGCT

GTAGCGGGTA GCTATTTAAA GAAAACAATT GATAAAGGCT ATGTTCCCAT AAAAAATGAT
TATAATGAAG CGCAAAATAA AGATAGTCAA TCGTTTTTGA TTATGGGGCT AGACAATACA
ATTGAACGGA AATTAGGCAC AACTAGGACT GATGCTATGA TGGTGATTAC CGTGAATAAC
AAGACGAAGA AAATAACCTA TTAAAGTTTG CCACGGGATA GTTTTGTTCA AATTGATGCG
AAAAATTACC AAGGGATGCA GCGAATTGAA GCCGCCTATA CCTACGATGG ACCAACAGCT
TCTGTTAACA CAGTTGAGAA ATTATTGAAT ATTCCAATCA ATCATTACGT TGTGTTTAAAC
TTTTTATCTT TTATTAAGTT AATTGATGCG GTTGGCGGCA TAGATGTCAA TGTCAAGCAG
GCGTTTGATG GTGTCACCAA AGACGGGCCA GGATCCATTC ATTTTGATGC AGGGAAACAG
CATTTAGATG GTACGAAAGC TTTATCTTAT GCGCGTAAA GACATAGCGA TAACGATATT
ATGCGTGGAT TCCGACAACA AGAAATTATT CAAGCAGTTG AAGACAAGTT GAAATCTGGT
CAATCAATCA TGAAAAAAT GGACATTATT GATTCGTTAA ATGGAAACAT TCAAACATGAT
GTGGATTCCA ATGAAATTGAC TCATTTAGTC AAAGAAGGTT TGACTTGGAC CAATTATGAT
AAACAACAGC TTTCTTTTGA CTGGCGCACT TTTAGTAATG AAGGGCGCAG TATGGTTGAA
CTATACCCAG ATAGTATTGA AAATGTCCGT CATCAATTAC GTGTGTCTTT AAATTTAGAA
AAGCCAGATG AACGAGATCA AGACGGCTAT GTCTCCATA CGAACGGTGA ATTTTATAT
CAAAGTGATT ATACCGTTCA AGATGAAGCA GCTGAGGAAA ACGAAATGAC TTCCATCAAC
GGCAATACGT ATATTGTTGT TCCTGGTAAT ACACAGACCG GCGCGTTGCC ATCAGTTAAA
ACGGAAAAATG GCTTTATAAA A

EF014-4 (SEQ ID NO:52)

AV AGSYLKKTID KGYVPIKNDY

NEAQNKDSQS FLIMGLDNTI ERKLGTTTRTD AMMVITVNNK TKKITYLSLP RDSFVQIDAK
NYQGMQRIEA AYTYDGPTAS VNTVEKLLNI PINHYVVFNF LSFILKLIDAV GGIDVNVKQA
FDGVTKDGP SIHFDAGKQH LDGTKALSIA RERHSDNDIM RGFRQOEIIQ AVEDKLKSGQ
SIMKIMDIID SLNGNIQTDV DSNEHLHLVK EGLTWTNYDK QQLSFDWRTF SNEGRSMVEL
YPDSIENVRH QLRVSLNLEK PDERDQDGYV FHTNGEFLYQ SDYTVQDEAA EENEMTSING
NTYIGVPGNT QTGPLPSVKT ENGFIK

EF015-1 (SEQ ID NO:53)

TAATTAATAA TGTGTAAAAA GGGTCTGATG AAAAAAGGAG ACATAATAGT TATTATCTTT
TTAATAGCTA TCTCTTTTTC TCCATATTTT ATTTTTTTTC ACAATAATCC ATTTAACTCC
AAAAGTTTTC ACGACACTAA ATATGCTGTG GTCAAGATAG ATGGGAAAGA GATTGAGCGT
ATAAATTTAG ATGATTCAAA AGAATTTATC AAAACATATT ATCCATCAAA AGGGCAATAT
AATACTATAG AAGTTAAAAA TGCGCACGTT CGTGTAATAA AAGATAATAG TCCAGATCAA
ATTGCGGTGA AAACAGGATG GATATCAGAA CCAGGGCNAA CTAGTATCTG TATTCTCTAC
AGATTCATTT TAGAAATTGT TCAACAATAT TCTAAGGATT ATTATATTTA CTAA

EF015-2 (SEQ ID NO:54)

MK KGDIIIVIFL IAISFSPYFI FFHNNPFNSK SFDDTKYAVV KIDGKEIERI
NLDDSKFIK TTYPSKGQYN TIEVKNGHVR VKKDNSPDQI AVKTGWISEP GXTSICIPHR
FILEIVQQYS KDYYIY

EF015-3 (SEQ ID NO:55)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAATAATCC ATTTAACTCC
 AAAAGTTTTG ACGACACTAA ATATGCTGTG GTCAAGATAG ATGGGAAAGA GATTBAGCGT
 ATAAATTTAG ATGATTCAAA AGAATTTATC AAAACATATT ATCCATCAAA AGGGAAATAT
 AATACTATAG AAGTTAAAAA TGGGCACGTT CGTGTAAAAA AAGATAATAG TCCAGATCAA
 ATTGCGGTGA AAACAGGATG GATATCAGAA CCAGGGCNAA CTAGTATCTG TATTCTCTAC
 AGATTCATTT TAGAAATTGT TCAACAATAT TCTAAGGATT ATTATATTTA C

EF015-4 (SEQ ID NO:56)

NNPFNSK SFDDTKYAVV KIDGKEIERI
 NLDDSKFEIK TYPSKQYN TIEVKNGHVR VKKDNSPDQI AVKTGWISEP GXTSICIPHR
 FILEIVQQYS KDYYIY

EF016-1 (SEQ ID NO:57)

TGACGGTTGC CCCCSTCCAA TAGAAAGGAG TTTATGATGA AAAAGAAATA TTCTTTAGCC
 TTGCTGGTTA TGTGTGTAG TTTACTCCTA TTTGCAGGTT GTGGTAAAAG AAAAGCAAC
 GAAGATCAAT GSACACGGAT TAACGAAGAA AAACGGATTA TTATTGGCTT AGATGACTCC
 TTTGTGCCCC TGGGTTTTCA AGATAAATCA GGCAAAATTG TCGGCTTTGA TGTCGACTTA
 GCCAAAGCGG TTTTAAACT TTATGGCATT TCCGTTGACT TCCAACCGAT TGATTGGTCT
 ATGAAAGAAA CAGAATTACA AAATCAAACC ATTGATCTTA TTTGGAACGG CTACACTAAA
 ACGAGCGAGC GGGCCGAAAA AGTTCAATTC ACACAACCTT ACATGACGAA CGACCAAGTA
 CTTGTTTCTT TAAAAGAAAA AAACATTGCA ACAGCGAGCG ACATGCAAGG CAAAATTTTA
 GGGGTTCAAA ACGGCTCTTC TGGCTATGAT GGCTTCGAAA GTCAGCCTGA CGTTTTGAAA
 AAATTTGTTA AAGACCAAAC ACCTATTTTA TATGACGGCT TTAATGAAGC TTTCTTAGAT
 TTAAATCTG GTCGAATTGA CGGACTCCTA ATCGATCGCG TTTACGCCAA CTACTATCTT
 TCCCACGAAG ATAATTTAAA AAATATACT ATTTCTCATG TAGGCTATGA CAATGAAGAT
 TTTGCTGTGG GCGTCCGCAA ATCAGACAAT CAATTAGTCC AAAAAATCAA TACTGCCTTT
 GAAACGTTAC GAAAAGATGG CACCCTTAGT AAAATTTCTC AAAAAATGTT TGGAGAGGAC
 GTTACAAATA ACACAAAAAT AACTAA

EF016-2 (SEQ ID NO:58)

MMKKKSLAL LVICCSLLLF AGCGKRKSNE DQWTRINEEK RIIIGLDDSF
 VPMGFQDKSG KIVGFDVLA KAVFKLYGIS VDFQPIDWSM KETELQNQTI DLIWNGYTKT
 SERAEKVQFT QPYMTNDQVL VSLKEKNIAT ASDMQGKILG VQNGSSGYDG FESQPDVLKK
 FVKDQTPILY DGFNEAFLDL KSGRIDGLLI DRVYANYLS HEDNLKNYTI SHVGYDNEFD
 AVGVKSDNQ LVQKINTAFE TLRKDGTLSK ISQKWFGEVD TNNTKIN

EF016-3 (SEQ ID NO:59)

AAGCAAC
 GAAGATCAAT GGACACGGAT TAACGAAGAA AAACGGATTA TTATTGGCTT AGATGACTCC
 TTTGTGCCCC TGGGTTTTCA AGATAAATCA GGCAAAATTG TCGGCTTTGA TGTCGACTTA
 GCCAAAGCGG TTTTAAACT TTATGGCATT TCCGTTGACT TCCAACCGAT TGATTGGTCT
 ATGAAAGAAA CAGAATTACA AAATCAAACC ATTGATCTTA TTTGGAACGG CTACACTAAA
 ACGAGCGAGC GGGCCGAAAA AGTTCAATTC ACACAACCTT ACATGACGAA CGACCAAGTA
 CTTGTTTCTT TAAAAGAAAA AAACATTGCA ACAGCGAGCG ACATGCAAGG CAAAATTTTA
 GGGGTTCAAA ACGGCTCTTC TGGCTATGAT GGCTTCGAAA GTCAGCCTGA CGTTTTGAAA
 AAATTTGTTA AAGACCAAAC ACCTATTTTA TATGACGGCT TTAATGAAGC TTTCTTAGAT
 TTAAATCTG GTCGAATTGA CGGACTCCTA ATCGATCGCG TTTACGCCAA CTACTATCTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCCACGAAG ATAATTTAAA AAACATATACT ATTTCTCATG TAGGCTATGA CAATGAAGAT
 TTTGCTGTGG GCGTCCGCAA ATCAGACAAT CAATTAGTCC AAAAAATCAA TACTGCCTTT
 GAAACGTTAC GAAAAGATGG CACCCTTAGT AAAATTCTC AAAAAATGGT TGGAGAGGAC
 GTTACAAATA ACACAAAAAT AAC

EF016-4 (SEQ ID NO:60)

SNE DQWTRINEEK RIIIGLDDSF
 VPMGFQDKSG KIVGFDVDLA KAVFKLYGIS VDFQPIDWSM KETELQNTI DLIWNGYTKT
 SERAEKVQFT QPYMTNDQVL VSLKEKNIAT ASDMQGKILG VQNGSSGYDG FESQPDVLKK
 FVKDQTPILY DGFNEAFLDL KSGRIDGLLI DRVYANYYLS HEDNLKNYTI SHVGYDNEDF
 AVGVKSDNQ LVQKINTAFE TLRKDGTLK ISQKWFGEDV TNNTKIN

EF017-1 (SEQ ID NO:61)

TGAGGTGTTT TTATGAAAAG GGCAACAAAG CAAAGGCTGT CTTTGGCAGC AATCATGGTT
 CTACTTCTCT CGGGCTGTGG AAGTGTGGG AAAGAAACCA AAAAGCAAGA ACAACAGGTA
 TTACGGGTCG GGATTGATTC GGAATTATCA ACGGCAGACG TGTCTGTGGC AATGGATAAT
 ACCGCAGCAG ATGTAATGAG CCAAGTAGGG GAGGGACTTT TCTCTTTGA CGAAAAAGGA
 GAAGCGAAAC CAGCATTTGGC AACTGAAAAA GTACAGCCCT CCAATGATGG TTAAAGCTAT
 ACTTTTACGA TTGAAAAGA TGCAAAATGG AGTAACGGCG AGCCAATCAC AGCAAATGAT
 TTTGAATACT CTTGGAAGCG CACAGTGGAC CAAAAACAG CTTCCCCGCA AGCGTATTAC
 TTTGAAGGGT TAAAAAATTA TCGTGCTATT GTTGACGGTA GCAAATCTAA AGAAGAGTTA
 GGGGTAACAG CCATTGATGA CCATACCTTG GAAGTAGAGC TAAGCTATCC TATGAGTTAT
 TTTCAACAAT TATTGGCGGT ACCAGCTTTT TATCCTTTAA ATGAAGCATT TGTGAAAAA
 ACGGGCAAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTACATTA
 GAAGGTTGGG ATGGCAGCAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT
 CAAGCGAATG TTTCGCTAGA TAAGGTGGAT GTCCAAGTAG TTAAAGAAAG CAATACTGGG
 AAAAACTTT TCGAAGGGAA AGAATTAGAT GTTGTAAGAA TTCTGGAGA AATTGTTGCA
 CAAGAACAAG GCAATGCAGC TTTGAAAATT CGTGAAATTC CTGGAACGTA TTATATCCAA
 TTAAATACGC AAAAAGATCT TTTGGCAAAT AAGAATGCAC GTCGAGCAAT AGCATATCA
 TTGAATTCTG AGCGTTTAGC TAAAAATGTT TTAATGATG GCTCAAAAAA AGCACTTGGC
 TTCGTGCCAA CAGGTTTCAC TAATCAAGAA ACGCAAAAAG ATTTTCGAGA GGAATTAGGA
 GATTTAAATC CTAGTGAACC AGAAAAAGCG AAAGAGTTAT GGCAACGGC TAAAAAGAA
 TTAGGAATTG AAAAAAGCGA GCTAACGATT TTAAGTTCCG ATACAGAAAA TGCTAAAAA
 ATCAGTGAGT ATGTTCAAGG AGCTTTAGCA GATAATTAG AAAAAATTAAC AGTCAATGTT
 TCACCAGTTC CTTTAAATAA TCGTTTAGAA AAAAGTCGCA GCGGAGATTT CGACATTGTG
 GTTGGTGGCT GGACGCCAGT ATATGCTGAT CCAATCGATT TCTTAACTT ACTGCAATCA
 AAAAAATCCA ATAATTTTGG TAAATGGTCT AATAAGACCT TTGATCAGTT GCTTCAAGAA
 GCAAACGTAA CTTATGCAAA TAAATATGAA GAACGTTGGA AAACATTACA AAAAGCGGAT
 CAATTGGTTG CGGAAGAAGC CCCCCTAGTT CCTCTTTATC AATTAACAGA AGCAGCCTTA
 GTGGCCGATT CTGTCCAAAA TTTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA
 GTCTCTATCG GCGACAAGTA A

EF017-2 (SEQ ID NO:62)

MKRATKQ RLSLAAIMVL LLSGCGSVGK ETKKQEQQVL RVGIDSELST ADVSLAMDNT
 AADVMSQVGE GLFSFDEKGE AKPALATEKV QPSNDGLSYT FTIRKDAKWS NGEPIITANDF
 EYSWKRTVDP KTASPQAYYF EGLKNYRAIV DGSKSKEELG VTAIDDHLE VELSYPMYSYF
 QQLLAVPAFY PLNEAFVEKT GKNYGTSAES TLYNGAFTLE GWDGNTNNTWS YVKNKNYWDQ
 ANVSLDKVDV QVVKEVNTGK NLFEGKELDV VKISGEIVAQ EQGNAALKIR EIPGTYIQL
 NTQKDLLANK NARRAIALSL NSERLAKNVL NDGSKKALGF VPTGFTNQET QKDFAEELGD

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LNPSEPEKAK ELWQTAKKEL GIEKAELTIL SSDTENAKKI SEYVQGALAD NLENLTVNVS
 PVPFNNRLEK SRSGDFDIVV GGWTPVYADP IDFLNLLQSK NSNNFGKWSN KTFDQLLQEA
 NVTYANKYEE RWKTLQKADQ LVAEEAPLVP LYQLTEARLV ADSVQNLVYG PLGSGYYKSV
 SIGDK

EF017-3 (SEQ ID NO:63)

CTGTGG AAGTGTGGG AAAGAAACCA AAAAGCAAGA ACAACAGGTA
 TTACGGGTGCG GGATTGATTC GGAATTATCA ACGGCAGACG TGTCGTTGGC AATGGATAAT
 ACCGCAGCAG ATGTAATGAG CCAAGTAGGG GAGGGACTTT TCTCCTTTGA CAAAAAGGA
 GAACCGAAAC CAGCATTGCT AACTGAAAAA GTACAGCCCT CCAATGATGG TTTAAGCTAT
 ACTTTTACGA TTGAAAAA TAACAAAATGG AGTAACGGCG AGCCAATCAC A3CAAAATGAT
 TTTAATACT CTTGGAAGCG CACAGTGGAC CCAAAAACAG CTTCCCGCA ABCGTATTAC
 TTTAAGGGT TAAAAAATTA TCGTGTCTATT GTTGACGGTA GCAATCTAA AGAAGAGTTA
 GGGTAACAG CCATTGATTA CCATACCTTG GAAGTAGAGC TAAGCTATCC TATGAGTTAT
 TTTCAACAAT TATTGGCGGT ACCAGCTTTT TATCCTTTAA ATGAAGCATT T3TCGAAAAA
 ACGGCACAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTACATTA
 GAAGTTGGG ATGGCAGCAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT
 CAAGCGAATG TTTGCTATA TAAGGTGAT GTCCAAGTAG TTAAGAAGT CAATACTGGG
 AAAAACTTT TCGAAGGGAA AGAATTAGAT GTTGTAAGAA TTTCTGGAGA AATTGTTGCA
 CAAGAACAAG GCAATGCAGC TTTGAAAATT CGTGAAATTC CTGGAACGTA TTATATCCAA
 TTAATACGC AAAAAATCT TTTGGCAAT AAGAATGCAC GTCGAGCAAT AGCATTATCA
 TTGAATCTG AGCGTTTAGC TAAAAATGTT TTAATGATG GCTCAAAAAA AGCACTTGGC
 TTCGTGCCAA CAGTTTCAC TAATCAAGAA ACGCAAAAAG ATTTTGCAGA GGAATTAGGA
 GATTTAATC CTAGTGAACC AGAAAAAGCG AAAGAGTTAT G3CAACGCG TAAAAAGAA
 TTAGGAATTG AAAAAAGCGA GCTAACGATT TTAAGTTCCG ATACAGAAAA TGCTAAAAAA
 ATCAGTGAGT ATGTTCAAGG AGCTTTAGCA GATAATTTAG AAAATTTAAC AGTCAATGTT
 TCACCAAGT CTTTTAATA TCGTTTAGAA AAAAGTCGCA GCGGAGATT CACATTGTG
 GTTGGTGGCT GGACGCCAGT ATATGCTGAT CCAATCGATT TCTTAACTT ACTGCAATCA
 AAAAAATCCA ATAATTTTGG TAAATGGTCT AATAAGACCT TTGATCAGTT GCTTCAAGAA
 GCAAACGTAA CTTATGCAA TAAATATGAA GAACGTTGGA AAACATTACA AAAAGCGGAT
 CAATTGGTTG CGGAAGAAGC CCCCTAGTT CCTCTTTATC AATTAACAGA AGCACGCTTA
 GTGGCCGATT CTGTCCAAA TTTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA
 GTCTCTATCG GCGACAAG

EF017-4 (SEQ ID NO:64)

CGSVGK ETKKQEQVL RVGIDSELST ADVSLAMDNT
 AADVMSQVGE GLFSFDEKGE AKPALATEKV QPSNDGLSYT FTIRKDAKWS NGEPIITANDF
 EYSWKRTVDP KTASPQAYYF EGLKNYRAIV DGSKSKEELG VTAIDDHTLE VELSYMSYF
 QQLLAVPAFY PLNEAFVEKT GKNYGTSAES TLYNGAFTLE GWDGTNNTWS YVKNKNYWDQ
 ANVSLDKVDV QVVKEVNTGK NLFEGKELDV VKISGEIVAQ EQGNAALKIR EIPGTYIIQL
 NTQKDLLANK NARRAIALSL NSERLAKNVL NDGSKKALGF VPTGFTNQET QKDFAEELGD
 LNPSEPEKAK ELWQTAKKEL GIEKAELTIL SSDTENAKKI SEYVQGALAD NLENLTVNVS
 PVPFNNRLEK SRSGDFDIVV GGWTPVYADP IDFLNLLQSK NSNNFGKWSN KTFDQLLQEA
 NVTYANKYEE RWKTLQKADQ LVAEEAPLVP LYQLTEARLV ADSVQNLVYG PLGSGYYKSV
 SIGDK

EF018-1 (SEQ ID NO:65)

TGTCATTACA ACGATACCAA TTTTAATCAT TTATCCATTA CTACAAAAAC ACTTTATCGG
 CGGTATGATG GCCGGTGCAG TAAAAGAATA AAGAAAGTAG GGAACAATAT GAAAAAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

TTAGGCGGTT TATTGGTGGC AACGGCGGTC GTTAGTTTAG CGGCCTGTAG CCGTGGGGAA
AAGAAAGCTA GCTCAGATGT CTCAATTAAG GATCGGTATG AATTAGATGA AAAGACGCCT
GCTTGGAAGT TAGATAAGAA GAAAGAACCG ACCAAGATTA AATGGTATAT TAACCTCAGAT
TGGACGGCGC TGCCTTTTGG AAAAGACGTG ACCACTGCGC AGATTAAAAA AGACTTAAAT
GTGGATATTG AATTTATTTC CGGCGATGAT TCAAAATTAA ATGCCATGAT TTCAAGTGGA
GATATGCCTG ATATCGTGAC ATTAAC TGAA AAAACTGGAC AAGCAGCATT GAAAGCAGAT
TCTTGGGCCT ATTCTTTAAA CGATTTAGCT AAAAAATATG ACCCCTATTT AATGAAAGTT
GTTAACCAAG ATACGTTTAA ATGGTATGCC TTAGAGGATG GAAAAACATA TGGTTACCCT
AATTACTCTA ATACAAAAGC GGATTATGAA AGTGGAATA TCCCAGTAAA TGATAATTTT
GTTATTTCGTG AAGATGTCTA TAATGCATTA GGCAAGCCAG ACGTTTCAAC ACCAGAAAAT
TTTGAAAAAG TCATGCAACA GATTAAAGAA AAATATCCTG AGATGACCCC AATGGGCTTC
ACCACAGTGG GCGATGGTGC AGGACCATT TTAGACAAAT TACAAGACTT CTTAGGTGTT
CCTTTAGAGG ATAAAAATGG TAAATACTAT GATCGAAAT TAGATAAAGA ATATTTAGAA
TGGTTAAAAA CATTTAATGA TGTTTACCGA GCAGGCAATA TTAGTGATGA TAGCTTCACA
GATGATGGGG CAACGTTTGA TGAAAAAGTG AAACAAGGAA ATTATGCAAC CATGCTCGTT
GCTGGAACCA GTGGTCAAGG TGGGAACCTC ACAGAATTGA TGAAAAATC TGGCACACGT
TATATAGCCA TTGATGGACC AAGTAGCACT TCTGGCCGAA AACCAACATT AAATCAAAACC
GGCATTTCAG GTTGGTTAAG TAATTACATT ACGAAAGATG CGAAAGATCC AGCAAAAGTC
ACTCAACTGT TCACATATTT AATTGATGAA CCGGGACAAA TTTTAACAAA ATATGGCGTT
GAAGGAGTTA CTTATGCGTA CAATGATCAA GGAAAAATTG ATTATTTACC AGAAGTGAAA
AAATTAGAAC AAACAGACAA TGATGCCTAC AACAAAAAAT ATGGCATTAG TCGTTTCCTA
TACTTTAACA ACGACCGTGT CAATAAATA AAAGTACCAA TGGAAAGTGC TTTAACGCAA
ATGCAAGAAT GGGGCAAAG AAAATTAGTC CCACATTTTCG TAATTGAAAA TATTAATCCA
GATGCAGGAA CGCCGGAAG TCGTGCGAAT GAAGCGATTG AAACCAAAT AAATACAACC
GTTATTTCAA TGATTCGTGC GAAAGATGAT AAAGCCTTTG ACAAATCTTT AGAAGACTAC
AAAGCATTCT TAAATCAAA TAAATGGGAT GCAATTGAAA AAATAAAATC TGAGAAAATG
GCGGAAAACA GAGACAACT TAAGTAA

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EF018-2 (SEQ ID NO:66)

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MKKV LGLLVATAV VSLAACSGGE
KKASSDVSIK DRYELDEKTP AWKLDKKKEP TKIKWYINS WTALPFGKDV TTAQIKKDLN
VDIEFISGDD SKLNAMEISS DMPDIVTLTE KTGQAALKAD SWAYSLNDLA KKYDPYLMKV
VNQDTFKWYA LEDGKTYGYP NYSNTKADYE SGNIPVNDNF VIREDVYNAL GKPDVSTPEN
FEKVMQIQKE KYPEMTPMGF TTVGDGAGPF LDKLQDFLGV PLEDKNGKYY DRNLDEKEYLE
WLKTFNDVYR AGNISDDST DDGATFDEKV KQGNATMLV AGTSGQGGNF TEFMKKSGTR
YIAIDGPSST SGRKPTLNQT GISGWSNYI TKDAKDPKV TQLFTYLIDE PGQILTKYGV
EGVTYAYNDQ GKIDYLPEVK KLEQTDNDAY NKKYGISRFL YFNNDRVNKL KVPMESALTQ
MQEWGKGKLV PHFVIENINP DAGTPEARAN EAIETKLNTT VISMIRAKDD KAFDKSLEDY
KAFLKSNKWD AIEKIKSEKM AENRDKLK

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EF018-3 (SEQ ID NO:67)

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CTGTAG CCGTGGGGAA
AAGAAAGCTA GCTCAGATGT CTCAATTAAG GATCGGTATG AATTAGATGA AAAGACGCCT
GCTTGGAAGT TAGATAAGAA GAAAGAACCG ACCAAGATTA AATGGTATAT TAACCTCAGAT
TGGACGGCGC TGCCTTTTGG AAAAGACGTG ACCACTGCGC AGATTAAAAA AGACTTAAAT
GTGGATATTG AATTTATTTC CGGCGATGAT TCAAAATTAA ATGCCATGAT TTCAAGTGGA
GATATGCCTG ATATCGTGAC ATTAAC TGAA AAAACTGGAC AAGCAGCATT GAAAGCAGAT
TCTTGGGCCT ATTCTTTAAA CGATTTAGCT AAAAAATATG ACCCCTATTT AATGAAAGTT
GTTAACCAAG ATACGTTTAA ATGGTATGCC TTAGAGGATG GAAAAACATA TGGTTACCCT
AATTACTCTA ATACAAAAGC GGATTATGAA AGTGGAATA TCCCAGTAAA TGATAATTTT
GTTATTTCGTG AAGATGTCTA TAATGCATTA GGCAAGCCAG ACGTTTCAAC ACCAGAAAAT
TTTGAAAAAG TCATGCAACA GATTAAAGAA AAATATCCTG AGATGACCCC AATGGGCTTC

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ACCACAGTGG GCGATGCTGC AGGACCATTT TTAGACAAAT TACAAGACTT CTTAGGTGTT
CGTTTAGAGG ATAAAAATGG TAAATACAT GATCGAAATT TAGATAAAGA ATATTTAGAA
TGSTTAAAAA CATTTAATGA TGTTTADCGA GCAGGCAATA TTAGTGATGA TAGCTTCACA
GATGATGGGG CAACGTTTGA TGA AAAASTG AAACAAGGAA ATTATSCAAC CATGCTCGTT
GCTGGAACCA GTGGTCAAGG TGGGAATTC ACASAATTTA TGAAAAATC TGGCACACGT
TATATAGCCA TTGATGGAAC AAGTAGSACT TCTGCGGAA AACCAACATT AAATCAAACC
GGTATTCGAG GTTGGTTAAG TAATTACATT ACGAAAGATG CGAAAGATCC AGCAAAAGTC
ACTCAACTGT TCACATATTT AATTGATGAA CCGGGACAAA TTTTAACAAA ATATGGCGTT
GAAGGAGTTA CTTATGCGTA CAATGATCAA GSA AAAATTG ATTATTTACC AGAAGTGAAA
AAATTAGAAC AAACAGACAA TGATGCCTAC AACAAAAAAT ATGGCATTAG TCGTTTCCTA
TACTTTAACA ACGACCGTGT CAATAAAATA AAAGTACCAA TGGAAAGTGC TTTAACGCAA
ATSCAAGAAT GGGGCAAAGG AAAATTASTC CCACATTTCC TAATTGAAAA TATTAATCCA
GATGCAGGAA CCGCGGAAGC TCGTGCGAAT GAAGCGATTG AAACCAAAC AAATACAACC
GTTATTTCAA TGATTCGTGC GAAAGATGAT AAAGCTTTG ACAAATCTTT AGAAGACTAC
AAAGCATTCT TAAAATCAAA TAAATGSSAT GCAATTSAAA AAATAAAATC TGAGAAAATG
GCGGAAAACA GAGACAAACT TAAG

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EF018-4 (SEQ ID NO:68)

CSGGE

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KKASSDVSIK DRYELDEKTP AWKLDKKKEP TKIKWYINS WTALPFGKDV TTAQIKKDLN
VDIEFISGDD SKLNAMEISSG DMPDIVTLTE KTGQAALKAD SWAYSLNDLA KKYDPYLMKV
VNQDTFKWYA LEDGKTYGYP NYSNTKADYE SGNIPVNDNF VIREDVYNAL GKPVDSTPEN
PEKVMQIQIE KYPEMTPMGF TTVGDGAGPF LDKLQDFLGV PLEDKNGKYY DRNLDKEYLE
WLKTFNDVYR AGNISDDSFT EDGATFDEKV KQGNATMLV AGTSGQGGNF TEFMKKSGTR
YIAIDGPSST SGRKPTLNQT GISGWSNYI TKDAKDPKV TQLFTYLIDE PGQILTKYGV
EGVTYAYNDQ GKIDYLPVK KLEQTDNDAY NKKYGISRFL YFNNDRVNKL KVPMESALTQ
MQEWGKGLV PHFVIENINP DAGTPEARAN EAIETKLNNT VISMIRAKDD KAFDKSLEDY
KAFLKSNKWD AIEKIKSEKM AENRDKLK

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EF019-1 (SEQ ID NO:69)

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TAAAGGAGTT ACACAATGAA ACTTTTAAAA AAGACGGTCC TAATTGGTAC AACCCTTCTT
CTTGGTTCAT TCTTACTCGC AGCTTGTGGT AATACGAATA AAGAAGCCAA CAACGCTGAC
AAAACACATG AAGTAACAGA TACCTTAGGC AATAAAGTAA CCGTCCCCGC GAAACCCAAA
CGGATTATTG CGAGTTATTT AGAAGATTAT CTAGTTGCAT TAGGAGAAAA ACCAGTGGCA
CAATGGACAG TTGGACAAGG CAGCATTCAA GATTATTTAG CGAAAGAATT GAAAGATGTC
CCCACTATTT CCTATGACTT GCCATATGAA GCGGTTCTAA AATTTGAACC TGACTTATTA
TTAATCAGTT CATCTGCTCT AGTTGAAGGC GGTAAATACA AAGAATACAG TAAAATTGCG
CCAAC TTATG TAGTCAAAAA CGGCGAAAAT GTCACCTGGC GTGATCAATT GGAAGATATT
GCCACTGTTT TAGATAAAAA AGAACAAGCG AAAAAAGTGT TAGAAGATTA TGATACCTTA
ACCAAAGGCG TCCAAGAATA TCTTGCAAAA AAAGATGCTG GCAAATCTGC GGCAGTCTTA
TGGGTAAACA ACAACCAAGT CTTTATGGTT AGCGATAATC GCTCAAGCGG AACCGTGCTC
TATCAGGACT TAGGCCTCCA AGTTCCAAAA TTAGTGGAAG AAATTTCTAA AAACGCTACT
GCGGATTGGA ATCAAGTTTC TTTAGAAAAA TTAGCTGAGC TTGACGCAGA CCACATTTTC
CTTGTAACAA GCGATGAATC AGCACCTCTT TTCCAAGAAG CAATTTGGAA GAACTTACCT
GCTGTGAAAA ATAACCAAGT TCATACCTAT GATAAAAAAA GTAGTTGGTT ATACAACGGA
CCTATTGCGA TACTCAAAAT TGTGAAGAT GTAAAAAAG CGCTCTTAAA TTAA

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EF019-2 ((SEQ ID NO:70)

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MKLLKK TVLIGTTLLL GSFLAACGN TNKEANNADK THEVDTLGN KVTVPKPKR
IIASYLEDYL VALGEKPVAQ WTVGQSSIQD YLAKELKDVP TISYDLPEYA VLKFEPLDLL

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ISSSALVEGG KYKEYSKIAP TYVVKNGENV TWRDQLEDIA TVLDKKEQAK KVLEDYDTLT
 KGVQEYLGGK DAGKSAAVLW VTNNQVFMVS DNRSSGTVLY QDLGLQVPKL VEEISKNATA
 DWNQVSLEKL AELDADHIFL VNSDESAPLF QEAIWKNLPA VKNNQVHTYD KKSSWLYNGP
 IANTQIVEDV KKALLN

EF019-3 (SEQ ID NO:71)

TTGTGGT AATACGAATA AAGAAGCCAA CAACGCTGAC
 AAAACACATG AAGTAACAGA TACCTTAGGC AATAAAGTAA CCGTCCCCGC GAAACCCAAA
 CGGATTATTG CGAGTTATTT AGAAGATTAT CTAGTTGCAT TAGGAGAAAA ACCAGTGGCA
 CAATGGACAG TTGGACAAGG CAGCATTCAG GATTATTTAG CGAAAGAATT GAAAGATGTC
 CCCACTATTT CCTATGACTT GCCATATGAA GCGGTTCTAA AATTGTAACC TGACTTATTA
 TTAATCAGTT CATCTGCTCT AGTTGAAGGC GGTAAATACA AAGAATACAG TAAAATGCG
 CCAACTTATG TAGTCAAAAA CGGCGAAAAAT GTCACCTGGC GTGATCAATT GGAAGATATT
 GCCACTGTTT TAGATAAAAA AGAACAAGCG AAAAAAGTGT TAGAAGATTA TGATACCTTA
 ACCAAAGGCG TCCAAGAATA TCTTGGCAAA AAAGATGCTG GCAAATCTGC GGCAGTCTTA
 TGGGTAACCA ACAACCAAGT CTTTATGGTT AGCGATAATC GCTCAAGCGG AACCGTGCTC
 TATCAGGACT TAGGCCTCCA AGTTCCAAAA TTAGTGGAAG AAATTTCTAA AACCGTACT
 GCGGATTGGA ATCAAGTTTC TTTAGAAAAA TTAGCTGAGC TTGACGCAGA CCACATTTTC
 CTTGTAAACA GCGATGAATC AGCACCTCTT TTCCAAGAAG CAATTTGGAA GAACTTACCT
 GCTGTGAAAA ATAACCAAGT TCATACCTAT GATAAAAAAA GTAGTTGGTT ATACAACGGA
 CCTATTGCGA ATACTCAAAT TGTTGAAGAT GTAAAAAAG CGCTCTTAAA T

EF019-4 (SEQ ID NO:72)

CGN TNKEANNADK THEVTDTLGN KVTVPAPKPR
 IIASYLEDYL VALGEKPVAQ WTVGQGSIQD YLAKELKDVP TISYDLPYEA VLKFEPLDLLL
 ISSSALVEGG KYKEYSKIAP TYVVKNGENV TWRDQLEDIA TVLDKKEQAK KVLEDYDTLT
 KGVQEYLGGK DAGKSAAVLW VTNNQVFMVS DNRSSGTVLY QDLGLQVPKL VEEISKNATA
 DWNQVSLEKL AELDADHIFL VNSDESAPLF QEAIWKNLPA VKNNQVHTYD KKSSWLYNGP
 IANTQIVEDV KKALLN

EF020-1 (SEQ ID NO:73)

TGAGGAGATG AGAAAATGAA AAAGGTAGTT TCAATTTTGT TGATGGTTGT TGCAGTCTTC
 ACATTAAGTG CATGTAATGG TTCTAAATTA GATAAACAG GTGAAGAATT TAAAAATTCT
 ATAATGAAAG ATTCCTTCATA TGGTGATGAA TATTCAGAAG ATGGTTTATG TTTTAAATA
 TATAAAGATA AAGACACTAA TCGTTATTTG GCTGATGTTT GGGTTCCTGT TAAAGATGAA
 ACTAGCGCAT TGGAGTATTT TTATTATTAT GATGAAGATA AGCGATTAGA TAGTACTAAA
 AGTAAAGTAA CCTTTGATGA TATGAAAGCT AGTGGAAGCT ATGAAGTAGT GTATAAATCA
 GGGAAATTTA AATAA

EF020-2 (SEQ ID NO:74)

MKKVVS ILLMVAVFT LTACNGSKLD KTGEFEKNSI MKDSSYGDEY SEDGFSFLIY
 KDKDNTNRYLA DWVVPVKDET SALEYFYFYD EDKRLDSTKS KVTFFDMKAS GNYEVVYKSG
 KFK

EF020-3 (SEQ ID NO:75)

ATGTAATGG TTCTAAATTA GATAAACAG GTGAAGAATT TAAAAATTCT

100

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATAATGAAAG ATTCTTCATA TGSTGATGAA TATTCAGAAG ATGCTTTTATG TTTTITTAATA
 TATAAAGATA AAGACACTAA TCGTTATTMG GCTGATGTTT GGSTTCCTGT TAAAGATGAA
 ACTAGCGCAT TGGAGTATTT TTATTATTAT GATGAAGATA AGCGATTAGA TAGTACTAAA
 AGTAAAGTAA CCTTTGATGA TATCAAAAGCT AGTGAAGACT ATGAAGTAGT GTATAAATCA
 GGGAAATTTA AA

EF020-4 (SEQ ID NO:76)

CNGSKLD KTGEFKNSE MKDSSYGDEY SEDGFSFLIY
 KDKDNTNRYLA DWWVPVKDET SALEYFYIYD EDKRLDSTKS KVTFDMMKAS GNYEVVYKSG
 KFK

EF021-1 (SEQ ID NO:77)

TAGTTGTTTA AATACATTAA ACTATTTTTTA GGAGGCTTTA CAGAAATGAA AAAAGCAAAA
 TTATTCGGTT TTAGTTTGAT TGCATTAGGT TTATCAGTTT CACTGCGAGC ATGTGGTGGT
 GGCAAAGGCA AAACCGCTGA AAGCGGCGGT GGCAAAGGGG ATGCAGCGCA TAGTGCTGTA
 ATCATTACAG ATACAGGCGG CGTGGATGAC AAGTCGTTCA ACCAATCTTC TTGGGAAGGA
 TTGCAAGCTT GGGGTAAAGA ACATGATTTA CCAGAAGGTT CAAAAGGGTA TGCATATATT
 CAATCGAATG ATGCAGCTGA CTATACAACC AATATTGACC AAGCGGTATC AAGTAAATTC
 AACACAATCT TTGGTATTGG CTACTTGCTA AAAGATGCAA TTTCTTCTGC AGCAGATGCC
 AACCCTGATA CAAACTTTGT TTTAATCGAT GATCAAATCG ATGGCAAAAA GAATGTCGTT
 TCTGCAACAT TTAGAGATAA TGAAGCAGCT TACTTAGCCG GTGTGCTGCTG TGCATAATGAA
 AAAAAACGA ACAAAGTCGG TTTTGTGGT GGTGAAGAAG GGGTCGTAAT TGACCGTTTC
 CAAGCTGGTT TTGAAAAAGG TGTGGCTGAT GCTGCGAAAG AATTAGGTAA AGAAATTACT
 GTTGATACGA AATATGCGGC TTCATTTGCT GATCCTGCCA AAGGGAAAGC TTTAGCTGCT
 GCAATGTACC AAAACGGCGT TGATATCATC TTCCATGCTT CTGGTGCGAC TGGACAAGGG
 GTCTTCCAAG AAGCAAAAGA CTTGAATGAA TCAGGTTCCTG GCGACAAAGT TTGGGTAATC
 GGCGTTGACC GCGATCAAGA TGCTGATGGC AAGTACAAAA CAAAAGACGG CAAAGAAGAC
 AACTTCACGT TAACCTCAAC GCTTAAAGGT GTCGGCACAG CGGTTCAAGA TATTGCCAAC
 CGTGCGTTAG AAGACAAATT CCTGGTGGC GAACATTTAG TTTATGGATT AAAAGATGGT
 GGCGTTGACT TAACAGACGG CTATTTAAAC GACAAAACAA AAGAAGCTGT TAAACAGCA
 AAAGATAAAG TAATCTCAGG TGACGTAAAA GTCCAGAAA AACCAGAATA A

EF021-2 (SEQ ID NO:78)

MKKAKL FGFSIALGL SVSLAACGGG KGKTAESGGG KGDAHSAVI
 ITDTGGVDDK SFNQSSWEGL QAWGKEHDL ESKGYAYIQ SNDAADYTTN IDQAVSSKFN
 TIFGIGYLLK DAISAAADAN PDTNFVLIDD QIDGKKNVVS ATFRDNEAAY LAGVAAANET
 KTNKVGTVGG EGVVIDRFQ AGFEKGVADA AKELGKEITV DTKYAASFAD PAKGKALAAA
 MYQNGVDIIF HASGATGQGV FQEAKDLNES GSGDKVWVIG VDRDQDADGK YKTKDGKEDN
 FTLTSTLKG VTAQVDIANR ALEDKFPGE HLTVGLKDGG VDLTDGYLND KTKEAVKTAK
 DKVISGDVKV PEKPE

EF021-3 (SEQ ID NO:79)

ATGTGGTGGT
 GGCAAAGGCA AAACCGCTGA AAGCGGCGGT GGCAAAGGGG ATGCAGCGCA TAGTGCTGTA
 ATCATTACAG ATACAGGCGG CGTGGATGAC AAGTCGTTCA ACCAATCTTC TTGGGAAGGA
 TTGCAAGCTT GGGGTAAAGA ACATGATTTA CCAGAAGGTT CAAAAGGGTA TGCATATATT
 CAATCGAATG ATGCAGCTGA CTATACAACC AATATTGACC AAGCGGTATC AAGTAAATTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

AACACAATCT TTGGTATTGG CTAATTGCTA AAAGATGCAA TTTCTTCTGC AGCAGATGCC
AACCCTGATA CAAACTTTGT TTTAATCGAT GATCAAATCG ATGGCAAAAA GAATGTCGTT
TCTGCAACAT TTAGAGATAA TGAAGCAGCT TACTTAGCCG GTGTTGCTGC TGCAAATGAA
ACAAAAACGA ACAAAGTCGG TTTTGTGGT GGTGAAGAAG GGGTCGTAAT TGACCGTTTC
CAAGCTGGTT TTGAAAAAGG TGTGGCTGAT GCTGCGAAAG AATTAGGTAA AGAAATTACT
GTTGATACGA AATATGCGGC TTCATTGCT GATCCTGCCA AAGGGAAAGC TTTAGCTGCT
GCAATGTACC AAAACGGCGT TGATATCATC TTCCATGCTT CTGGTGCGAC TGGACAAGGG
GTCTTCCAAG AAGCAAAAGA CTTGAATGAA TCAGGTTCTG GCGACAAAGT TTGGGTAATC
GGCGTTGACC GCGATCAAGA TGCTGATGGC AAGTACAAAA CAAAAGACGG CAAAGAAGAC
AACTTCACGT TAACCTCAAC GCTTAAAGGT GTCGGCACAG CGGTTCAAGA TATTGCCAAC
CGTGCGTTAG AAGACAAATT CCCTGGTGGC GAACATTTAG TTTATGGATT AAAAGATGGT
GGCGTTGACT TAACAGACGG CTATTTAAAC GACAAAACAA AAGAAGCTGT TAAAACAGCA
AAAGATAAAG TAATCTCAGG TGACGTAAAA GTCCAGAAA AACCAGAA

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EF021-4 (SEQ ID NO:80)

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CGGG KGKTAESGGG KGDAAHSAVI
ITDTGGVDDK SFNQSSWEGL QAWGKEHDLF EGSKGYAYIQ SNDAADYTTN IDQAVSSKFN
TIFGIGYLLK DAISSAADAN PDTNFVLIDD QIDGKKNVVS ATFRDNEAAY LAGVAAANET
KTNKVG FVGG EEGVVIDRFQ AGFEKGVADA AKELGKEITV DTKYAASFAD PAKGKALAAA
MYQNGVDIIF HASGATGQGV FQEA KDLNES GSGDKVWVIG VDRDQDADGK YKTKDGKEDN
FTLTSTLKV GTAVQDIANR ALEDKFPGGE HLVYGLKDGG VDLTDGYLND KTKAEVKTAK
DKVISGDVKV PEKPE

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EFO22-1 (SEQ ID NO:81)

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TAAGAGCATA AAAAAATGAA GAGTTATAGG AGAAAGAAGA TGAAAAAGTA TTTAAAAATC
ACAATGGTTT GTATTTTATT GGTAGGATTT TTAGCTGGGT GTACCAATAA AAATGAAAAT
AAAAAGAAAC AGAAAAATAC CAAAGAAGCC GTTCAACTGA TGTCACCCTC GGAATTAACA
ACGCTCAACA CCTCTGTATT ATTGGATTIT CCAGATGCTA TTGTCCAAAC TGCAGCGTTT
GAAGGGTTAT ATAGTTTAGA TGAACAAGAC CAATTGGTAC CAGCCGTAGC AAAAGCATTG
CCGATGATTT CAGAAGATGG AAAAACCTAC ACGATTCTT TGAGAAAAGA AGCGGTTTGG
AGTAACGATG ATCCTGTAC AGCACATGAT TTTGAATATG CTTGGA AAAA AATGATTGAT
CCTAAAAACG GCTTTGTTTA TAGCTTCCTC ATCGTTGAAA CAATTCAAAA TGGTGCAGAA
ATCTCAGCGG GGAAATTAGC ACCCAATGAA CTAGGTGTCA CAGCTGTGGA TGATTATACA
TTAAAGGTGA CGCTCAAAGA GCCAAAACCG TACTTTACGT CCTTGTTAGC TTTTCCGACA
TTTTTCCCGC AAAATCNAAG AGTAGTCGAA CAATTTGGTG CGGACTATGG AACTGCTAGT
GATAAAGTCG TCTATAATGG TCCGTTCTGT GTAAAAGATT GGCAGCAAAC AAAGATGGAC
TGCAACTAG CAAAAAATAA TCGCTATTGG GATCACCAGA ACGTGCGCTC AGACATTATC
AATTATACAG TTATCAAAGA AACATCTACC GCATTGAATC TTTTGAAGA TGGACAATTA
GATGTGGCTA CACTAAGTGG TGAAC TGGCG CAACAGAATA AAAATAATAC GTTGATCAT
TCGTATCCAA CAGCGACAAT GAATATTG CGCTTAAATC AAAAACGGNA AGGGCAAGCN
ACGCCGCTTG CAAACGAAAA CCGTGGTAAA GCATTGGCTT TAGGAATAGA TAAAGAAAAAT
CTAGTCAATA ATATTATTGC AGATGGTTCT AAAGCGCTAC ATGGTGCAT TACGGAAGGC
TTTGTGGCGA ATCCACAAC GGGTCTCGAT TTTCTGCAAG AAGCAGGTAA TTTAATGGTT
TATAACAAAG AAAAAGCGCA AAGTTATTGG AAAAAGCAC AAGCAGAATT AGGAGAAAAG
GTTAACGTTG AATTGATGGT AACAGATGAT GGTCTTACA AAAAAATTGG TGAAGTTTG
CAAGGCTCGC TACAAGAATT GTTTCCTGGT TTGACAATAG AGCTAACCGC ATTGCCGACT
GAAGCTGCAT TGAAC TTTGG GCGAGAAAGT GACTATGATT TATCTTAAT TTACTGGACA
CCAGACTATC AAGACCCTAT TTCTACCCTG ATGACTTTAT ACAAGGGCAA TGATCGCAAT
TATCAGAAC CTGTCTATGA CAAATTATTA GATGAAGCAG CCACAACCTA TGCCTTAGAG
CCAGAAAAAA GATGGGCGAC ACTGATTGCA GCTGAAAAAG AAGTGATTGA AACGACTGCT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GGCATGATTC CACTTAGCCA AAATGAACAA ACAGTCTGTC AAAATGATAA AGTCAAAGGC
TTGAATTTTC ATACCTTTGG CGCTCCATTA ACSTTAAAAA ATGTTTATAA GGAAAAATAA

EF022-2 (SEQ ID NO:82)

KKKYLKIT MVCILLVGF AGCTNKNENK KKQKNTKEAV QLMSPSELTT
LNTSVLLDFP DAIVQTAAFE GLYSLDEQDQ LVPAAKALP MISEDGKTYT ISLRKEAVWS
NDDPVTAHDF EYAWKKMIDP KNGFVYSFLI VETIQNGAEI SAGKLAPNEL GVTAVDDYTL
KVTLLKEPKPY FTSLLAPPTF FPQXKXVVEQ FGADYGTASE KVVYNGPFV KDWQQTMDW
QLAKNNRYWD HQNVRSDIIN YTVIKETSTA LNLFEQDQLD VATLSGELAQ QNKNNTLYHS
YPTATMNYLR LNQKRXGQAT PLANENLRKA LALGIDKENL VNNIADGSK ALHGAITEGF
VANPTTGLDF RQEAGNLMVY NKEKAQSYWK KAQAELEGKV NVELMVTDDG SYKKIGESLQ
GSLQELFPGI TIELTALPTE AALNFGRESL YDLFLIYWTF DYQDPISLTM TLYKGNDRNY
QNPVYDKLLD EAATTYALEP EKRWATLIAA EKEVIETTAG MIPLSQNEQT VLQNDKVKGL
NFHTFGAPLT LKNVYKEK

EF022-3 (SEQ ID NO:83)

GT GTACCAATAA AAATGAAAAAT
AAAAAGAAAC AGAAAAATAC CAAAGAAGCC GTTCAACTGA TGTCACCCCTC GGAATTAACA
ACGCTCAACA CCTCTGTATT ATTGGATTTT CCAGATGCTA TTGTCCAAAC TGCAGCGTTT
GAAGGGTTAT ATAGTTTAGA TGAACAAGAC CAATTGGTAC CAGCCGTAGC AAAAGCATTG
CCGATGATTT CAGAAGATGG AAAACCTAC ACGATTCTTT TGAGAAAAGA AGCGGTTTGG
AGTAACGATG ATCCTGTCTAC AGCACATGAT TTTGAATATG CTTGGAAAAA AATGATTGAT
CCTAAAAACG GCTTTGTTTA TAGCTTCCTC ATCGTTGAAA CAATCAAAA TGCTGCAGAA
ATCTCAGCGG GGAAATTAGC ACCCAATGAA CTAGGTGTCA CAGCTGTGGA TGATTATACA
TTAAAGGTGA CGCTCAAAGA GCCAAAACCG TACTTTACGT CCTGTGTAGC TTTTCCGACA
TTTTTCCCGC AAAATCNAAA AGTAGTCGAA CAATTGGTGG CGGACTATGG AACTGCTAGT
GATAAAGTCG TCTATAATGG TCCGTTCTGT GTAAAAGATT GGCAGCAAAC AAAGATGGAC
TGGCAACTAG CAAAAAATAA TCGCTATTGG GATCACCAGA ACGTGCCTC AGACATTATC
AATTATACAG TTATCAAAGA AACATCTACC GCATTGAATC TTTTGAAGA TGGACAATTA
GATGTGGCTA CACTAAGTGG TGAAGTGGCG CAACAGAATA AAAATAATAC GTTGATCAT
TCGTATCCAA CAGCGACAAT GAATATTG CGCTTAAATC AAAACGGNA AGGCAAGCN
ACGCCGCTTG CAAACGAAAA CCTGCGTAAA GCATTGGCTT TAGGAATAGA TAAAGAAAAT
CTAGTCAATA ATATTATTGC AGATGGTTCT AAAGCGCTAC ATGGTGCGAT TACGGAAGGC
TTTGTGGCGA ATCCCACAAC GGGTCTCGAT TTTCGTCAAG AAGCAGGTAA TTTAATGGTT
TATAACAAAG AAAAAGCGCA AAGTTATTGG AAAAAAGCAC AAGCAGAAAT AGGAGAAAAG
GTTAACGTTG AATTGATGGT AACAGATGAT GGTTCTTACA AAAAAATTGG TGAAAGTTTG
CAAGGCTCGC TACAAGAATT GTTCCCTGGT TTGACAATAG AGCTAACCGC ATTGCCGACT
GAAGCTGCAT TGAACCTTGG GCGAGAAAGT GACTATGATT TATTCTTAAT TTACTGGACA
CCAGACTATC AAGACCCTAT TTCTACCCTG ATGACTTTAT ACAAGGGCAA TGATCGCAAT
TATCAGAACC CTGTCTATGA CAAATTATTA GATGAAGCAG CCACAACCTA TGCCTTAGAG
CCAGAAAAAA GATGGGCGAC ACTGATTGCA GCTGAAAAAG AAGTGATTGA AACGACTGCT
GGCATGATTC CACTTAGCCA AAATGAACAA ACAGTCTGTC AAAATGATAA AGTCAAAGGC
TTGAATTTTC ATACCTTTGG CGCTCCATTA ACGTTAAAAA ATGTTTATAA GGAAAAA

EF022-4 (SEQ ID NO:84)

CTNKNENK KKQKNTKEAV QLMSPSELTT
LNTSVLLDFP DAIVQTAAFE GLYSLDEQDQ LVPAAKALP MISEDGKTYT ISLRKEAVWS
NDDPVTAHDF EYAWKKMIDP KNGFVYSFLI VETIQNGAEI SAGKLAPNEL GVTAVDDYTL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KVTLKEPKPY FTSLLAFPTF FPQNXKVVEQ FGADYGTASD KVVYNGPFV V KDWQQTKMDW
 QLAKNRYWD HQNVRSIIN YTVIKETSTA LNLFDGQLD VATLSGELA Q QNKNNTLYHS
 YPTATMNYLR LNQKRXGQAT PLANENLRKA LALGIDKENL VNNIADGSK ALHGATEGF
 VANPTTGLDF RQEAGNLMVY NKEKAQSYWK KAQAELGEKV NVELMVTDDG SYKKIGESLQ
 GSLQELFPGL TIELTALPTE AALNFGRES D YDLFLIYWTP DYQDPIS TLM TLYKCNDRNY
 QNPVYDKLLD EAATTYALEP EKRWATLIAA EKEVIETTAG MIPLSQNEQT VLQNDKVKGL
 NFHTFGAPLT LKNVYKEK

EF023-1 (SEQ ID NO:85)

TAAATGGAG GGATCGGTAT GAAGAAATTA AAAATGTTAG GATGCGTCGG GTTGCTTTTA
 GCTTTAACGG CTTGTCAGGC GGGAACGGGA AACTCGGCTG ATAGTAACAA AGCAGCGGAA
 CAAAAAATG CAATTAGTTC TGAAGCGGCT ATTTGACAA TGGAACCACA CACAGCGGGG
 GATACGACCT CGACTTTAGT CATGAATCAA GTTTATGAAG GACTCTATGT TTTAGGTAAA
 GAAGATGAAT TAGAGTTGGG GGTCGCTGCC GAAGAACCAG CGATTCTGA AGATGAAACC
 GTTTATACAT TTAAGATTAG AGAAGATGCC AAATGGTCGA ATGATGATCC AGTAACAGCA
 AACGACTTTG TTTATGCATG GCAACAAGTT GCTTCCCTA AATCAGGATC GATTTCATCA
 GCTTTATTTT TTGATGTCAT TAAAAATGCT AAGGAAATG CTTTAGAAGG CGCAGATGTG
 AATACTCTTG GGGTTAAGGC GCTAGATGAT AAAACGTTAG AAATAACTTT AGAACGGCCC
 ACCCCTTATT TGAAATCATT ACTTTCGTTT CCTGTTTGT TTCCACAAA TGAATAATAT
 ATCAAAGAAC AAGGGGATAA ATATGCTACT GATGCAGAAC ATTTGATTTA TAATGGTCCT
 TTTAAATGTA AAGAATGGGA TAATGCCTCT TCTGATGACT GGACCTACGA AAAAAATGAT
 ACGTATTGGG ATGCTGAAAA AGTTAAATTA ACAGAAGCGA AAGTTTCAGT AATTAAGAGC
 CCAACGACAG CCGTGAATTT GTTTGACTCG AATGAATTGG ATGTAGTGAA TAAGCTAAGT
 GGTGAATTTA TTCCTGGTTA TGTTGATAAT CCAGCCTTTC TTTCAATTCC TCAATTCGTC
 ACATACTTTT TAAAAATGAA CAGCGTTCTG GATGGAAAAG AAAATCCGGC TTTAGCGAAC
 AACAATATTC GTAAAGCGTT GGCACAAGCT TTTGATAAAG AAAGTTTGT AAAAGAAGTC
 TTGCAAGATC AATCAACGGC TACAGATCAA GTAATTCGC CGGGACAAAC GATTGCGCCA
 GATGGAACAG ATTTACAAA ACTAGCTGCT AAGAAAAATA ACTACTTAAC CTACGATACA
 GCGAAAGCAA AAGAATTCG GGAAGAGGG AAAAAAGAAA TTGGGCTGGA TAAATCAAA
 TTAGAATTTT TAACAGATGA TACAGACAGC GCCAAAAAG CTGCTGAGTT TTTCCAATTT
 CAATTGGAAG AAAATCTAGA TGGATTAGAA GTGAATGTTA CTCAAGTTCC TTTTACTATT
 CGTGTGATC GTGATCAAAC GAGAGACTAT GATTTAGAAT TATCTGGTTG GGGAACCGAT
 TATCGTGATC CATTAACAGT TATGCGCATC TTTACTTCGG ATAGTACCTT GGGCGGCGTA
 ACGTTCAAGA GTGATACGTA TGATCAATTA ATTCAAGAAA CTAGAACAAC ACATGCGGCT
 GATCAAGAGG CTCGTTTAAA TGACTTTGCT CAAGCACAAG ATATTTTGGT GAATCAGGAA
 ACGGTTTTAG CACCAATCTA CAATCGAAGC ATTTCTGTAT TAGCTAATCA AAAAAATCAAG
 GATCTGTATT GGCATTTCATT TGGACCCACG TACAGTTTAA AATGGGCTTA TGTTAACTAA

EF023-2 (SEQ ID NO:86)

MKKLK MLGCVGLLLA LTACQAGTGN SADSNAKEQ KIAISSEAAI STMEPHTAGD
 TTSTLVMNQV YEGLYVLGKE DELELGVAE EPAISEDTV YTFKIREDAK WSNDPVTAN
 DFVYAWQQVA SPKSGSIHQ LFFDVIKNAK EIALEGADVN TLGVKALDDK TLEITLERPT
 PYLKSLLSFP VLFPPQNEKYI KEQGDKYATD AEHLIYNGPF KLKEWDNASS DDWTYEKNDT
 YWDAEKVKLT EAKVSVIKSP TTAVNLFDSN ELDVVNKLSG EFIPGYVDNP AFLSIPQFVT
 YFLKMNSVRD GKENPALANN NIRKALAQAF DKESFVKEVL QDQSTATDQV IPPGQTIAPD
 GTDFTKLA AKNNYLT YDTA KAKEFWK GK KEIGLDKIKL EFLTDDTDSA KKAEEFFQFQ
 LEENLDGLEV NVTQVPFTIR VDRDQTRDYD LELSGWGTDY RDPLTVMRIF TSDSTLGGVT
 FKSDTYDQLI QETRTTHAAD QEARLNDFAQ AQDILVNQET VLAPIYNRSI SVLANQKIKD
 LYWHSFGPTY SLKWAYVN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF023-3 (SEQ ID NO:87)

GGGAACGGGA AACTCGGCTG ATAGTAACAA AGCAGCGGAA
CAAAAAATTG CAATTAGTTG TGAAGCGGCT ATTCGACAA TGGAAACCACA CACAGCGGGG
GATACGACCT CGACTTTAGT CATGAATCAA GTTTATGAAG GACTCTATGT TTTAGGTAAA
GAAGATGAAT TAGASTTGGG GGTGCTGTCG GAAGAACCAG CGATTTCTGA AGATGAAACC
GTTTATACAT TTAAGATTAG AGAAGATGCG AAATGGTCGA ATGATGATCC AGTAACAGCA
AACGACTTTG TTTATGCATG GCAACAAGTT GCTTCCCTTA AATCAGGATC GATTCATCAA
GCTTTATTTT TTGATGTCAT TAAAAATGCT AAGGAAATTG CTTTAGAAGG CGCAGATGTG
AATACTCTTG GGGTTAAGGC GCTAGATGAT AAAACGTTAG AAATAACTTT AGAACGGCCC
ACCCCTTATT TGAAATCATT ACTTTCGTTT CTTGTTTTGT TTCCACAAAA TGAAAAATAT
ATCAAAGAAC AAGGGGATAA ATATGCTACT GATGAGAAC ATTTGATTTA TAATGGTCCT
TTTAAATTGA AAGAATGGGA TAATGCCTCT TCTGATGACT GGACCTACGA AAAAAATGAT
ACGTATTGGG ATGCTGAAAA AGTTAAATTA ACAGAAGCGA AAGTTTCAGT AATTAAGAGC
CCAACGACAG CGGTGAATTT GTTGACTCG AATGAATTGG ATGTAGTGAA TAAGCTAAGT
GGTGAATTTA TTCCTGGTTA TGTGATAAAT GCAGCCTTTC TTTCAATTCC TCAATTCTGC
ACATACTTTT TAAAAATGAA CAGCGTTTCG GATGGAAGG AAAATCCGGC TTTAGCGAAC
AACAAATATC GTAAAGCGTT GGCACAAGCT TTGATAAAG AAAGTTTTGT AAAAGAAGTC
TTGCAAGATC AATCAACGGC TACAGATCAA GTAATTCCGC CGGGACAAAC GATTGCGCCA
GATGGAACAG ATTTACAAA ACTAGCTGCT AAGAAAAATA ACTACTTAAC CTACGATACA
GCGAAAGCAA AAGAATTCTG GGAAAAAGG AAAAAGAAA TTGGGCTGGA TAAAAATCAA
TTAGAAATTT TAACAGATGA TACAGACAGC GCCAAAAAAG CTGCTGAGTT TTTCCAATTT
CAATTGGAAG AAAATCTAGA TGGATTAGAA GTGAATGTTA CTCAAGTTCC TTTTACTATT
CGTGTGATC GTGATCAAAC GAGAGACTAT GATTAGAAT TATCTGGTTG GGAACCGAT
TATCGTGATC CATTAAACAGT TATGCGCATC TTTACTTCGG ATAGTACCTT GGGCGCGGTA
ACGTTCAAGA GTGATACGTA TGATCAATTA ATTCAAGAAA CTAGAACAAC ACATGCGGCT
GATCAAGAGG CTCGTTTAAA TGACTTTGCT CAAGCACAAG ATATTTTGGT GAATCAGGAA
ACGGTTTTAG CACCAATCTA CAATCGAAGC ATTTCTGTAT TAGCTAATCA AAAAAATCAAG
GATCTGTATT GGCATTCATT TGGACCCACG TACAGTTTAA AATGGGCTTA TGTAAAC

EF023-4 (SEQ ID NO:88)

GTGN SADSNAAEQ KIAISSEAAI STMEPHTAGD
TTSTLVMNQV YEGLYVLGKE DELELVAAE EPAISEDETV YTFKIREDAK WSNDPVTAN
DFVYAWQQVA SPKSGSIHQ LFFDVIKNAK EIALEGADVN TLGVKALDDK TLEITLERPT
PYLKSLLSFP VLFPQNEKYI KEQGDYATD AEHLIYNGPF KLKEWDNASS DDWTYEKNDT
YWDAEKVKLT EAKVSVIKSP TTAVNLFDSN ELDVVKLSG EFIPGYVDNP AFLSIPQFVT
YFLKMNSVRD KENPALANN NIRKALAQAF DKESFVKEVL QDQSTATDQV IPPGQTIAPD
GTDFTKLAKE KNNYLTIDTA KAKEFWEKKG KEIGLDKIKL EFLTDDTDSA KKAAEFFQFQ
LEENLDGLEV NVTQVPFTIR VDRDQTRDYD LELSGWGTDY RDPLTVMRIF TSDSTLGGVT
FKSDTYDQLI QETRTTHAAD QEARLNDFAQ AQDILVNQET VLAPIYNRSI SVLANQKIKD
LYWHSFGPTY SLKWAYVN

EF024-1 (SEQ ID NO:89)

TAATGGCCGT TTCGTCTACT AATAAAGAGG ATGAAGCTAC TCAAATGGCG TTGGCAATGG
AACAAAGGATC ATAAAAAAGG AGAAGTGAGC ATGAAAAAAG TACTACCTTT TATTGCCTTA
GTCGGCTTGT TATTGTTGTC AGGTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
GGTGGTAAAT GGAAAGTGGA AGAAACACGT GCAACTTACA CTTTTTTTGA TGACGGTAAA
TTTTTCAGCTA ATGACTCAGA GGATAGTGTT AGTGGGACAT ACACTTATGA TGAAAAAAAT
AAAAAAATAA CCTTTGACNT TACTAGCAGN AACTCTTCA TTATGAAAAA AGTNGANTNC
AANGNTANCA AGATTACAGG GGAAATTGGC GAAAAACAAA GAACACTTAT AAAACAAAAA
ACAGAATAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF024-2 (SEQ ID NO:90)

M KKVLPFIALV GLLLLSGCGT DMKKILTADG
 GKWKVEETRA TYTFFDDGKF SANDSEDSVS GTYTYDEKNK KITFDXTSXN SFIMEKVXXX
 XXXKITGEIGE KQRTLIKQKT E

EF024-3 (SEQ ID NO:91)

ATT GACTGCCGAT
 GGTGGTAAAT GGAAAGTGGA AGAAACACGT GCAACTTACA CTTTTTTTGA TGACGGTAAA
 TTTTCAGCTA ATGACTCAGA GGATAGTGTT AGTGGGACAT ACACTTATGA TGAAAAAAT
 AAAAAAATAA CCTTTGACNT TACTAGCAGN AACTCTTCA TTATGGAAAA AGTNGANTNC
 AANGNTANCA AGATTACAGG GGAAATTGGC GAAAAACAAA GAACACTTAT AAAACAAAAA
 ACAGAA

EF024-4 (SEQ ID NO:92)

LTADG
 GKWKVEETRA TYTFFDDGKF SANDSEDSVS GTYTYDEKNK KITFDXTSXN SFIMEKVXXX
 XXXKITGEIGE KQRTLIKQKT E

EF025-1 (SEQ ID NO:93)

TGAATGAAAC ATATTAAAGG AATGTTGGTT TTTATCGGAT TATTTATTTT GGTGGTTGT
 GCGCCAGATC AAGAGCCAAC GAAACAAACA ACAAGTGGTC CGCAAGAGAC AAAGCAAGTG
 AAGCAAGTTA CCGTCACCAA TCAAACGACT TCTGCGGTGG AAAAAACAAGC GCCGACTAAA
 AATGACGAAC TGATTGCTAA TCAATTGACT TTTGATTCTC ATGAATACAC GTACGAAGTG
 GTTACAGGGG CCACACAAAC GACATTTGGA ACAACCCAC CAGCAAAATA TACACCGGAA
 GAAAAAAGA AAAAAATGTT TTGGTCCAAT CAACCGCCTT TGGGATTAAT GACGGGTAAC
 TATTATAAAA ATGAAGGTGT ATTTACTGGC GGAAATTACG GCATTGTAGA GATTATTACG
 GAACCTGAAA CGCAAAGGAT TCTGAATGTT GAGTTTACAG AGTTTGCTAG TGATCCTTAT
 TATGATACAC GCTATTCCGG TGTCAACAAA CGCCTGTCGG ATTATCCTGA ATTCAAGCA
 AGCAACACGC GTACAGACGA TACGTTAGTC ACCGTTGTTA ATGGTATTAC TTATGTAGAA
 AAACAAATGC GTGACGAAAA TCGTGTTACA GGTAATTTTT ATACGGTACG CGGTTTCATCA
 ACTTCTGCGC GTGAAGGATT AATGCCTTTA GCAGCAGAGA TGGACACTTG GCTAAAAGAG
 CCATCGAAAG AAACGTATAT CGGTTACGCA GAAGATTTAG GCAATGGCCT AATCGCTCGA
 CTTCAAGTGA TAACAGAAGA GCAGAAAATA AAACATGTCA GCTATGATGA ATACTTTTCA
 GATGAACAGG AAAAAATCAC AGAAACAGCC TCGGCGCTTT TTATCGTCAA TCGAAATATT
 ATTCACCAGG ATACAATAAA CAAACCAACA ATTCCTTTTAT TCATTTTGTA G

EF025-2 (SEQ ID NO:94)

MKHIKMLVF IGLFILVGCA PDQEPKQTT SGPQETKQVK QVTVTNQTTS AVEKQAPTKN
 DELIANQLTF DSHEYTYEVV TGATQTTFGT TPPAKYTPEE KKKKMFWSNQ PPLGLMTGNY
 YKNEGVFTGG NYGIVEIITE PETQRILNVE FTEFASDPY DTRYSGVNKR LSDYPEFQAS
 NTRTDDTLVT VVNGITYVEK QMRDENRVTG NFYTVRGSST SAREGLMPLA AEMDTWLKEP
 SKETYIGYAE DLGNGLIARL QVITEEQKIK HVSYDEYFSD EQEKITETAC GLFIVNRNII
 HQDTINKPTI LLFIL

EF025-3 (SEQ ID NO:95)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAC GAAACAAADA ACAAAGTGGTC CGGAAGAGAC AAAGCAAGTC
 AAGCAAGTTA CCGTCACCAA TCAAAAGCACT TCTGCGGTGG AAAAACAAGC GCGGACTAAA
 AATGACGAAC TGATTGCTAA TCAATTGACT TTTGATTCTC ATGAATACAC GTACGAAGTG
 GTTACAGGGG CCACACAAAC GACATTTGGA ACAACCCAC CAGCAAAATA TACACCGGAA
 GAAAAAAGA AAAAAATGTT TGGGTCCAAT CAACCGGCTT TGGGATTAAT GACGGGTAAC
 TATTATAAAA ATGAACTGT ATTTACTGCG GAAATTACG GATTGTAGA GATTATTACG
 GAACCTGAAA CCGAAAGGAT TCTGAATGTT GAGTTTACAG AGTTTGCTAG TATCCTTAT
 TATGATACAC GGTATTCGGG TGTCAACAAA CGCCTGTCGG ATTATCCTGA ATTTCAAGCA
 AGCAACACGC GTACAGACGA TACGTTAGTC ACCCTTGTTA ATGGTATTAC TTATGTAGAA
 AAACAAATGC GTGACGAAAA TCGTGTACGA GATAATTTTT ATACGGTACG CGSTTCATCA
 ACTTCTGCGC GTGAAGGATT AATGCTTTTA GACACAGAGA TGGACACTTG GCTAAAAGAG
 CCATCGAAAG AAACGTATAT CGGTTACGCA GAAGATTTAG GCAATGGCCT AATCGCTCGA
 CTTCAAGTGA TAACAGAAGA GCAGAAAATA AAACATGTCA GCTATGATGA ATACTTTTCA
 GATGAACAGG AAAAAATCAC AGAAACAGCC TCGCGCCTTT TTATCGTCAA TCGAAATATT
 ATTCACCAGG ATACAATAAA CAAACCAACA ATTCTTTTAT TCATTTTG

EF025-4 (SEQ ID NO:96)

TKQTT SGPQETKQVK QVTVTNQITS AVEKQAPTKN
 DELIANQLTF DSHEYTYEVV TGATQTFGT TPPAKYTPPE KKKKMFWSNQ PPLGLMTGNY
 YKNEGVTGG NYGIVEIITE PETQRILNVE FTEFASDPY DTRYSGVNKR LSDYPEFQAS
 NTRTDDTLVT VVNGITYVEK QMRDENRVTG NFYTVRGSST SAREGLMPLA AEMDTWLKEP
 SKETYIGYAE DLGNGLIARL QVITEEQKIK HVSYDEYFSD EQEKITETAC GLFIVNRNII
 HQDTINKPTI LLFIL

EF026-1 (SEQ ID NO:97)

TGAGTGTATG ATTACTCATT TCCCTTTGAA TCAGTTATGA TAAAGGAAGA AATAAAATAA
 TTTTITGGAG GGATTTTCAT GAAAATGTCT AAAGTACTCA CCACTGTTTT GACGGCAACT
 GCTGCTCTTG TGTTGCTTAG TGCTTGTTCA TCTGATAAAA AAACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACCTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATTTCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAATTAA

EF026-2 (SEQ ID NO:98)

MKMSK VLTTVLTATA ALVLLSACSS DKKTDSSSSS
 KETANSSTEVS GASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSSENFNIHV GTVKGDIIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF026-3 (SEQ ID NO:99)

AACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACCTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCAACGATG TCTATCGTAA ATTAGCACTT TATTCCCAAG ATGATAATAA AAAAGTAAC
 GCTGAAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAAT

EF026-4 (SEQ ID NO:100)

TDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLLALY SQDDNKKVTA EYEITVPKLI VSSENFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF027-1 (SEQ ID NO:101)

TTTGGTATGA AACAGAAAAA GTGGTTAATC GGACTTGTTC CACTGGGCTT GGTTTTAGCA
 GCATGTGGAA GTGGCGGTTC GAAAACGACC TCAAACGAAC CAGCTACACA GAAAATTAAC
 GTCGCATCTG GTGGTGAACCT CTCGACATTA GACAGCGCTC ATTATACAGA TGTCTATAGT
 TCCGATATGA TTGGTCAAGT AGTTGAAGGC TTGTATCGAC AAGATAAAAA CGGAGATCCT
 GAGCTAGCTA TGGCGAAAGC AGAGCCACAA GTTAGTGAAG ACGGGTTAGT CTATACATTC
 AAGTTACGAG AAGCAAAATG GACAAACGGG GATCCAGTTA AAGCAGGGGA TTTTGTAGTT
 GCGTTTAGAA ACGTGGTCGA TCCAGCATAC GGTTCAGTA GCAGTAATCA AATGGATATT
 TTTAAAAATG GCGTGCAGT GCGGGAAGGA CAAGCCACGA TGGAGAATT TGGTGTCAAA
 GCAATCGATG ACCAGACACT AGAATAACA TTGGAAAAATC CAATTCCTTA TTTAGCCCAA
 GTCTTGGTTG GGACACCTTT TATGCCTAAA AATGAAGCCT TTGCCAAAGA AAAAGGTACT
 GCCTATGGGA CTTCTGCAGA TAATTTTGTG GGCAATGGGC CGTTTGTAAAT TTCAGGTTGG
 GATGGCAATT CCGAAACTTG GAAATTGAAG AAGAATGATC ATTATTGGGA TAAAGAACAC
 GTAAAATTGA ATGAAATTGA TGTTCAAGTA GTGAAAGAAA TTGGCACAGG AGCCAATCTT
 TTTGATAATG GCGACTTAGA TTACACTGTT TTAGCAGATA CTTATGCACT TCAGTATAAA
 GAGTCAAAAC AAGCGCATTT TGTACCTAAA GCCATGGTGG GTTATTTAAG CCCCATCAT
 CGCCGTGAAA TTACCGGCAA CGAACATGTT CGAAAAGCTT TTTTACAAGC GATTGACAAA
 GAAACTTTTG CAAAAGAAAT TTTAGGAGAT GGCTCGACAG CTTTAAATGG NTTTGTACCA
 GCTAATTTTG CAAAATCCA GATACAGGTG AAGATTTCG CAAAGAAAAT GGTGATTAT
 TGCCATATAA TATTAAAGAA GCCCAAGCTA ACTGGAACAA TT

EF027-2 (SEQ ID NO:102)

MKQKKWLI GLVALGLVLA ACGSGSKTT SNEPATQKIN VASGGELSTL DSAHYTDVYS
 SDMIGQVVEG LYRQDKNGDP ELAMAKAEPQ VSEDGLVYTF KLREAKWTNG DPKAGDFV
 AFRNVDPAY GSSSSNQMDI FKNGRAVREG QATMEEFVVK AIDDQTELENT LENPIPYLAQ
 VLVGTPFMPK NEAFAKEKGT AYGTSADNFV GNGPFVISGW DGNSETWKLK KNDHYWDKEH
 VKLNEIDVQV VKEIGTGANL PDNGDLDTV LADTYALQYK ESKQAHFVPK AMVGYLSPNH
 RREITGNEHV RKAFLQAIK ETFKEILGD GSTALNGFVP ANFAKIQIV KISAKKMIY
 CHILKKPKL TGTI

EF027-3 (SEQ ID NO:103)

AACGACC TCAAACGAAC CAGCTACACA GAAAATTAAC
 GTCGCATCTG GTGGTGAACCT CTCGACATTA GACAGCGCTC ATTATACAGA TGTCTATAGT
 TCCGATATGA TTGGTCAAGT ACTTGAAGGC TTGTATCGAC AAGATAAAAA CGGAGATCCT
 GAGCTAGCTA TGGCGAAAGC AGAGCCACAA GTTAGTGAAG ACGGGTTAGT CTATACATTC
 AAGTTACGAG AAGCAAAATG GACAAACGGG GATCCAGTTA AAGCAGGGGA TTTTGTAGTT
 GCGTTTAGAA ACGTGGTCGA TCCAGCATAC GGTTCAGTA GCAGTAATCA AATGGATATT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TTTAAAAATG GGGGTGGGT GCGGGAAGGA CAAGCCACGA TGAAGAATT TGGTGTCAAA
GCAATCGATG ACCAGACACT AGAACTAACA TTGGAATAAG CAATTCCTTA TTTAGCCCCAA
GTCTTGCTTG GACACCTTTT TATGCTTAAA AATGAAGCCT TTGCCAAAGA AAAAGGTACT
GCCTATGGGA GTTCTGAGA TAATTTTGTT GGAATGGGG CGTTTGTAAT TTCAGGTTGG
GATGSCAATT CCGAAACTTG GAAATTGAAG AAGAATGATC ATTATTGGGA TAAAGAACAC
GTAAATTTGA ATGAAATTGA TGTTCAGTA GTGAAAGAAA TTGGCACAGG AGCCAATCTT
TTTGATAATG GCGACTTATA TTACACTGTT TTACGAGATA CTTATGCACT TCAGTATAAA
GAGTCAAAAC AAGCGCATTT TGTACCTAAA GCGATGCTGG GTTATTTAAG CCCCATCAT
CGCGTGAAA TTACCGGCAA CGAACATGTT CGAAAAGCTT TTTTACAAGC GATTGACAAA
GAAAGCTTTT CAAAAGAAAT TTTAGGAGAT GCGTCGACAG CTTTAAATGG NTTTGTACCA
GCTAATTTTG CAAAATCCA GATACAGGTG AAGATTTCG CAAAGAAAAT GGTGATTTAT
TGCCATATAA TATTAAAGAA GCCCAAGCTA A

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EF027-4 (SEQ ID NO:104)

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TT SNEPATQKIN VASGGELSTL DSAHYTDVYS
SDMIGQVVEG LYRQDNKNDP ELAMAKAEPQ VSEDGLVYTF KLREAKWTNG DPVKAGDFVV
AFRNVDPAY GSSSSNQMDI FKNGRAVREG QATMEEFQVK AIDDQTLLELT LENPIPYLAQ
VLVGTPEMPK NEAFAKEKGT AYGTSADNFV GNGPFVISGW DGNSETWKLK KNDHYWDKEH
VKLNEIDVQV VFEIGTGANL FDNGLDYTV LADTYALQYK ESKQAHFVVK AMVGYLSPNH
RREITGNEHV RKAFLQAIK EFAKEILGD GSTALNGFVP ANFAKIQIQV KISAKKMIY
CHIILKKPKL

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EF028-1 (SEQ ID NO:105)

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TAACAGAAGC AATACAACAA CTTAACACTT TGTTTACTTG TTATTTATCA GAAATCAACT
AAGACTTGTT ATAGTCAATG TATGGGTAGA TATGAAGGAG GAAACAAGGA AATGAAGAAA
AGAGCTTTGC TAGGGGTAC CTTATTAACA TTCACAACAT TAGCGGGTTG TACAAATTTA
TCTGAACAGA AAAGCGGCGA AAAACAACA GAGGTTGCTG AAGCGAAGGC AACTGAATCT
GAAAAAGCAT CAGTAAAAAA TGTTATTTT ATGATTGGAG ATGGCATGGG GAATCCGTAT
ACAACGGGCT ATCGCTATTT CAAAGCCAAT CACTCAGACA AGCGTGTTCC CCAAACAGCT
TTTGATACCT ATTTGGTCGG ACAGCAAGCC ACTTATCCAG AAGATGAAGA AGAGAATGTC
ACCGATTGAG CTTCCGCGAG GACAGCGATG GCTGCCGAG TGAACACCTA TAATAATGCT
ATTGCACTCG ATATGACAA GTCCAAAACA GAAACAGTGC TCGAACGTGC GAAAAAAGTG
GGGAAATCAA CGGGTCTTGT AGCAACATCT GAAATAACAC ATGCAACCCC TGCTGCATAT
GGCGCACATA ATGTTTCAG CAAAATATG GCAGAAATCG CCGATGACTA TTTTGATGAT
CAAATCGAGC GACAACACAA AGTCGATGTG TTACTTGGCG GCGGCTCCGA ATTATTTGCC
CGGAAAGATC GTGATTTAGT CAAAGAATTT TCCCAAGCGG GTTATGGTCA TGTCACAGAC
AAAAAGTCGT TAAATGAGAA CCAAGACGAC AAAATTTTAG GCTTGTTTGC ACCAGGCGGG
CTACCTAAAA TGATTGACCG AACGGAAGAA GTCCCTTCAT TAGCTGATAT GACAGAAGCG
GCTCTTCAAC GGTAGATAA AAATGAAAAA GGTTTCTTT TAATGGTTGA AGGTAGTCAA
ATTGATTGGG CCGGGCATAG CAATGATATT GTTGGCGCGA TGAGCGAAAT GCAAGACTTC
GAAGCGGCGT TTGAAAAGGC CATCGATTTT GCCAAAAAG ATGGTGAACA TTGGTGGTTA
CAACTGCAGA TCATTCACAA GGGGGCTTGT CTTTAG

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EF028-2 (SEQ ID NO:106)

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MKKR ALLGVTLTLTF TLAGCTNLS
EQKSGEKQTE VAEAKATESE KASVKNVIFM IGDGMGNPYT TGYRYFKANH SDKRVPQTAF
DTYLVGQQAT YPEDEEENV DSASATAMA AGVKTYNNAI ALDNDKSKTE TVLERAKKVG
KSTGLVATSE ITHATPAAYG AHNVSRRNMA EIADDFDDQ IDGQHKVDVL LGGSESELFAR
KDRDLVKEFS QAGYGHVTDK KSLNENQDDK ILGLFAPGGL PKMIDRTEEV PSLADMTEAA
LQRLDKNEKG FFLMVEGSI DWAGHSNDIV GAMSEMDFE AAFKAIDFA KKDGEHWWLQ

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LQIIQQGACL

EF028-3 (SEQ ID NO:107)

ACAGA AAAGCGGCGA AAAACAAACA GAGGTTGCTG AAGCGAAGGC AACTGAATCT
 GAAAAAGCAT CAGTAAAAAA TGTTATTTT ATGATTGGAG ATGGCATGGG GAATCCGTAT
 ACAACGGGCT ATCGCTATTT CAAAGCCAAT CACTCAGACA AGCGTGTTCC CCAAACAGCT
 TTTGATACCT ATTTGGTCGG ACAGCAAGCC ACTTATCCAG AAGATGAAGA AGAGAATGTC
 ACCGATTTCAG CTTCCGCAGC GACAGCGATG GCTGCCGGAG TGAAAACCTA TAATAATGCT
 ATTGCACCTCG ATAATGACAA GTCCAAAAACA GAAACAGTGC TCGAACGTGC GAAAAAAGTG
 GGGAAATCAA CGGGTCTTGT AGCAACATCT GAAATAACAC ATGCAACCCC TGCTGCATAT
 GGGCGACATA ATGTTTCACG CAAAAATATG GCAGAAATCG CCGATGACTA TTTTGATGAT
 CAAATCGACG GACAACACAA AGTCGATGTG TTAATTGGCG GCGGCTCCGA ATTATTTGCC
 CGGAAAGATC GTGATTTAGT CAAAGAATTT TCCCAAGCGG GTTATGGTCA TGTCACAGAC
 AAAAAGTCGT TAAATGAGAA CCAAGACGAC AAAATTTTAG GCTTGTTTGC ACCAGGCGGG
 CTACCTAAAA TGATTGACCG AACGGAAGAA GTCCCTTCAT TAGCTGATAT GACAGAAGCG
 GCTCTTCAAC GGTTAGATAA AAATGAAAAA GGTTCCTTT TAATGGTTGA AGGTAGTCAA
 ATTGATTGGG CCGGGCATAG CAATGATATT GTTGCGCGCA TGAGCGAAAT GCAAGACTTC
 GAAGCGGCGT TTGAAAAGGC CATCGATTTT GCCAAAAAG ATGGTGAAACA TTGGTGGTTA
 CAACTGCAGA TCATTCAACA GGGGGCTTGT CTT

EF028-4 (SEQ ID NO:108)

QKSGEKQTE VAEAKATESE KASVKNVIFM IGDGMGNPYT TGYRYFKANH SDKRVPQTAF
 DTYLVGQQAT YPEDEEENV DSASAATAMA AGVKTYNNAI ALDNDKSKTE TVLERAKKVG
 KSTGLVATSE ITHATPAAYG AHNVSRRNMA EIADDYFDDQ IDGQHKVDVL LGGSELFAR
 KDRDLVKEFS QAGYGHVTDK KSLNENQDDK ILGLFAPGGL PKMIDRTEEV PSLADMTEAA
 LQRLDKNEKG FFLMVEGSQI DWAGHSNDIV GAMSEMQDFE AAFEKAIDFA KKDGEHWWLQ
 LQIIQQGACL

EF029-1 (SEQ ID NO:109)

TGAAGGAGGG AGAAAATGAA AAAGTTAATC GGTAAAAAGT GGCTGCTGCT TACAGCAGTA
 GCCACTTTTT TATTATCAGG ATGCGCAAGT CTTGAACAAA AAGCACAGGA TAGTGTAATA
 GAAGTTACTG AAAATGTTAC TCAAACATATT TCAAACGATC AACGTATACC AGCTGATTTT
 GTTAGGCACG TGGATGGCGA TACCACAGTA TTAATAATTG ACGGAAAAGA ACAAAGGTT
 CGGTTTTTAT TAATTGACAC ACCCGAGACT GTGAAACCGA AAACAAAAGT TCAGCCGTTT
 GGATTGGAAG CTAGCAAACG CACAAAAGAG CTTTTGTCTA CTGCTTCAGA AATTACGTTT
 GAATATGATA AGGGCGATAA AACAGATCGT TACGGACGAG CGTTGGGCTA CATATTCGTA
 GATGGAACAT TACTACAAAA AACGCTTGTA AGTGAAGGAT TAGCTCGTGT TGCCTATGTA
 AAAGAGCCTA CAACTAAGTA TTTGGCAGAA CTAGAGCAAG CCCAAGAACA GGCTAAAAAT
 GAGTCACTCG GAATCTGGAG CATACCAGGT TATGTGACAC AACGGGGGTT TAGTAAATAA

EF029-2 (SEQ ID NO:110)

MKKLIG KKWLLTAVA TFLLSGCASL EQKAQDSVKE VTENVQTIS NDQRIPADTV
 RHVDGDTTVL KIDGKEQKVR FLLIDTPETV KPKTKVQPPG LEASKRTKEL LSTASEITFE
 YDKGDKTDY GRALGYIFVD GTLLQKTLVS EGLARVAVVK EPTTKYLAEL EQAQEQAKNE
 SLGIWSIPGY VTQRGFSK

EF029-3 (SEQ ID NO:111)

AAATGTTAC TCAAACATATT TCAAACGATC AACGTATACC AGCTGATTTT
 GTTAGGCACG TGGATGGCGA TACCACAGTA TTAATAATTG ACGGAAAAGA ACAAAGGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGGTTTTTAT TAATTGACAC AAGCGAGACT GTGAAACCGA AAACAAAAGT TCAGCCCGTTC
 GGATTGGAAG CTAGDAAACG CACAAAAGAG TTTTGTCTA CTGCTTCAGA AATTACGTTT
 GAATATGATA AGGCGGATAA AACAGATCGT TACCGACGAG CGTTGGGCTA CATATTCGTA
 GATGGAACAT TACTACAAA AACGCTTGT AGTBAAGGAT TAGCTCGTGT TGCCTATGTA
 AAAGAGCCTA CAACTAAGTA TTTGCGAGAA CTAGAGCAAG CCCAAGAACA GGCTAAAAAT
 GAGTCACTCG GAATCTGGAG CATACGAGGT TATGTGACAC AACGGGGGTT TAGTAAA

EF029-4 (SEQ ID NO:112)

NVTQTIS NDQFIPADFV
 RHVGDPTTVL KIDGKEQKVR FLLIDTPETV KPKTKVQPFQ LEASKRTKEL LSTASEITFE
 YDKGDKTDY GRALGYIFVD GTLLQKTLVS EGLARVAYVK EPTTKYLAEL EQAQEQAKNE
 SLGIWSIPGY VTQRGFSK

EF030-1 (SEQ ID NO:113)

TGATTGACAC ATAGGGGAGAA TAGTATGAAA AAGTTAAAAA TGATGGGGAT TATGTTATTT
 GTTAGTACCG TCTTGGTAGG TTGTGGCACA ACAGCAGANA CAAAAATAGA CGAGAAAGCA
 ACTGAGAAAA CCAGTGTCTC GAAAAAAGTT TTAAATTTAA TGGAGAACTC GGAAATCGGT
 TCAATGGATT CTATTTTAC ACAAGATGAA GCCAGTATTA ACGCACAGTC CAATGTCTTT
 GAAGGGTTAT ATCAATTGGA TGAAAAAGAT CAACTAATAC CTGCTGCTGC TAAAGAGATG
 CCAGAAATTT CTGAGGATGG CAAACGATAT ACCATTAAAC TAAGAGAAGA TGGCAAGTGG
 TCCAATGGTG ATGCTGTAAC AGCCAATGAT TTCGTTTTTG CTGGCGTAA ATTAGCGAAT
 CCCAAAAACC AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
 ATTACAAAAG AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
 TTGGAGGTTA CTTTAGAAAA GCCTGTACCA TATTTTACGT CGTTATTGGC ATTTTCTCCA
 TTTTTCACAC AAAACGAAGC ATTCGTGAAA GAAAAAGGAC AAGCCTATGG CACTTCTAGT
 GAAATGATTG TATCTAATGG TCCGTTTTTA ATGAAAAATT GGGATCAGTC AGCGATGTCTG
 TGGGATTTTG TCGTAATCC CTACTATTAC GATAAAGAAA AAGTAAATC AGAAACGATT
 CATTTTGAAG TTTTAAAGA AACCAATACC GTTTATAATT TGTACGAATC AGGTGAATTA
 GATGTGGCTG TCTTAACAGG AGATTTTGCT AAACAAAATC GAGACAACCC AGACTATGAA
 GCAATCGAAC GGTCAAAAGT CTATTCCTTA CGTTTAAACC AAAAAAGAAA CGAAAAACCA
 TCCATTTTTG CAAATGAGAA TGTCCGCAAA GCTTTAGCTT ATGCTTTGGA TAAAAAAGT
 TTAGTCGATA ATATTTTACG AGATGGCTCA AAAGAAATTT ATGGGTACAT TCCAGAAAAA
 TTTGTATATA ACCCAGAAAC GAATGAAGAT TTTCTCAAG AAGCAGGCGC TCTTGTCAAA
 ACAGACGCCA AAAAAGCCAA AGAGTATTTA GATAAAGCAA AAGCAGAGCT AAACGGAGAT
 GTAGCCATTG AACTTCTTTC AAGAGATGGT GATAGTGACC GA

EF030-2 (SEQ ID NO:114)

MKK LKMMGIMLFV STVLVGCCTT AXTKIDEKAT EKTSVSKKVL NLMENSEIGS
 MDSIFTQDEA SINAQSNVFE GLYQLDEKDQ LIFAAAKEMP EISEDGKRYT IKLREDGKWS
 NGDAVTANDF VFAWRKLANP KNQANYFFLL EGTILNGTAI TKEEKAPPEL GVKALDDYTL
 EVTLEKPVYP FTSLALFSPF FPQNEAFVKE KGQAYGTSSE MIVSNGPFLM KNWDQSAMSW
 DFVRNPYYID KEKVKSETIH FEVLKETNTV YNLYESGELD VAVLTGDFAK QNRDNPDIYA
 IERSKVYSLR LNQKRNEKPS IFANENVRKA LAYALDKKSL VDNILADGSK EIYGYIPEKF
 VYNPETNEDF RQEGALVKT DAKKAKEYLD KAKAELNGDV AIELLSRDGD SDR

EF030-3 (SEQ ID NO:115)

GAGAAAGCA
 ACTGAGAAAA CCAGTGTCTC GAAAAAAGTT TTAAATTTAA TGGAGAACTC GGAAATCGGT
 TCAATGGATT CTATTTTAC ACAAGATGAA GCCAGTATTA ACGCACAGTC CAATGTCTTT
 GAAGGGTTAT ATCAATTGGA TGAAAAAGAT CAACTAATAC CTGCTGCTGC TAAAGAGATG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGAAATTT CTGAGGATGG CAAACGATAT ACCATTAAAC TAAGAGAAGA TGGCAAGTGG
 TCCAATGGTG ATGCTGTAAC AGCCAATGAT TTCGTTTTTG CTTGGCGTAA ATTAGCGAAT
 CCCAAAAACC AAGCCAATTA CTTTTTCTTG TTAGAAGGAA CGATTCTGAA CGGAACAGCT
 ATTACAAAAG AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
 TTGGAGGTTA CTTTAGAAAA GCCTGTACCA TATTTTACGT CGTTATTGGC ATTTTCTCCA
 TTTTTCACAC AAAACGAAGC ATTTCGTGAA GAAAAAGGAC AAGCCTATGG CACTTCTAGT
 GAAATGATTG TATCTAATGG TCCGTTTTTA ATGAAAAATT GGGATCAGTC AGCGATGTCC
 TGGGATTTTG TCGGTAATCC CTACTATTAC GATAAAGAAA AAGTAAATC AGAAACGATT
 CATTTTGAAG TTCTTAAAGA AACCAATACC GTTTATAATT TGTACGAATC AGGTGAATTA
 GATGTGGCTG TCTTAACAGG AGATTTTGCT AAACAAAATC GAGACAACCC AGACTATGAA
 GCAATCGAAC GGTCAAAAGT CTATTCCTTA CGTTTAAACC AAAAAAGAAA CGAAAAACCA
 TCCATTTTTG CAAATGAGAA TGTCCGCAAA GCTTTAGCTT ATGCTTTGGA TAAAAAAGT
 TTAGTCGATA ATATTTTAGC AGATGGCTCA AAAGAAATTT ATGGGTACAT TCCAGAAAAA
 TTTGTATATA ACCCAGAAAC GAATGAAGAT TTTCTCAAG AAGCAGGCGC TCTTGTCAAA
 ACAGACGCCA AAAAAGCCAA AGAGTATTTA GATAAGCAA AAGCAGAGCT AAACGGAGAT
 GTAGCCATTG AACTTCTTTC AAGAGATGGT

EF030-4 (SEQ ID NO:116)

EKAT EKTSVSKKVL NLMENSEIGS

MDSIFTQDEA SINAQSNVFE GLYQLDEKDQ LIPAAAKEMP EISEDGKRYT IKLREDGKWS
 NGDAVTANDF VFAWRKLANP KNQANYFFLL EGTILNGTAI TKEEKAPEEL GVKALDDYTL
 EVTLEKVPY FTSLLAFSPF FPQNEAFVKE KGQAYGTSSE MIVSNGPFLM KNWDQSAMSW
 DFVRNPYYD KEVKSETIH FEVLKETNTV YNLYESGELD VAVLTGDFAK QNRDNPDYEA
 IERSKVYSLR LNQKRNEKPS IFANENVRKA LAYALDKKSL VDNILADGSK EIYGYIPEKF
 VYNPETNEDE RQEGALVKT DAKKAKEYLD KAKAELNGDV AIELLSRDG

EF031-1 (SEQ ID NO:117)

TGAGAAATTA GTTATTTTAG AAAAATAAAA ACCATTTTGG AGGAAGATTT AAAAATGAAA
 AAACGCGTAA TTTTAGGGAC ATTAGTCGCT GCAACGTTAT TAATGACTGC TTGTGGAAAC
 AGCGAAGCAA CTACGAAAAG CGAGAGCAAA GGTGGAAGTA ATGCTTTAGT CGTTTCAACT
 TTCGGATTAA GTGAAGATAT TGTCAAAAAA GACATTATCG CTCCATTTGA AAAAGAGAAAT
 GAAGCGAAAG TTACCTTGA AGTAGGCAAT AGCGCAGACC GCTTTACGAA ATTAATAAAT
 AATCCCAATG CGGGAATTGA TGTCATTGAA TTAGCACAAG CAAATGCAGC ACAAGGTGGA
 AAAGATGGGT TATTGAAAA AATTACAGAA AAAGAAGTAC CTAATTTAAG TCAGTTAACG
 CCGGGAGCAA AAGAGGTTT TGAAAGTGGT GCTGGCGTAC CAATCGCTGT AAACAGTATC
 GGGATTGTTT ACAACAAAGA AAAATTAGGC AAAGAAATTA AAAACTGGGA TGACTTATGG
 TCAGCTGATT TGAAAGGTAA AATTCTGTT CCAGACGTTG CCACGACGGC AGGTCTTTTA
 ATGTTATACG TTGCTAGTGA ACATGCTGGT CAAGATATTA CAAAAGATAA CGGGAAGGCC
 GCTTTTGAAG CGATGAAAGA ATTAACCA AACGTTGTTA AAACGTATTC AAAATCGTCA
 GACTTAGCNA ATATGTTCCA ATCTGGTGAA ATTGAAGCAG CTGTGGTTGC TGATTTTGGC
 GTTGATATTA TTCAAGGCGC ACAGAAAACG TGA

EF031-2 (SEQ ID NO:118)

MKK RVILGTLVAA TLLMTACGNS EATTKSESKG GSNALVVSTF

GLSEDIVKDD IIAPFEKENE AKVTLEVGN ADRFTKLKNN PNAGIDVIEL AQANAAQGGK
 DGLFEKITEK EVPNLSQLTP GAKEVFESGA GVPIAVNSIG IVYNKEKLGK EIKNWDDLWS
 ADLKGKISVP DVATTAGPLM LYVASEHAGQ DITKDNGKAA FEAMKELKPN VVKTYSSSD
 LANMFQSGEI EAAVADFV DIIQGAQKT

EF031-3 (SEQ ID NO:119)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AA CTACGAAAAG CGAGAGCAAA GGTGGAAGTA ATGCTTTAGT CGTTTCAACT
 TTCCGATTAA GTGAAGATAT TGTCAAAAA GACATTATCG CTCCATTGTA AAAAGAGAAT
 GAAGCGAAAG TTACCTTAGA AGTAGGCAAT AGCGCAGACC GCTTTACGAA ATTAAAAAAT
 AATCCCAATG CGGGAATTGA TGTCAATTGAA TTAGCACAAG CAAATGCAGC ACAAGGTGGA
 AAAGATGGGT TATTTGAAAA AATTACAGAA AAAGAATAC CTAATTTAAG TCAGTTAACG
 CCGGGAGCAA AAGAGGTTTT TBAAGTGGT GCTGGCCTAC CAATCGCTGT AAACAGTATC
 GGGATTGTTT ACAACAAAGA AAAATTAGGC AAAGAAATTA AAAACTGGGA TGACTTATGG
 TCAGCTGATT TGAAAGGTAA AATTTCTGTT CCAGACCTTG CCACGACGGC AGGTCCTTTA
 ATGTTATACG TTGCTAGTGA ACATGCTGCT CAATATATTA CAAAAGATAA CCGGAAGGCC
 GCTTTTGAAG CGATGAAAGA ATTAAAACTA AACCTTGTTA AAACGTATTC AAAATCGTCA
 GACTTAGCNA ATATGTTCCA ATCTGCTGAA ATTGAAGCAG CTGTGGTTGC TGATTTTGGC
 GTTGATATTA TTCAAGGCGC ACAGAAAA

EF031-4 (SEQ ID NO:120)

TTKSESKG GSNALVVSTF
 GLSEDIVKDD IAPFEKENE AKVTLEVGNL ADRFTKLKNN PNAGIDVIEL AQANAAQGGK
 DGLFEKITEK EVPNLSQLTP GAEVFESEA GVPIAVNSIG IVYNKEKLGK EIKNWDLLWS
 ADLKGKISVP DVATTAGPLM LYVASEHAGQ DITKDNKAA FEAMKELKPN VVKTYSSSD
 LANMFQSGEI EAAVVADFAV DIIQGAQK

EF032-1 (SEQ ID NO:121)

TGAATAAATT ATTTAGGAGG AATTATGATG AAAAAATTAA TTAGTTTAGG ATTGGTTTGT
 GTTTGTGGTA TTCTACTACT TACTGCTTGT NCGGAAATA ATGATAATAA AGATACTGAA
 AAGTCAACCA GTCAATCTAG CAGCACAGTT AAACAACCGA ATTCAAAGA CTTTGTGGC
 TCAGGGGAAT ATTCAGTTGG AAAAGATATT GATCCTGGAG ATTACTATGC TGTATTAACT
 CAACTAGATG ATAAATCGAG CATAGTTCTT ATTACCGTCA AATCAGGCGG AGAAAATAGT
 AACCATGACT TATACGGAGT GGGAAACAAG AAAAAAGTAT CTCTTAAAAA GGGAGATACT
 CTCACATTTCG AAACCTGCCG CAAAGATTTT GTTGTAGAT TTTTAAATGA AAAAGATTTT
 CAAGAATATA TGAAAAATCC AGTATCNAGT ACTGAACTA GCAAACANAA AACAGTAAAC
 TCTGATGTTT CTAAGTAG TAGCCAAGAT AATAACAAT CTGATGTATC TGAAAAAATA
 GAAGTAAGTA CTGAAGCGAA GTCTGATGTA GCTACTAATA CTTTACCGAG CGAAGATAAA
 AATACTAATG ACATTACTAA GCTAGCAGAT GAGCCAACCT TAGAACAACA AACCGTCTTA
 GATACTTTAG CTAAGCATCA ATTTAATGAT ATGTATCCTT ATAAAGGAAG CAAAATGCAT
 TCAATTATCG GCGTCATCCC AACCATGGAC GCAAAAAGAT GGTA

EF032-2 (SEQ ID NO:122)

MK KLISLGLVCV CGISLLTACX GNNDNKDTEK STSQSSSTVK QPNSKDFVAS
 GEYSVGKIDID PGDYYAVLTQ LDDKSSIVLI TVKSGGENSN HDLYGVGNKK KVSLLKGDITL
 TFETADKDFV VRFLNEKDFQ EYMKNPVSST ETSKXKTVNS DVSKSSSQDN KQSDVSEKKE
 VSTEAKSDVA TNTLPSEDKN TNDITKLADE PTLEQQTVLD TLAKHQFNMD YPYKSGSKMHS
 IIGVIPTMDA KRW

EF032-3 (SEQ ID NO:123)

TA ATGATAATAA AGATACTGAA
 AAGTCAACCA GTCAATCTAG CAGCACAGTT AAACAACCGA ATTCAAAGA CTTTGTGGC
 TCAGGGGAAT ATTCAGTTGG AAAAGATATT GATCCTGGAG ATTACTATGC TGTATTAACT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAACTAGATG ATAAATCGAG CATAGTTCCTT ATTACCGTCA AATCAGGCGG AGAAAATAGT
 AACCATGACT TATACGGAGT GGGAAACAAG AAAAAAGTAT CTCTTAAAAA GGGAGATACT
 CTCACATTCG AAACGTCCGA CAAAGATTTT GTTGTTAGAT TTTTAAATGA AAAAGATTTT
 CAAGAATATA TGAAAAATCC AGTATCNAGT ACTGAACTA GCAAACANAA AACAGTAAAC
 TCTGATGTTT CTAAGAGTAG TAGCCAAGAT AATAACAAT CTGATGTATC TGAAAAAAA
 GAAGTAAGTA CTGAAGCGAA GTCTGATGTA GCTACTAATA CTTTACCGAG CGAAGATAAA
 AATACTAATG ACATTACTAA GCTAGCAGAT GAGCCAACCT TAGAACAACA AACCGTCTTA
 GATACTTTAG CTAAGCATCA ATTTAATGAT ATGTATCCTT ATAAAGGAAG CAAAATGCAT
 TCAATTATCG GCGTCATCCC AACCATGGAC GCAAAAAGAT GG

EF032-4 (SEQ ID NO:124)

NDNKDTEK STSQSSSTVK QPNSKDFVAS
 GEYSVGKID PGDYYAVLTQ LDDKSSIVLI TVKSGGENSN HDLYGVGNKK KVSLLKGDTL
 TTFETADKDFV VRFLNEKDFQ EYMKNPVSSST ETSKXKTVNS DVSKSSSQDN KQSDVSEKKE
 VSTEAKSDVA TNTLPSEKDN TNDITKLADE PTLEQQTVLD TLAKHQFNDM YPYKSGSMHS
 IIGVIPTMDA KRW

EF033-1 (SEQ ID NO:125)

TGACTGCTTT TTTTCTATTG GAGAAAAAAG TGGTTTTTTT GTATTGTTTT GACGTTGAGA
 CAAAGGAGGT TCATTTCAGA AAATTTTCCC CAAAATAAAA TAGACGAATG CGAGGATGAA
 AAAATGAAAA AATTTACTTT AACAAATGATG ACTTTAGGTT TAGTAGCAAC ACTTGGCTTA
 GCAGGATGTG GTAAACAGGA AAAGAAAGCA ACTACCTCTT CTGAAAAAAC AGAAGTAACG
 TTACCAACCA AAGACCGTAG CGGCAAAGAA ATTACTTTAC CCAAAGAAGC AACCAAAATT
 ATTTCCCTAG TGCCATCAAC AACAGAAGTG ATTGAAGACT TAGGTAAAAC CGACCAATTA
 ATCGCAGTTG ATACTCAAAG TAGTACAATG ATGACTGATT TAAAAAAATT ACCACAAATG
 GATATGATGG CTGTCGATGC CGAAAAATTG ATTGCCTTGA AACCACAAAT TGTTTATGTG
 AATGACATCA ATTTAGCTAG CTCAGAAAGT GTTTGGAAGC AAGTGGAAGA TGCTGGAATT
 ACAGTCGTTA ATATCCCCAC TAGTACAAGC ATCAAAGCAA TCAAAGAAGA CGTCCAATTC
 ATCGCTGATA GCTTATCTGA ACATGAAAAA GGACAAAAGT TAATCAAAAC AATGGATCAA
 GAAATCGACG AGTAG

EF033-2 (SEQ ID NO:126)

MKKFTLTMMT LGLVATLGLA
 GCGKQEKAT TSSEKTEVTL PTKDRSGKEI TLPKEATKII SLVPSTTEVI EDLGKTDQLI
 AVDTQSSTMM TDLKKLPQMD MMAVDAEKLI ALKPQIVYVN DINLASSESV WKQVEDAGIT
 VVNIPTSTSI KAIKEDVQFI ADSLSEHEKG QKLIKTMDE IDE

EF033-3 (SEQ ID NO:127)

CTCTT CTGAAAAAAC AGAAGTAACG
 TTACCAACCA AAGACCGTAG CGGCAAAGAA ATTACTTTAC CCAAAGAAGC AACCAAAATT
 ATTTCCCTAG TGCCATCAAC AACAGAAGTG ATTGAAGACT TAGGTAAAAC CGACCAATTA
 ATCGCAGTTG ATACTCAAAG TAGTACAATG ATGACTGATT TAAAAAAATT ACCACAAATG
 GATATGATGG CTGTCGATGC CGAAAAATTG ATTGCCTTGA AACCACAAAT TGTTTATGTG
 AATGACATCA ATTTAGCTAG CTCAGAAAGT GTTTGGAAGC AAGTGGAAGA TGCTGGAATT
 ACAGTCGTTA ATATCCCCAC TAGTACAAGC ATCAAAGCAA TCAAAGAAGA CGTCCAATTC
 ATCGCTGATA GCTTATCTGA ACATGAAAAA GGACAAAAGT TAATCAAAAC AATGGATCAA
 GAAATCGACG AGTAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF033-4 (SEQ ID NO:128)

SSEKTEVTL PTKDRSGKEI TLPKEATKII SLVPSTTEVI EDLGKTDQLI
 AVDTQSSTMM TDLKKLPQMD MMAVDAEKLI ALKPQIVVYN DINLASSESV WKQVEDAGIT
 VVNIPTSTSI KAIKEDVQFI ADSESEHEKG QKLIKTMQDE IDF

EF034-1 (SEQ ID NO:129)

TAGGAGGGAG TAATCATSAA AAAAATCGGG TATTTTAGTT GTATTATTTT TTTCATGTTT
 TTGGTAGGTT GTAGTAATAA CAAAAAAGAA AACGGCAATC TTTTGAATGC CAGTTCGTTT
 CCTTTAATAC TCACCACGAT TATTGAAAAA GAAGAAGACC TAACGAAAGG TTCAATTTTT
 TTCAACAAGG ATAAAACCAT GACGCTTGAA AAAGAATATT TAGTTAATCC CAATAATGAA
 GACACAAAAA AAACAAGTAG AACAGAAAAA AAGGTATATA AAAATATTAA AATACAAGAA
 AATAAAGAGA GCTATGAAAT TATAGGTCAA TTGACAAAAA AAACGAAAAA AATAGAGTTT
 AAAAAAGTTG ATGAAGGTAA ACGTATATCT GATGCAGAAG GTAATGTGTA TGGTGATTTT
 GGTGGTAAAT AG

EF034-2 (SEQ ID NO:130)

MKKIGY FSCIIFFMFL VGCSNNKKN GNLLNASSFP LILTTIEKE EDLTGSIFF
 NKDKTMTLEK EYLVNPNED TKKTSRTEKK VYKNIKIQEN KESYEIIGQL DKKTKKIEFK
 KVDEGKRISD AEGNVYGDFG GK

EF034-3 (SEQ ID NO:131)

AGAA AACGGCAATC TTTTGAATGC CAGTTCGTTT
 CCTTTAATAC TCACCACGAT TATTGAAAAA GAAGAAGACC TAACGAAAGG TTCAATTTTT
 TTCAACAAGG ATAAAACCAT GACGCTTGAA AAAGAATATT TAGTTAATCC CAATAATGAA
 GACACAAAAA AAACAAGTAG AACAGAAAAA AAGGTATATA AAAATATTAA AATACAAGAA
 AATAAAGAGA GCTATGAAAT TATAGGTCAA TTGACAAAAA AAACGAAAAA AATAGAGTTT
 AAAAAAGTTG ATGAAGGTAA ACGTATATCT GATGCAGAAG GTAATGTGTA TGGTGATTTT
 GGTGGTAAAT AG

EF034-4 (SEQ ID NO:132)

KEN GNLLNASSFP LILTTIEKE EDLTGSIFF
 NKDKTMTLEK EYLVNPNED TKKTSRTEKK VYKNIKIQEN KESYEIIGQL DKKTKKIEFK
 KVDEGKRISD AEGNVYGDFG GK

EF035-1 (SEQ ID NO:133)

TAAACGAGAG GTGAGTTTAT GAAAACAAAA ATCGGAAAAA CAGTTATCTT GTCAGCATTT
 TTATTACAA GTTTCCTTT ACTGAGTGGT TGTACCTCGG CTGGCGAAGA GATGGAAAAA
 ACAATTGATC GACAGAAAGA AAAAGTCGAT AAAACGGTCG ATAAGCAGAA ACATAAAAAT
 GAAAATTCCA TGGAAAGTTA CGACGAAAAA GTTGACCGTT CTTTAGATAG TCAAGAAGAC
 AAAATCGATA CTACTGAGTA A

EF035-2 (SEQ ID NO:134)

MKTKI GKTVILSAFL FTSFLLLSGC TSAGEEMEKT IDRQKEKVDK TVDKQKHKNE
 NSMESYDEKV DRS LDSQEDK IDTTE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF035-3 (SEQ ID NO:135)

GATGGAAAAA

ACAATTGATC GACAGAAAAGA AAAAGTCGAT AAAACGGTCG ATAAGCAGAA ACATAAAAAAT
 GAAAATTCCA TGGAAAGTTA CGACGAAAAA GTTGACCGTT CTTTAGATAG TCAAGAAGAC
 AAAATCGATA CTACTGAG

EF035-4 (SEQ ID NO:136)

MEKT IDRQKEKVDK TVDKQKHKNE
 NSMESYDEKV DRS LDSQEDK IDTTE

EF036-1 (SEQ ID NO:137)

TAATTTTCAA GTCCTACATA TAATGGTAAA ATAGAATGGA TTGAAATTAA TTGGAGGAAT
 AATGAATCGA TGAAAAAAG ATTGCTATTA TTTATTGGTT TGGCAAGTAT ACTTACTTTG
 ACAGGATGTG CAAAATGGAT TGATCGTGGT GAATCCATCA CAGCGGTAGG CTCATCAGCT
 TTACAACCAT TAGTAGAGAC AGCGAGTGAG GAATATCAAA GCCAAAATCC GGGAAGATTT
 ATTAATGTCC AAGGTGGCGG AAGCGGAACA GGTCTGAGTC AAGTCCAATC TGGCGCGGTA
 GACATTGGTA ATTCTGATTT ATTTGCAGAA GAGAAAAAGG GCATCAAAGC GGAAGACTTA
 ATTGATCATA AAGTTGCTGT CGTTGGGATT ACACCAATCG TTAACAAAAA TGTCGGTGTC
 AAAGATATCT CAATGGAAAA TTAAAGAAA ATCTTTT TAG GTGAAGTAAC AAAGTGGAAA
 GAAGTTGGCG GGAAAGACCA AAAAATTGTT ATTTTGAATA GAGCGGCCGG TAGTGGTACG
 CGTGCGACTT TTGAAAAGTG GGTCTTGGGA GATAAACAG CCATTCGTGC GCAAGAACAA
 GATTCCAGCG GCATGGTTCG TTCCATTGTT TCTGATACAC CAGGAGCGAT TAGTTATACC
 GCATTTTCAT ATGTTACTGA TGAAGTAGCT ACSTTAAGTA TTGATGGTGT TCAGCCAACA
 GATGAAAATG TAATGAACAA TAAATGGATT ATTTGGTCTT ATGAACACAT GTACACTCGT
 AAAAAATCCAA GTGATTTAAC CAAAGAGTTT TTAGACTTTA TGTGTCAGA TGATATCCAA
 GAACGTGTGA TTGGTCAATT AGGGTATATT CCTGTTTCGA AAATGGAAAT TGAACGGGAT
 TGGCAAGGAA ATGTCATTAA ATAA

EF-36-2 (SEQ ID NO:138)

MKKRLLLF IGLASILT LT GCAKWIDRGE SITAVGSSAL
 QPLVETASEE YQSQNPGRFI NVQGGSGTG LSQVQSGAVD IGNSDLFAEE KKGIIKAEDLI
 DHKVAVVGIT PIVKNVGVK DISMENLKKI FLGEVTNWKE LGGKDQKIVI LNRAAGSGTR
 ATFEKWVLGD KTAIRAQEQD SSGMVRISVS DTPGAISYTA FSYVTDEVAT LSIDGVQPTD
 ENVMNNKWI WSYEYMYTRK NPSDLTKEFL DFMLSDDIQE RVIGQLGYIP VSKMEIERDW
 QGNVIK

EF036-3 (SEQ ID NO:139)

GAT TGATCGTGGT GAATCCATCA CAGCGGTAGG CTCATCAGCT
 TTACAACCAT TAGTAGAGAC AGCGAGTGAG GAATATCAAA GCCAAAATCC GGGAAGATTT
 ATTAATGTCC AAGGTGGCGG AAGCGGAACA GGTCTGAGTC AAGTCCAATC TGGCGCGGTA
 GACATTGGTA ATTCTGATTT ATTTGCAGAA GAGAAAAAGG GCATCAAAGC GGAAGACTTA
 ATTGATCATA AAGTTGCTGT CGTTGGGATT ACACCAATCG TTAACAAAAA TGTCGGTGTC
 AAAGATATCT CAATGGAAAA TTAAAGAAA ATCTTTT TAG GTGAAGTAAC AAAGTGGAAA
 GAAGTTGGCG GGAAAGACCA AAAAATTGTT ATTTTGAATA GAGCGGCCGG TAGTGGTACG
 CGTGCGACTT TTGAAAAGTG GGTCTTGGGA GATAAACAG CCATTCGTGC GCAAGAACAA
 GATTCCAGCG GCATGGTTCG TTCCATTGTT TCTGATACAC CAGGAGCGAT TAGTTATACC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCATTTTCAT ATGTTACTGA TGAAGTAGCT ACGTTAAGTA TTGATGGTGT TCAGCCAACA
 GATGAAAAATG TAATGAACAA TAAATGGATT ATTTGGTCTT ATGAACACAT GTACACTCGT
 AAAAATCCAA GTGATTTAAC CAAAGAGTTT TTAGACTTTA TGTGTCAGA TGATATCCAA
 GAACGTGTGA TTGGTCAATT AGGGTATATT CCTGTTTCGA AAATGGAAAT TGAACGGGAT
 TGGCAAGGAA ATGTCATTAA A

EF036-4 (SEQ ID NO:140)

IDRGE SITAVGSSAL

QPLVETASEE YQSQNPGRFI NVQGGGSGTG LSQVQSGAVD IGNSDLFAEE KKGIIKAEDLI
 DHKVAVVGIT PIVNKNVGK DISMENLKKI FLGEVTNWKE LGGKDQKIVI LNRAAGSGTR
 ATFEKWVLGD KTAIRAEQD SSGMVRSIVS DTPGAISYTA FSYVTDEVAT LSIDGVQPTD
 ENVMNNKWII WSYEHMYTRK NPSDLTKEFL DFMLSDDIQE RVIGQLGYIP VSKMEIERDW
 QGNVIK

EF037-1 (SEQ ID NO:141)

TGAGTGATG ATTACTCATT TCCCTTTGAA TCAGTTATGA TAAAGGAAGA AATAAATAAA
 TTTTGTGGAG GGATTTTCAT GAAAATGTCT AAAGTACTCA CCACTGTTTT GACGGCAACT
 GCTGCTCTTG TGTGCTTAG TGCTTGTTC TCTGATAAAA AACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAA

EF037-2 (SEQ ID NO:142)

MKMSK VLTTVLTATA ALVLLSACSS DKKTDSSSSS
 KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSENFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF037-3 (SEQ ID NO:143)

AACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA A

EF037-4 (SEQ ID NO:144)

TDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSENFNIVH GTVKGDIEVK ANGFTLNGTK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF038-1 (SEQ ID NO:145)

TAATGGCCAT TTCGTCTACT AATAAAGAGG ATGAAGCTAC TCAAATGGCG TTGGCAATGG
 AACAAGSATC AAAAAAAGG AGAAGTGAGC ATGAAAAAAG TACTACCTTT TATTGCCTTA
 GTCGGCTTGT TATTGTGTC AGGTTSTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGGAACTAGA AAATAAAAGT CCAACTACTA CTTACACTTT TTTTGATGAT
 GAAACTTTTT CGAGGTATAA TTCAAAAATT AGTGATAGTG GAACGTACTC TTACGATGAA
 AATAATAAAA AACTCACTTT GGATATAAAA AATAAAGAAC AATTAATAAT GGAAAATGTT
 GAATATAAAG ACGGTAAATT AAAAGGTGAA ATTGGAGGCG AGAAGGACTC TGATAAAAAA
 TNGAATAAGA GGTGTCTTTG A

EF038-2 (SEQ ID NO:146)

M KLLKWRWQWN KDHKKGEVSM KKVLPFIALV GLLLLSGCGT DMKKILTADG
 KWELLENKSP TTTYTFFDDE TFSRYNSKIS DSGTYSYDEN NKKLTLDIKN KEQLIMENVE
 YKDGKLGKEI GGEKDSKX NKRCL

EF038-3 (SEQ ID NO:147)

TTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGGAACTAGA AAATAAAAGT CCAACTACTA CTTACACTTT TTTTGATGAT
 GAAACTTTTT CGAGGTATAA TTCAAAAATT AGTGATAGTG GAACGTACTC TTACGATGAA
 AATAATAAAA AACTCACTTT GGATATAAAA AATAAAGAAC AATTAATAAT GGAAAATGTT
 GAATATAAAG ACGGTAAATT AAAAGGTGAA ATTGGAGGCG AGAAGGACTC TGATAAAAAA
 TNGAATAAGA GGTGTCTTTG A

EF038-4 (SEQ ID NO:148)

CGT DMKKILTADG
 KWELLENKSP TTTYTFFDDE TFSRYNSKIS DSGTYSYDEN NKKLTLDIKN KEQLIMENVE
 YKDGKLGKEI GGEKDSKX NKRCL

EF039-1 (SEQ ID NO:149)

TAAATATATC AAAAAGAAAA AAGGGGATTA CCAACCATGA AAAAGAAAA AGTTTTTAGT
 GCGCTTACCT TATTAACCTT TAGTACGTTG TTGATTGCAG GCTGTGCTGG CGGAGCCAAC
 TCTGCAACAG ATAAATCAAG TGCAGCTAGC TCAAGCACTG CAGTCTCTAG TTCAGCAGAA
 GCAGCTAAAG AGCAATCAAA AGGACAAGAA TTAACAGAAA TTTTATCCAG TACTGATTGG
 CAAGGCACAA AAGTTTACGA CAAAAATNAT AATAATTTAA CAGCAGAAAA TGCTAATTTT
 ATTGGTTTTAG CAAAATATGA TGGTGAAACA GGTTTTTATG AATTTTTCGA CAAAGAAACA
 GGTGAAACCC GTGGCGATGA AGGCACATTC TTTGTGACAG ACGATGGCGA AAAGCGTATC
 TTAATTTCCG ATACACAAAA CTATCAAGCG GTGGTCGATT TAACGGAAGT GACGAAAGAT
 AAATTTACCT ATAAGCGAAT GGGTAAAGAT AAAGACGGGA AAGATGTAGA AGTCTTTGTA
 GAACATATCC CTTATTCTGA CGAGAAATTA ACCTTTACGA ACGGCCGTAA AGATTTAGAA
 ACAGAACTG CCAAGATTGT TACCAATGAA CCTGGGGATG ACATTTTAGG GGCCACATTA
 TGGAATGGCA CGAAAGTTT AGATGAAGAC GGTAAACGATG TTACTGAAGC AAATAAAATG
 TTTATTAGTT TAGCGAAATT TGATAATAAA ACAAGTAAAT ATGAATTCCT TGATTTAGAA
 ACGGGTAAAA CACGTGGAGA TTTTGGTTAC TTCCAAGTAA TTGATAATAA CAAAATCCGT
 GCTCACGTTT CAATTGGTGA CAATAAATAT GGAGCTGCAT TAGAATTAAC AGAATTAAT
 GATAACGTT TTACGTATAC ACGAATGGGT AAAGACAACA ATGGCAAAGA AATTAAAGTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTTGTAGAAC ATGAACCATA TGAAGGAGAC TTTACGCCAG ACTTCACGTT CTAA

EF039-2 (SEQ ID NO:150)

MKKKKVFSALTLTTFSTLLIAGCAGGANSATDKSSAASSSTAVSSSAEA
 AKEQSKGQELTEILSSTDWQGTKVYDKNXNLTAEANANFI GLAKYDGETG FYEFFDKETG
 ETRGDEGTFFVTDDGEKRILISDTQNYQAVVDLTEVTKDKFTYKRMGKDKDGKDVEVFVE
 HIPYSDEKLTFTNGRKDLETETGKIVTNPEGDDILGATLWNGTKVLDEGNDVTEANKMF
 ISLAKFDNKT SKYEFFDLETGKTRGDFGYFQVIDNNKIRAHVSIKDNKYGAALELTELND
 KRFTYTRMGKDNNGKEIKVFVEHEPYEGDFTPDFTF

EF039-3 (SEQ ID NO:151)

TGCAACAGATAAATCAAGTGCAGCTAGCTCAAGCACTGCAGTCTCTAGTTCAGCAGAA
 GCAGCTAAAGAGCAATCAAAAGGACAAGAAATAACAGAAAATTTATCCAGTACTGATTGG
 CAAGGCACAAAGTTTACGACAAAATNATAATAATTTAACAGCAGAAAA TGCTAATTTT
 ATTGGTTTAGCAAAATATGATGGTGAAACAGGTTTTTTATGAATTTTTCGACAAAGAAACA
 GGTGAAACCCGTGGCGATGAGGCACATTC TTTGTGACAGACGATGGCGA AAAGCGTATC
 TTAATTTTCGATACACAAAACTATCAAGCGGTGGTTCGATT TAACGGAAGTGACGAAAGAT
 AAATTTACCTATAAGCGAATGGGTAAAGATAAGACGGGAAGATGTAGAAGTCTTTGTGA
 GAACATATCCCTTATTCTGACGAGAAATTAACCTTTACGACGGCCGTAAAGATTAGAA
 ACAGAACTGCAAGATTGTACCAATGAACTGGGGATGACATTTTAGGGGCCACATTA
 TGAATGGGACGAAAGTTTTAGATGAAGACGGTAACGATGTTACTGAAGCAAAATAAATG
 TTTATTAGTTTACGCAAAATTGATAATAAAACAAGTAAATATGAATTCCTTGTATTAGAA
 ACGGGTAAAAACGTGGGAGATTTTGGTTACTTCCAAGTAAATGATAATAACAAATCCGT
 GCTCACGTTTCAATTGGTGAATAAATATGGAGTGCATAGAAATTAACAGAATTAAT
 GATAACGTTTACGTATACACGAATGGGTAAAGACAACAATGGCAAAGAATTAAGATC
 TTTGTAGAACATGAACCATA TGAAGGAGAC TTTACGCCAGACTTCACGTTCTAA

EF039-4 (SEQ ID NO:152)

ATDKSSAASSSTAVSSSAEA
 AKEQSKGQELTEILSSTDWQGTKVYDKNXNLTAEANANFI GLAKYDGETG FYEFFDKETG
 ETRGDEGTFFVTDDGEKRILISDTQNYQAVVDLTEVTKDKFTYKRMGKDKDGKDVEVFVE
 HIPYSDEKLTFTNGRKDLETETGKIVTNPEGDDILGATLWNGTKVLDEGNDVTEANKMF
 ISLAKFDNKT SKYEFFDLETGKTRGDFGYFQVIDNNKIRAHVSIKDNKYGAALELTELND
 KRFTYTRMGKDNNGKEIKVFVEHEPYEGDFTPDFTF

EF040-1 (SEQ ID NO:153)

TAGATTAGAA CCACTGGAGA AAAATCTCATATTTCTCTCGAGGAAAGGAA GTTGAGCACA
 ATGAACAAAAAATTTTAATGGGGCTATTAAGTGTCTGTA CCATTCCATTACTTGCTGCG
 TGTCAAGGAGGAGAAACACC TTCCGCAGCGTCAAAAAATA GTCAAACGGTGACTACTCAA
 AGTAGTGCAA AACTGAAAGCACCAGTACAACCCGTTCCGTAGCTCAAAC AACATCAAAA
 GAGGAAGTGAAGAACCAGATGAAGACCTATGAAGTGGGTGCGCTTTTAGAAGCAGCCAAT
 CAACGAGATACGAAGAAGGTCAAGGAAATT TTACAAGATACTACTTATCAAGTGGATGAA
 GTCGACACAG AAGGCAACACACCGCTCAATATCGCTGTTCACAATAATGACATTGAGATT
 GCAAAAGCGTGTATTGATCGGGGTGCCGATATTAATCTGC AAAACAGCATTAGTGATAGT
 CCTATCTTTATGCGGGAGCGCAAGGACGTACGGAGATTTAGCGTATATGTTAAACAT
 GCGACCCAGATTTAAATAAGCATAACCGTTACGGTGGCAATGCGTTAAT TCCGGCAGCT
 GAAAAAGGACATATTGACAA TGTGAAGCTC TTGTTAGAAGATGGACGAGAAGACATAGAT
 TTCCAAAATGACTTTGGCTATACAGCATTTATTGAGGCAGTGGGTTACGTGAAGGGAAC
 CACTTTTACC AAGATATTGTAAAATTGTTATGGAAAAATG GTGCGGATCAATCCATTAA
 GACAATTCTGTCGAACAGCAATGGACTATGCCAATCAAAAGGTTATACGGAAATTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAATTTTAG TACAGTACAA CTAA

EF040-2 (SEQ ID NO:154)

M NKKILMGLLS VVTIPLAAC QGGETPSAAS KNSQTVTTQS
 SAKTESTSTT RSVAQTTSKE EVKEPMKTYE VGALLEAANQ RDTKKVKEIL QDTTYQVDEV
 DTEGNTPLNI AVHNNIDIEIA KALIDRGADI NLQNSISDSP YLYAGAQRRT EILAYMLKHA
 TPDLNKHNRK GGNALIPAAE KGHIDNVKLL LEDGREDIDF QNDFGYTALI EAVGLREGNQ
 LYQDIVKLLM ENGADQSIKD NSGRTAMDYA NQKGYTEISK ILAQYN

EF040-3 (SEQ ID NO:155)

AGCG TCAAAAAATA GTCAAACGGT GACTACTCAA
 AGTAGTGCAA AAACGTAAAG CACCAGTACA ACCCGTTCCG TAGCTCAAAC AACATCAAAA
 GAGGAAGTGA AAGAACCGAT GAAGACCTAT GAASTGGGTG CGCTTTTAGA AGCAGCCAAT
 CAACGAGATA CGAAGAAGGT CAAGGAAAT TACAAAGATA CTACTTATCA AGTGGATGAA
 GTCSACACAG AAGGCAACAC ACCGCTCAAT ATCGCTGTTC ACAATAATGA CATTGAGATT
 GCAAAAGCGT TGATTGATCG GGGTGCCGAT ATTAATCTGC AAAACAGCAT TAGTGATAGT
 CCTATCTTT ATGCGGGAGC GCAAGGACGT ACGGAGATT TAGCGTATAT GTTAAACAT
 GCGACCCAG ATTTAAATAA GCATAACCGT TACGGTGGCA ATGCGTTAAT TCCGGCAGCT
 GAAAAAGGAC ATATTGACAA TGTGAAGCTC TTGTTAGAAG ATGGACGAGA AGACATAGAT
 TTCCAAATG ACTTTGGCTA TACAGCATTG ATTGAGGCAG TGGGGTTACG TGAAGGGAAC
 CAACCTTACC AAGATATTGT AAAATTGTTA ATGGAAATG GTGCGGATCA ATCCATTAAA
 GACAATTCTG GTCGAACAGC AATGGACTAT GCCAATCAAA AAGGTTATAC GGAAATTAGT
 AAAATTTTAG CACAGTACAA C

EF040-4 (SEQ ID NO:156)

AS KNSQTVTTQS
 SAKTESTSTT RSVAQTTSKE EVKEPMKTYE VGALLEAANQ RETKKVKEIL QDTTYQVDEV
 DTEGNTPLNI AVHNNIDIEIA KALIDRGADI NLQNSISDSP YLYAGAQRRT EILAYMLKHA
 TPDLNKHNRK GGNALIPAAE KGHIDNVKLL LEDGREDIDF QNDFGYTALI EAVGLREGNQ
 LYQDIVKLLM ENGADQSIKD NSGRTAMDYA NQKGYTEISK ILAQYN

EF041-1 (SEQ ID NO:157)

TAATTATTAA NTTCTGATTT TTCAGAAAAT ACAGATTGCA TTATTTTAGG AGGCAACACT
 ATGAAATTGA AAAAGTCATT AACATTCGGT GTGATTACAT TATTTAGCGT AACAACTTTA
 GCGGCTGTG GAGGCGGCGG AACGTCAGAT AGCTCAAGCG CGTCTGGTGG CGGTAAGGCA
 AGTGGCGAAC AAGTTTTACG TGTCACAGAA CAACAAGAAA TGCCAACAGC TGATTTATCA
 CTAGCAACAG NCAGAATTAG TTTTATTGCA TTAAATAATG TATATGAAGG AATTATCGT
 TTAGACAAAG ATAACAAAGT CCAACCTGCA GGTGCAGCGG AAAAAGCAGA AGTTTCTGAA
 GATGGACTAA CATAAAAAT TAAATTAAAT AAAGATGCAA AATGGTCAGA CGGTAAACCA
 GTGACTGCTA ATGACTATGT TTACGGATGG CAACGAACAG TTGATCCAGC GACAGCTTCT
 GAATATGCTT ATCTGTATGC CTCTGTAAAA AATGGTGATG CCATTGCTAA AGGGGAAAAA
 GATAAATCAG AATTAGGAAT TAAAGCAGTC AGTGATACAG AATTAGAAAT CACTTTAGAA
 AAAGCAACAC CATACTTTGA TTAATTATTA GCTTTCCCAT CATTCTTCCC GCAACGTCAA
 GACATTGTGG AAAAATATGG TAAAAATTAT GCATCAACA GCGAAAGTGC TGTCTACAAT
 GGTCCATTG TCTTAGACGG CTTTGATGGT CCTGGTACAG ATACAAAATG GTCATTCAAG
 AAAACGATC AATATTGGGA TAAAGATACT GTGAAACTGG ACTCAGTAGA TGTGAATGTC
 GTGAAAGAAT CACCAACCGC GTTGAACCTG TTCCAAGATG GACAAACAGA CGATGTCGTT
 CTTTCTGGTG AATTAGCCCA ACAAATGGCC AATGACCCAG CTTTGTAGT TCAAAAAGAA
 GCATCAACAC AATATATGGA ACTAAATCAA CGTGATGAAA AATCACCATT TAGAAATGCC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACTTACGTA AAGCAATTTC TTACTCAATC GACCGTAAAG CGTTAGTTGA ATCAATCCTT
AGGGGATGG

EF041-2 (SEQ ID NO:158)

M KLKKSITFGV ITLFSVTTLA ACGGGGTSDDS SSASGGGKAS
GEQVLRVTEQ QEMPTADLSL ATXRISFIAL NNVYEGYRL DKDNKVQPAG AAKEAEVSED
GLTYKIKLNK DAKWSDGKPV TANDYVYGWQ RTVDPATASE YAYLYASVKN GDAIAKGEKD
KSELGIKAVS DTELEITLEK ATPYFDYLLA FPSFFPQRQD IVEKYGKNYA SNSESAVYNG
PFVLDGFDGP GTDTKWSFKK NDQYWDKDTV KLDSVDVNVV KESPTALNLF QDGQTDVVVL
SGELAQQMAN DPAFVSQKEA STQYMELNQR DEKSPFRNAN LRKAISYSID RKALVESILR
GW

EF041-3 (SEQ ID NO:159)

TTGTG GAGGCGGCGG AACGTCAGAT AGCTCAAGCG CGTCTGGTGG CGGTAAGGCA
AGTGGCGAAC AAGTTTTACG TGTCACAGAA CAACAAGAAA TGCCAACAGC TGATTTATCA
CTAGCAACAG NCAGAATTAG TTTTATTGCA TTAAATAATG TATATGAAGG AATTTATCGT
TTAGACAAAG ATAACAAAGT CCAACCTGCA GGTGCAGCGG AAAAAGCAGA AGTTTCTGAA
GATGGACTAA CATACAAAAT TAAATTAAAT AAAGATGCAA AATGGTCAGA CGGTAAACCA
GTGACTGCTA ATGACTATGT TTACGGATGG CAACGAACAG TTGATCCAGC GACAGCTTCT
GAATATGCTT ATCTGTATGC CTCTGTAAAA AATGGTGATG CCATTGCTAA AGGGGAAAAA
GATAAATCAG AATTAGGAAT TAAAGCAGTC AGTGATACAG AATTAGAAAT CACTTTAGAA
AAAGCAACAC CATACTTTGA TTACTTATTA GCTTTCCCAT CATTCTTCCC GCAACGTCAA
GACATTGTGG AAAAATATGG TAAAAATTAT GCATCAAACA GCGAAAGTGC TGTCTACAAT
GGTCCATTCG TCTTAGACGG CTTTGATGGT CCTGGTACAG ATACAAAATG GTCATTCAAG
AAAAACGATC AATATTGGGA TAAAGATACT GTGAAACTGG ACTCAGTAGA TGTGAATGTC
GTGAAAGAAT CACCAACCGC GTTGAACCTG TTCCAAGATG GACAAACAGA CGATGTCGTT
CTTTCTGGTG AATTAGCCCA ACAAATGGCC AATGACCCAG CTTTGTGTTAG TCAAAAAGAA
GCATCAACAC AATATATGGA ACTAAATCAA CGTGATGAAA AATCACCATT TAGAAATGCG
AACTTACGTA AAGCAATTTC TTACTCAATC GACCGTAAAG CGTTAGTTGA ATCAATCCTT
AGGGGATGG

EF041-4 (SEQ ID NO:160)

CGGGGTSDDS SSASGGGKAS
GEQVLRVTEQ QEMPTADLSL ATXRISFIAL NNVYEGYRL DKDNKVQPAG AAKEAEVSED
GLTYKIKLNK DAKWSDGKPV TANDYVYGWQ RTVDPATASE YAYLYASVKN GDAIAKGEKD
KSELGIKAVS DTELEITLEK ATPYFDYLLA FPSFFPQRQD IVEKYGKNYA SNSESAVYNG
PFVLDGFDGP GTDTKWSFKK NDQYWDKDTV KLDSVDVNVV KESPTALNLF QDGQTDVVVL
SGELAQQMAN DPAFVSQKEA STQYMELNQR DEKSPFRNAN LRKAISYSID RKALVESILR
GW

EF044-1 (SEQ ID NO:161)

TAAGATAAAA TTAGTTATAG CGTCTATAGG AGGAATAGTA TGAAAAAATT AGTTTGTGTT
ATTTTAGTTA TTTTTTTAAC AGGTGTAGT TCTCAAAAAG CGAATGAACC TAAAAACAA
GAAAAATCTA CCAATCATAC AACATCAATA AAAAGCAGTA CTAATCATTA CAGTTCTAGC
ATAGAAACAA GCTCTAATAA TAACTAAAA GAAACTTCAG AAAGTGCCAG CACCCTCAA
ACTTCGTCAG AGTCGAAAAA TGAAGTATCT ACAAATGTCG AAGAAGCAAA TTCTTTAGAA
GCAACACCTT ATGCTGTCGA TCTTAGTAGC TTAAACAATC CACTCGTATT TAATTTTAAA
GGAATGAATG TGCCAACCTC AATTACGTTA GAGAACTTAA ATTCAACACC AACTGCTACC
TTCCGAACCTA AATTGTTTGG GGCTGAAAAT GGTCAAGTGA AAGAAGCCAT TAATAAATAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. jaccalis* Genes.

GAGGTATCTA TAAATACAAT TCCTACAAAA GAGATTAGAA TATTTTCAGC G3CCGATAAC
 AGTATTCGCA CCGTTAAAST AAATACAGAA TTAATTTTAG GAACTAATAT TTCTTCAAAC
 GATGAACAAA ATAGATCGGG CACTTTATAC TTATTCAACA ATAAAAATGG TTCGATATCT
 TTAATCACTC CTAACACG TGGCAATGTT ACGGATGATC AAAAAGACGT TATGCTAGAA
 GTAATTCAAT AA

EF044-2 (SEQ ID NO:162)

MKKLVCVI LVIFLTGSS QKANEPKKQE NSTNHTTSIK SSTNHYSSSI
 ETSSNNKLKE TSESASTTQT SSKSKNEVST NVEEANSLEA TPYAVDLSSL NNPLVFNFKG
 MNVPTSITLE NLNSTPTATF RTKLFGAENG QVKEAINKYE LSINTIPTKE IRIFSAADNS
 IRTVKVNTL ILGTNISSND EQNRSGTLYL FNNKNGSISL ITPNYAGNVT DDQKDVMLEV
 IQ

EF044-3 (SEQ ID NO:163)

TTGTAGT TCTCAAAAAG CGAATGAACC TAAAAAACAA
 GAAATTCTA CCAATCATAC AACATCAATA AAAAGCAGTA CTAATCATT AAGTTCTAGC
 ATAGAAACAA GCTCTAATAA TAACTAAAA GAACTTCAG AAAGTGCCAG CACCACTCAA
 ACTTCGTCAA AGTCGAAAAA TGAAGTATCT ACAAATGTCG AAGAAGCAAA TTCTTTAGAA
 GCAACACCTT ATGCTGTCCA TCTTAGTAGC TTAAACAATC CACTCGTATT TAATTTTAAA
 GGAATGAATG TGCCAACTTC AATTACGTTA GAGAACTTAA ATTCAACACC AACTGCTACC
 TTCCGAAC TAATTGTTTGG GGCTGAAAAT GGTCAAGTGA AAGAAGCCAT TAATAAATAT
 GAGCTATCTA TAAATACAAT TCCTACAAAA GAGATTAGAA TATTTTCAGC GGCCGATAAC
 AGTATTCGCA CCGTTAAAGT AAATACAGAA TTAATTTTAG GAACTAATAT TTCTTCAAAC
 GATGAACAAA ATAGATCGGG CACTTTATAC TTATTCAACA ATAAAAATGG TTCGATATCT
 TTAATCACTC CTAACACG TGGCAATGTT ACGGATGATC AAAAAGACGT TATGCTAGAA
 GTAATTCAA

EF044-4 (SEQ ID NO:164)

CSS QKANEPKKQE NSTNHTTSIK SSTNHYSSSI
 ETSSNNKLKE TSESASTTQT SSKSKNEVST NVEEANSLEA TPYAVDLSSL NNPLVFNFKG
 MNVPTSITLE NLNSTPTATF RTKLFGAENG QVKEAINKYE LSINTIPTKE IRIFSAADNS
 IRTVKVNTL ILGTNISSND EQNRSGTLYL FNNKNGSISL ITPNYAGNVT DDQKDVMLEV
 IQ

EF045-1 (SEQ ID NO:165)

TAGCCAAAAA ATGAGGGAGG AAAAGAGATG AACAAGAAAC GGATTTTAGG TGCAATCACG
 TTAGCTTCTG TGTTAGTATT CGGGTTAGCT GCATGTGGTG GCGGCAATAA AGGCGGGGGC
 AATAAAGCAA CGGAAACAGA AGACATTTCA AAAATGCCAA TCGCTGTTAA AAATGATAAA
 AAAGCAATTG ATGGCGGTAC ATTAGATGTC GCTGTAGTTA TGGATACACA ATTCCAAGGA
 CTTTTCAGC AAGAATTTTA TCAAGACAAC TATGATGCAC AATACATGCT TCCACGGTA
 CAGCCATTAT TTAACAATGA TGCAGACTTT AAGATTGTCG ATGGGGGTCC TGCGGATCTG
 AAATTAGATG AAGATGCCAA TACAGCAACC ATTAAATTAC GTGACAATTT GAAATGGTCT
 GACGGTAAAG ATGTGACAGC CGATGACGTG ATTTTCTCTT ATGAAGTCAT TGGTCATAAA
 GACTATACAG GGATTCGTTA TGATGATAAC TTTACGAATA TTGTTGGCAT GGAAGACTAC
 CATGATGGTA AATCGCCAAC CATTTCTGGC ATAGAAAAAG TCAATGATAA AGAAGTTAAA
 ATCACTTATA AAGAAGTTCA CCCAGGAATG CAACAATTAG GTGGCGGTGT TTGGGGCTCA
 GTTTTACCAA AACATGCCTT TGAAGGAATT GCTGTTAAAG ACATGGAATC AAGCGATGCA
 GTTCGTAAAA ACCCTGTGAC TATTGGACCA TACTACATGA GTAATATTGT GACAGGTGAA
 TCTGTTGAAT ACCTACCAA TGAGCATTAC TACGGTGGTA AACCTAAATT AGATAAATTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGTTCAAAT CTGTTCCCTTC TGCGAGCATT GTAGAAGCGA TGAAAGCGAA ACAATACGAT
 ATTGCAATTAT CAATGCCAAC AGATACGTAT CCAACATACA AAGATACTGA AGGGTATCAA
 ATCTTAGGAC GTCCCGAACA AGCCTACACG TATATTGGCT TTAAATGGG TACGTTTGAC
 AAAGAAACAA ATACAGTGAA ATACAATCCA AAAGCTAAAA TGGCAGATAA AAGCTTACGT
 CAAGCCATGG GCTATGCAAT TGACAATGAT GCAGTCGGCC AAAAATTCTA CAACGGCTTA
 CGAACAGGGG CAACAACGTT AATCCCACCA GTCTTCAAGA GCTTGCATGA TAGCGAAGCG
 AAAGGCTATA CGCTTGATTT AGACAAAGCG AAAAAATTAT TAGACGATGC TGGTTATAAA
 GACGTAGACG GCGATGGCAT TCGCGAAGAC AAAGAAGGCA AACCCTAGA AATCAAGTTT
 GCTTCAATGT CAGGCGGCGA AACTGCACAA CCACTTGCTG ATTACTATGT CCAACAATGG
 AAAGAAATTG GCTTAAACGT AACGTATACA ACAGGACGCT TAATTGATTT CCAAGCATTC
 TATGATAAAT TGAAAAATGA TGACCCAGAA GTAGATATCT ATCAAGGCGC GTGGGGCACA
 GGTTTCAGATC CTTCACCAAC CGGCTTATAT GGTCCAAACT CAGCCTTTAA CTATACACGT
 TTTGAGTCAG AAGAAAAATC TAAATTACTT GATGCGATTG ATTCAAAAGC ATCATTTGAT
 GAAGAAAAAC GTAAAAAAGC CTTCTACGAT TGGCAAGAGT ATGCCATTGA TGAAGCGTTT
 GTAATCCCAA CGCTTTACAG AAATGAAGTC TTGCCTGTCA ACGACCGTGT AGTTGACTTT
 ACTTGGGCAG TTGATACGAA AGATAATCCA TGGGCAACGG TGGGTGTCAC AGCAGACTCA
 CGGAAATAA

EF045-2 (SEQ ID NO:166)

MN KKRILGAIL ASVLVFLAA CGGNGKGGN KATETEDISK MPIAVKNDKK
 AIDGGTLDVA VVMDTQFQGL FQQEFYQDNY DAQYMLPTVQ PLFNNDADFK IVDGGPADLK
 LDEDANTATI KLRDNLKWSG GKDVTTADDVI FSYEVIGHKD YTGIRYDDNF TNIVGMEDYH
 DGKSPTISGI EKVDNKEVKI TYKEVHPGMQ QLGGGVWGSV LPKHAFEGIA VKDMESSDAV
 RKNPVTIGPY YMSNIVTGES VEYLPNEHYG GGKPKLDKLV FKSVPASIV EAMKAKQYDI
 ALSMPTDTYP TYKDTQYQI LGRPEQAYTY IGFKMGTDFK ETNTVKYNPK AKMADKSLRQ
 AMGYAIDNDA VGQKFYNGLR TGATTLIPPV FKSLHDSEAK GYTLDDLKAK KLLDDAGYKD
 VDGDGIREDK EGKPLEIKFA SMSGGETAQP LADYYVQQWK EIGLNVYTT GRLIDFQAFY
 DKLNDDPEV DIYQGAWGTG SDPSPTGLYG PNSAFNYTRF ESEENTKLLD AIDSASFDE
 EKRRKAFYDW QEYAIDEAFV IPTLYRNEVL PVNDRVVDFT WAVDTKDNPW ATVGVTADSR
 K

EF045-3 (SEQ ID NO:167)

ATGTGGTG GCGGCAATAA AGCGGGGGG
 AATAAAGCAA CGGAAACAGA AGACATTTCA AAAATGCCAA TCGCTGTAA AAATGATAAA
 AAAGCAATTG ATGGCGGTAC ATTAGATGTC GCTGTAGTTA TGGATACACA ATTCCAAGGA
 CTTTTCCAGC AAGAATTTTA TCAAGACAAC TATGATGCAC AATACATGCT TCCAACGGTA
 CAGCCATTAT TTAACAATGA TGCAGACTTT AAGATTGTCG ATGGGGGTCC TGCGGATCTG
 AAATTAGATG AAGATGCCAA TACAGCAACC ATTAAATTAC GTGACAATTT GAAATGGTCT
 GACGGTAAAG ATGTGACAGC CGATGACGTG ATTTTCTCTT ATGAAGTCAT TGGTCATAAA
 GACTATACAG GGATTCGTTA TGATGATAAC TTTACGAATA TTGTTGGCAT GGAAGACTAC
 CATGATGGTA AATCGCCAAC CATTTCTGGC ATAGAAAAAG TCAATGATAA AGAAGTTAA
 ATCACTTATA AAGAAGTTCA CCCAGGAATG CAACAATTAG GTGGCGGTGT TTGGGGCTCA
 GTTTTACCAA AACATGCCTT TGAAGGAATT GCTGTAAAG ACATGGAATC AAGCGATGCA
 GTTCGTAAAA ACCCTGTGAC TATTGGACCA TACTACATGA GTAATATTGT GACAGGTGAA
 TCTGTTGAAT ACCTACCAA TGAGCATTAC TACGTTGGTA AACCTAAAT AGATAAATTA
 GTGTTCAAAT CTGTTCCCTC TGCGAGCATT GTAGAAGCGA TGAAAGCGAA ACAATACGAT
 ATTGCAATTAT CAATGCCAAC AGATACGTAT CCAACATACA AAGATACTGA AGGGTATCAA
 ATCTTAGGAC GTCCCGAACA AGCCTACACG TATATTGGCT TTAAATGGG TACGTTTGAC
 AAAGAAACAA ATACAGTGAA ATACAATCCA AAAGCTAAAA TGGCAGATAA AAGCTTACGT
 CAAGCCATGG GCTATGCAAT TGACAATGAT GCAGTCGGCC AAAAATTCTA CAACGGCTTA
 CGAACAGGGG CAACAACGTT AATCCCACCA GTCTTCAAGA GCTTGCATGA TAGCGAAGCG
 AAAGGCTATA CGCTTGATTT AGACAAAGCG AAAAAATTAT TAGACGATGC TGGTTATAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GACGTAGACG GCGATGSCAT TCGCGAAGAC AAAGAAGSCA AACCCTAGTA AATCAAGTTT
 GCTTCAATGT CAGGCGGCGA AACTGCACAA CCACCTGCTG ATTACTATGT CCAACAATGG
 AAAGAAATTS GCTTAAAGST AACGTATACA ACAGGAGGCT TAATTGATTT CCAAGCATTC
 TATGATAAAT TGAAAAATGA T3ACCCAGAA GTAGATATCT ATCAAGGCGC GTGGGGCACA
 GGTTCAGATC CTTCACCAAC CGGCTTATAT GGTCCAACT CAGCCTTTAA CTATACACGT
 TTTGAGTCAG AAGAAAAATAC TAAATTACTT GATGCGATTG ATTCAAAAGC ATCATTTGAT
 GAAGAAAAAC GTAAAAAAGC CTTCTACGAT TGGCAAGAGT ATGCCATTGA TGAAGCGTTT
 GTAATCCCAA CGCTTTACAG AAATGAAGTC TTGCTGTCA ACGACCGTGT AGTTGACTTT
 ACTTGGGCAG TTGATACGAA AGATAATCCA TGGGCAACGG TGGGTGTCAC AGCAGACTCA
 CGGAAA

EF045-4 (SEQ ID NO:168)

CGGGNKGGG: KATETEDISK MPIAVKNDKK
 AIDGGTLDVA VVMDTQFQGL FQQEFYQDNY IAQYMLPTVQ PLFNNDADFK IVDGGPADLK
 LDEDANTATI KLRDNLKWSG GHDVTADDVI FSYEVIGHKD YTGIRYDDNF TNIVGMEDYH
 DGKSPTISGI EKVNDKEVKI TYKEVHPGMQ CLGGGVWGSV LPKHAFEGIA VKDMESSDAV
 RKNPVTIGPY YMSNIVTGES VEYLPNEHY GSKPKLDKLV FKSVPASIV EAMKAKQYDI
 ALSMPTDTYF TYKDTEGYQI LGRPEQAYTY IGFKMGTFDK ETNTVKYNPK AKMADKSLRQ
 AMGYAIDNDA VGQKPYNGLR TGATTLLIPPV FKSLHDSEAK GYTLDLKAK KLLDDAGYKD
 VGDGIREDF EGKPLEIKFA SMSGGETAQP LADYYVQQWK EIGLNVYTT GRLIDFQAFY
 DKLNDDPEV DIYQGAWGTG SDPSPTGLYG PNSAFNYTRF ESEENTKLLD AIDSASFDE
 EKRKKAIFYDW QEYAIDEAFV IPTLYRNEVL PVNDRVVDFT WAVDTKDNPW ATVGVTADSR
 K

EF046-1 (SEQ ID NO:169)

TAGGAGGATA TAATGAAAAA AAAACTTATT CTACTATTGT TAGCCTTATT TTAAACGGCA
 TGTAAGTAATA ATACTGGGGG AAAAAATAGC GACGCTTCAT CTACTGAAGT ATCAACTAAG
 CAGCAAATA CCCAGTCTTC TAAAAAAGAT AGTAGTAATC CGGACACAAC ACCAACTTCT
 ACATCATCTA TAACAATTGA AACAACCGAG AATTTAAAGA ATAGAGAATT GAATCCAACA
 GATGATGTTT CAAAACTAG ACGACAATTG TATGAACAAG GAATTAACAG TTCAACAATT
 ACGGATAAAG AACTAAAGGA ATATATATCA GAGGCTAAAG AACAAAAGAA AGATGTCATT
 AATTATATTA AGCAAAAA

EF046-2 (SEQ ID NO:170)

MKKKLIV LLLALFLTAC SNNTGGKNSD ASSTEVSTKQ QTTQSSKKDS SNPDTTPTST
 SSITIIETTEN LKNRELNPTD DVSKTRRQLY EQGINSSTIT DKELKEYISE AKEQKKDVIN
 YIKQK

EF046-3 (SEQ ID NO:171)

A

TGTAAGTAATA ATACTGGGGG AAAAAATAGC GACGCTTCAT CTACTGAAGT ATCAACTAAG
 CAGCAAATA CCCAGTCTTC TAAAAAAGAT AGTAGTAATC CGGACACAAC ACCAACTTCT
 ACATCATCTA TAACAATTGA AACAACCGAG AATTTAAAGA ATAGAGAATT GAATCCAACA
 GATGATGTTT CAAAACTAG ACGACAATTG TATGAACAAG GAATTAACAG TTCAACAATT
 ACGGATAAAG AACTAAAGGA ATATATATCA GAGGCTAAAG AACAAAAGAA AGATGTCATT
 AATTATATTA AGCAAAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF046-4 (SEQ ID NO:172)

C SNNTGGKNSD ASSTEVSTKQ QTTQSSKKDS SNPDTTPTST
 SSITTIETTEN LKNRELNPTD DVSKTRRQLY EGGINSSTIT DKELKEYISE AKEQKKDVIN
 YIKQK

EF047-1 (SEQ ID NO:173)

TAGGGAAAAC AAGGAGGAAT TCTTATGAAA AAGATAGGGC TTATTTCTAG TGCTTTTCTT
 TTAACCCCTTG CTTTAGCAGC ATGCGGCGGC GGAAAAAGTA CAGAAAATAC GGATAGTCGT
 TCCAGTGCTG CGGAAAGTAC CACAGTCGAG AGTACAAAAG CATCTGCTAC AAAAGAATCA
 AGTAGCAAAG CAACAACAAA ATCTAGTGAT GCGAAACCGT CAGGAACAAC AACAGCTGAT
 TCGAAAGCAA CAGCTTCTTC TACGAAGGAA GCGGCAAATA ATGGCTCAGC AGAGAAGCAA
 TCACCAGCGA AAAATGCGAA TCCAGATGAC CAAGCCAACC AAGTGCTTAA CCAGCTAGCA
 AACATGTTTC CTGGTCAAGG CTTACCGCAG GCAATTTTAA CGAGTCAAAC GAATAACTTT
 TTAAGTGCAG CGACAACCTC ACAAGCGGAT CAAAACAATT TCCGTGTTTT ATATTATGCA
 GAAAAAGAAG CGATTCCAGT GAATGATGCA CGTGTCATC AGTTAACGCC AATTAGTTCT
 TTTGAGAAAA AAACATATGG CTCTGATGCC GAAGCAAAAA ATGCAGTGAA CCAAATCATT
 GACAATGGCG GTCAACCACT AGATTTAGGT TACAATATTA CTGGGTATAA ACAAGGGGCG
 GCAGGTCTTA GTTACTTATC TTGGCAAGAA GGCAATTGGA GTTTAGTCGT ACGGGCCTCA
 AATATCAATG GTGAATCGCC TGATGATTTA GCGAAAAATG TTGTCAACAT TTTGGAACAA
 GAAACATTAC CAGCACCAGT TACCGTTGGT CAAATCACAC TGAACGTGGC AGGAACCACT
 GACTATAATC GAAACTCAGT AGTTTGGCAA GCCGGTACAG TCGTTTACTC TGTCCATCAT
 TTTGACCCAA TTCAAGCAGT GAAGATGGCA ACATCAATGT AA

EF047-2 (SEQ ID NO:174)

MKK IGLISSAFLL TLALAACGGG KSTENTDSRS SAAESTTVES TKASATKESS
 SKATTKSSDA KPSGTTTADS KATASSTKEA ANNGSAEKQS PAKNANPDDQ ANQVLNQLAN
 MFPQGQLPQA ILTSQTNNFL TAATTSQADQ NNFRVLYYAE KEAIPVNDAR VNQLTPISSF
 EKKTYSDDAE AKNAVNIQID NGGQPVDLGY NITGYKQGA GSSYLSWQEG NWSLVVRASN
 INGESPDDLA KNVVNILEQE TLPAPNTVQ ITLNVAGTTD YNRNSVVWQA GTVVVSVHFF
 DPIQAVKMAT SM

EF047-3 (SEQ ID NO:175)

ATGCGGCGGC GGAAAAAGTA CAGAAAATAC GGATAGTCGT
 TCCAGTGCTG CGGAAAGTAC CACAGTCGAG AGTACAAAAG CATCTGCTAC AAAAGAATCA
 AGTAGCAAAG CAACAACAAA ATCTAGTGAT GCGAAACCGT CAGGAACAAC AACAGCTGAT
 TCGAAAGCAA CAGCTTCTTC TACGAAGGAA GCGGCAAATA ATGGCTCAGC AGAGAAGCAA
 TCACCAGCGA AAAATGCGAA TCCAGATGAC CAAGCCAACC AAGTGCTTAA CCAGCTAGCA
 AACATGTTTC CTGGTCAAGG CTTACCGCAG GCAATTTTAA CGAGTCAAAC GAATAACTTT
 TTAAGTGCAG CGACAACCTC ACAAGCGGAT CAAAACAATT TCCGTGTTTT ATATTATGCA
 GAAAAAGAAG CGATTCCAGT GAATGATGCA CGTGTCATC AGTTAACGCC AATTAGTTCT
 TTTGAGAAAA AAACATATGG CTCTGATGCC GAAGCAAAAA ATGCAGTGAA CCAAATCATT
 GACAATGGCG GTCAACCACT AGATTTAGGT TACAATATTA CTGGGTATAA ACAAGGGGCG
 GCAGGTCTTA GTTACTTATC TTGGCAAGAA GGCAATTGGA GTTTAGTCGT ACGGGCCTCA
 AATATCAATG GTGAATCGCC TGATGATTTA GCGAAAAATG TTGTCAACAT TTTGGAACAA
 GAAACATTAC CAGCACCAGT TACCGTTGGT CAAATCACAC TGAACGTGGC AGGAACCACT
 GACTATAATC GAAACTCAGT AGTTTGGCAA GCCGGTACAG TCGTTTACTC TGTCCATCAT
 TTTGACCCAA TTCAAGCAGT GAAGATGGCA ACATCAATGT AA

EF047-4 (SEQ ID NO:176)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGGB KSTENTDSRS SAAESTTVES TKASATKESSE
 SKATTKSSDA KPSGTTTADS KATASSTKEA ANNSSAEMQS PAKNANPDDQ ANQVLNQLAN
 MFPGQGLPQA ILTSQTNNFL TAATTSQADQ NNFRVLYYAE KEAIPVNDAR VNQLTPISSE
 EKKTYSSEAE AKNAVNQIID NGGQPVLDGY NITGYKQGA GSSYLSWQEG NWSLVVRASN
 INGESPDDLA KNVVNILEQE TLPAPNTVGQ ITLNVAGTTD YNRNSVVWQA GTVVYSVHHF
 DPIQAVKMAT SM

EF048-1 (SEQ ID NO:177)

TAAGSAGAAA AGTTCATGAA AAAAAGAAAAG GTTTTATTTA CAGCAGTTAT GGTATTGGCA
 GGATTACAGT TGCTAAGTGG TTGCGGCAAA ACAGAAACCTT CGGCAAATGA TACGGTAGTC
 TTGCGCTATG CGTATGCTAG TAATAGCCAA CCAGTTATCG ATTCTATGAA GAAATTTCGGT
 GAATTAGTAG AGGAAAAAAC AGATGGTAAA GTTCAAATTG AATATTTTCC AGATGGTCAA
 TTAGSAGGAG AAACAGAACT AATTGAATTA ACACAAACAG GTGCAATTGA TTTTGCAAAG
 GTCAGTGGAT CAGCATTAGA AAGTTTTTCT AAAGATTATT CTGTATTTGC CATTCCGTAT
 ATTTTTGATA ATGAAAAACA TTTTTTTAAA GTAATGGATA ATCAAGCGCT AATGCAACCA
 GTGTATGATT CTACAAAAAA ATTAGGATTT GTTGGTTTAA CTTATTATGA CTCTGGTCAA
 CGAAGTTTTT ATATGAGCAA AGGGCCTGTT ACATCTCCAG ATGATTTGAA AGGTAAAAAA
 ATTCGGGTCA TGCAAAGTGA AACCGCCATC AAAATGGTAG AACTTTTAGG GGGTTCGCCA
 GTACCTATGG GTAGTTCGGA AGTATATACT TCTCTACAAT CTAATCTAAT CAACGGTGCA
 GAGAATAATG AGTTCGTTTT ATATACAGCT GGTCTATGGT GTGTGGCTAA GTATTATTCT
 TATGATGAGC ATACTCGAGT GCCAGATATT GTGATTATGA ACGAGGGAAC AAAAGAACGT
 TTGACAGCGA AACAAGAACA AGCGATTGAA GAAGCAGCAA AAGAATCGAC CGCTTTTGAA
 AAAACGGTCT TTAAGAAGC GGTGAAGAA GAAAAGAAA AAGCACAAGC AGAATATGGC
 GTTGTGTTCA ATCAAGTAGA CAGTGAACCA TCCAAAAAC TTGTTCAACC GTTGCATGAA
 TCATTCAAAA ATAGCTCAGA ACATGGCGAA CTGTATCAGG CTATTGCCA GTTGGCGGAC
 TAA

EF048-2 (SEQ ID NO:178)

MKKRKV LFTAVMVLG LQLLSGCGKT EASANDTVVL RYAYASNSQP VIDSMMKKFGE
 LVEEKTGKV QIEYFPDQQL GGETELIELT QTGAIDFAKV SGSALESFSK DYSVFAIPYI
 FDNEKHFFKV MDNQALMQPV YDSTKKLGFV GLTYYDSGQR SFYMSKGPVT SPDDLKGGKI
 RVMQSETAIK MVELLGGSPV PMGSSEVYTS LQSNLINGAE NNEFVLYTAG HGGVAKYYSY
 DEHTRVPDIV IMNEGTERL TAKQEQAIEE AAKESTAF EK TVFKEAVEEE KKKAQAEYGV
 VFNQVDSEPF QKLQPLHES FKNSEHGEL YQAIRQLAD

EF048-3 (SEQ ID NO:179)

TTGCGGCAAA ACAGAAGCTT CGGCAAATGA TACGGTAGTC
 TTGCGCTATG CGTATGCTAG TAATAGCCAA CCAGTTATCG ATTCTATGAA GAAATTTCGGT
 GAATTAGTAG AGGAAAAAAC AGATGGTAAA GTTCAAATTG AATATTTTCC AGATGGTCAA
 TTAGSAGGAG AAACAGAACT AATTGAATTA ACACAAACAG GTGCAATTGA TTTTGCAAAG
 GTCAGTGGAT CAGCATTAGA AAGTTTTTCT AAAGATTATT CTGTATTTGC CATTCCGTAT
 ATTTTTGATA ATGAAAAACA TTTTTTTAAA GTAATGGATA ATCAAGCGCT AATGCAACCA
 GTGTATGATT CTACAAAAAA ATTAGGATTT GTTGGTTTAA CTTATTATGA CTCTGGTCAA
 CGAAGTTTTT ATATGAGCAA AGGGCCTGTT ACATCTCCAG ATGATTTGAA AGGTAAAAAA
 ATTCGGGTCA TGCAAAGTGA AACCGCCATC AAAATGGTAG AACTTTTAGG GGGTTCGCCA
 GTACCTATGG GTAGTTCGGA AGTATATACT TCTCTACAAT CTAATCTAAT CAACGGTGCA
 GAGAATAATG AGTTCGTTTT ATATACAGCT GGTCTATGGT GTGTGGCTAA GTATTATTCT
 TATGATGAGC ATACTCGAGT GCCAGATATT GTGATTATGA ACGAGGGAAC AAAAGAACGT
 TTGACAGCGA AACAAGAACA AGCGATTGAA GAAGCAGCAA AAGAATCGAC CGCTTTTGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAACGGTCT TTAAGAAGC GGTTGAAGAA GAAAAGAAAA AAGCACAAGC AGAATATGGC
 GTTGTGTTCA ATCAAGTAGA CAGTGAACCA TTCCAAAAAC TTGTTCAACC GTTGCATGAA
 TCATTCAAAA ATAGCTCAGA ACATGGCGAA CTGTATCAGG CTATTGCGCA GTTGGCGGAG
 TAA

EF048-4 (SEQ ID NO:180)

CGKT EASANDTVVL RYAYASNSQP VIDSMKKFGE
 LVEEKTGDKV QIEYFPDQQL GGETELIELT QTGAIDFAKV SGSALESFSK DYSVFAIPYI
 FDNEKHFFKV MDNQALMQPV YDSTKKLGFV GLTYDSDGQR SFYMSKGPVT SPDDLKGGKI
 RVMQSETAIK MVELLGGSPV PMGSSEVYTS LQSNLINGAE NNEFVLYTAG HGGVAKYYSY
 DEHTRVPDIV IMNEGTERL TAKQEQAIEE AAKESTAFEK TVFKEAVEEE KKKAQAEYGV
 VFNQVDSEPF QKLVLPLHES FKNSSSEHGEL YQAIRQLAD

EF049-1 (SEQ ID NO:181)

TGAGACTCTT TCTTTTTCAG AATGAGGTAT GGTATAGTTA TAACAGANAT AAAACTANAA
 AAAACAGGAG TGCATAAGAG AATGAAGAAA AAATAATCT TAGCTGCAGC GGGCGCAATG
 GCCGTTTTTA GTTTAGCAGC GTGTTCAAGC GGTCAAAAAG ATATCGCAAC AATGAAAGGT
 TCAACAATTA CTGTTGATGA TTTTATAAC CAAATTAAAG AACAAAGCAC TAGCCAACAA
 GCCGTTTAGCC AAATGGTTAT TTATAAAGTC TTTGAAGAAA AATATGGCGA CAAAGTAACT
 GACAAAGANA TTCAAAAAAA CTTTGACGAA GCCAAAGAAC AAGTAGAAGC ACAAGGCGGA
 AAGTTCTCTG ATGCATTAAA ACAAGCTGGT TTAAGTAAA AAACATTCAA GAAACAGTTA
 AAACAAAGAG CAGCCTATGA TGCAGGTCTA AAAGCCCACT TAAAAATTAC AGATGAAGAC
 TTAATAACAG CTGGGCAAG TTTCCATCCA GAAGTAGAAG CACAAATTAT CCAAGTTGCT
 TCAGAAGATG ATGCCAAAGC TGTCAGAAA GAAATCACTG ACGGCGGCGA TTTTACAAAA
 ATTGCTAAAG AAAAAATCAAC AGATACTGCT ACGAAAAAAG ATGGCGGTAA AATTAAATTT
 GATTCAACAAG CAACAACACTGT TCCTGCCGAA GTTAAAGAAG CTGCCTTCAA ATTAAGAAT
 GGCGAAGTGT CAGAACCAAT TGCTGCAACA AATATGCAAA CCTACCAAAC AACCTACTAT
 GTAGTAAAA TGACGAAAA CAAAGCAAAA GGCAATGACA TGAAACCTTA TGAAAAAGAG
 ATCAAGAAAA TTGCTGAAGA AACAAAATTA GCCGATCAAA CATTTGTTTC GAAAGTCATT
 AGTGACGAAT TAAAGCGGC CAATGTGAAA ATTAAAGATG ATGCCTTCAA GAACGCTTTA
 GCAGGCTACA TGCAAACTGA ATCTTCAAGC GCTTCTTCA AGAAAAAGA ATCAAAATCA
 AGTGATTCTA AAACAAGCGA TACCAAAACA AGCGACTCTG AAAAAGCAAC AGATTCTTCA
 AGCAAAACAA CAGAATCTTC TTCTAAATAA

EF049-2 (SEQ ID NO:182)

MKKK LILAAAGAMA VFSLAACSSG SKDIATMKGS
 TITVDDFYNQ IKEQSTSQQA FSQMVYKVF EEKYGDKVTD KXIQKNFDEA KEQVEAQGGK
 FSDALKQAGL TEKTFKKQLK QRAAYDAGLK AHLKITDEEL KTAWASFHPE VEAQIIQVAS
 EDDAKAVKKE ITDGGDFTKI AKEKSTDTAT KKDGGKIKFD SQATTVPAAEV KEAFAKLKDG
 EVSEPIAATN MQTYQTTYV VKMTKNKAKG NDMKPYEKEI KKIAEETKLA DQTFVSKVIS
 DELKAANVKI KDDAFKNALA GYMQTESSA SSEKKESKSS DSKTSDTKTS DSEKATDSSS
 KTTESSEK

EF049-3 (SEQ ID NO:183)

GTGTTCAAGC GTTCAAAAAG ATATCGCAAC AATGAAAGGT
 TCAACAATTA CTGTTGATGA TTTTATAAC CAAATTAAAG AACAAAGCAC TAGCCAACAA
 GCCGTTTAGCC AAATGGTTAT TTATAAAGTC TTTGAAGAAA AATATGGCGA CAAAGTAACT
 GACAAAGANA TTCAAAAAAA CTTTGACGAA GCCAAAGAAC AAGTAGAAGC ACAAGGCGGA
 AAGTTCTCTG ATGCATTAAA ACAAGCTGGT TTAAGTAAA AAACATTCAA GAAACAGTTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AAACAAAGAG CAGCCTAT3A TGCAGGTCTA AAAGCCCACT TAAAAATTAC A3ATGAAGAC
TTAAAAACAG CTTGGGCAAG TTTCCATCCA GAAGTAGAAG CACAAATTAT CCAAGTTGCT
TCABAAGATG ATGCCAAAGC TGTCAAGAAA GAAATCACTG ACGGCGGCGA TTTCACAAAA
ATTGCTAAAG AAAAATCAAC AGATACTGCT ACGAAAAAG ATGGCGGTAA AATTAAATTT
GATTCACAAG CAACAACCTT TCCCTGCCGA GTTAAAGAA3 CTGCCTTCAA ATTTAAAGAT
GGC3AAGTGT CAGAACCAAT TGCTGCAACA AATATGCAAA CCTACCAAAC AACCTACTAT
GTATGTGAAA TGACGAAAAA CAAAGCAAAA GGCATGACA TGAAACCTTA T3AAAAAGAG
ATCAAGAAAA TTGCTGAAGA AACAAAATTA GCCGATCAAA CATTTGTTTC GAAAGTCATT
AGTGACGAAT TAAAAGCGGC CAATGTGAAA ATTAAAGATG ATGCCTTCAA GAACGCTTTA
GCAGGCTACA TGCAAACT3A ATCTTCAAGC GCTTTTTCAG AGAAAAAGA ATCAAAATCA
AGTGATTCTA AAACAAGCGA TACCAAAACA AGCGACTCTG AAAAAGCAAC AGATTCTTCA
AGCAAAACAA CAGAATCTTC TTCTAAATAA

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EF049-4 (SEQ ID NO:184)

CSSG SKDIATMKGS

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TITVDDFYNQ IKEQSTSQQA FSQMVYKVF EEKYGDKVTD KXIQKNFDEA KEQVEAQGGK
FSDALKQAGL TEKTFKKQLK QRAAYDAGLK AHLKITDEDL KTAWASFHPE VEAQIIQVAS
EDDAKAVKKE ITDGGDFTKI AKEKSTDAT KKGKGIKIFD SQATTVPAAV KEAFAFKLDG
EVSEPIAATN MQTYQTTYVY VKMTKNKAKG NDMKPYEKI KKIABETKLA DQTFVSKVIS
DELKAANVKI KDDAFKNALA GYMQTESSA SSEKKESKSS DSKTSDTKTS DSEKATDSSS
KTTESSSK

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EF050-1 (SEQ ID NO:185)

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TAGGGTCTGG AAAAGCAGTC AACTGACTTC TTTTCCAAGC CCTTTTTTAG TTCATCGCAG
AAAGGATGNA AAAAAATGAA CATGCCCAA AATATCNGTT ATTTTCTTTT GCTAATGGGT
CTTGTTCTAT TATTAAGTGC TTGCCAAAT GGGGCAACTA CGAAGGATGA CAACCAAGCC
GCCACAAAAG AAGCAACTGT TGAGTTAAAC CGCACAAACA CACCAACGCT TTTTTTTCAT
GGTTACGCAG GAACTAAAAA TTCGTTTGGC TCGTTACTGC ATCGCTTGGA GAAACAAGGT
GCCACAACCT AAGAATTAGT GCTACTCGTT AAACCTGATG GGACCGTGGT TAAAGAGCGA
GGAGCTTTAA GTGGCAAAGC GACGAATCCC AGTGTTCAAG TTCTATTTGA AGATAATAAA
AACAATGAAT GGAATCAAAC AGAATGGATA AAAAACACAT TACTCTATTT ACAAAAAAAT
TATCAAGTGA ACAAAGCCAA TATTGTCGGG CACTCTATGG GTGGTGTTAG TGGTTTACGT
TATTTAGGAA CCTATGGGCA AGATACATCG TTACCTAAAA TTGAAAAAAT CGTCAGCATT
GGAGCACCTT TCAATGATTT TATTGATACG AGTCAACAGC AAACCATCGA AACCGAACTA
GAAAACGGCC CCACAGAAAA AAGTAGCCGC TATTTGGATT ATCAAGAGAT GATTAATGTT
GTTCCAGAAA AACTGCCCAT TTTATTAATT GGTGGTCAAT TAAGTCCAAC AGATTTAAGT
GATGGAACGG TGCCGTATC TAGTGCCCTA GCAGTCAACG CCTTGCTAAG ACAGCGAGGA
ACTCAAGTCA CTAGCCAGAT TATTAAAGGA GAAAATGCAC AACATAGTCA ATTACATGAA
AATCCTGAAG TAGATCAATT CTAATCGAA TTTCTATGGC CGAGTAAAAA ATAG

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EF050-2 (SEQ ID NO:186)

MNMPKN IXYFSLMGL VLLSACQIG ATTKDDNQAA

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TKEATVELNR TTTPTLFFHG YAGTKNSFGS LLHRLEKQGA TTQELVLLVK PDGTVVKERG
ALSGKATNPS VQVLFEDNKN NEWNQTEWIK NTLlyLQKNY QVNKANIVGH SMGGVSLGRY
LGTYGQDTSI PKIEKFVSI APFNDPIDTS QQQTIELE NGPTEKSSRY LDYQEMINNV
PEKLPILLIG GQLSPTDLSD GTVPLSSALA VNALLRQRGT QVTSQIIGKE NAQHSQI LHEN
PEVDQLLIEF LWPSKK

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EF050-3 (SEQ ID NO:187)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTGCCAAATT GGGGCAACTA CGAAGGATGA CAACCAAGCC
 GCCACAAAAG AAGCAACTGT TGAGTTAAAC CGCACAACAA CACCAACGCT TTTTTTTCAT
 GGTACGCAG GAACTAAAAA TTCGTTTGGC TCGTTACTGC ATCGCTTGGA GAAACAAGGT
 GCCACAACCTC AAGAATTAGT GCTACTCGTT AAACCTGATG GGACCGTGGT TAAAGAGCGA
 GGAGCTTTAA GTGGCAAAGC GACGAATCCC AGTGTTCAG TTCTATTTGA AGATAATAAA
 AACAATGAAT GGAATCAAAC AGAATGGATA AAAAACACAT TACTCTATTT ACAAAAAAAT
 TATCAAGTGA ACAAAGCCAA TATTGTCTGGG CACTCTATGG GTGGTGTTAG TGGTTTACGT
 TATTTAGGAA CCTATGGGCA AGATACATCG TTACCTAAAA TTGAAAAATT CGTCAGCATT
 GGAGCACCTT TCAATGATTT TATTGATACG AGTCAACAGC AAACCATCGA AACGGAACCTA
 GAAAACGGCC CCACAGAAAA AAGTAGCCGC TATTGTGATT ATCAAGAGAT GATTAATGTT
 GTTCCAGAAA AACTGCCCAT TTTATTAATT GGTGGTCAAT TAAGTCCAAC AGATTTAAGT
 GATGGAACGG TGCCGTTATC TAGTGCCCTTA GCAGTCAACG CCTTGCTAAG ACAGCGAGGA
 ACTCAAGTCA CTAGCCAGAT TATTAAAGGA GAAAATGCAC AACATAGTCA ATTACATGAA
 AATCCTGAAG TAGATCAATT GCTAATCGAA TTTCTATGGC CGAGTAAAAA ATAG

EF050-4 (SEQ ID NO:188)

CQIG ATTKDDNQAA

TKEATVELNR TTTPTLFFHG YAGTKNSFGS LLHRLEKQGA TTQELVLLVK PDGTVVKERG
 ALSGKATNPS VQVLFEDNKN NEWNQTEWIK NTLLEYLQKNY QVNKANIVGH SMGGVSGRLRY
 LGTYGQDTSI PKIEKFVSIG APFNDFIDTS QQQTIELE NGPTEKSSRY LDYQEMINVV
 PEKLPILLIG GQLSPTDLSD GTVPLSSALA VNALLRQRGT QVTSQIIKGE NAQHSQLEHN
 PEVDQLLIEF LWPSKK

EF051-1 (SEQ ID NO:189)

TAAAAGAAAA GAGGCGTTCA AATGTCTAAA CAAAAAAGG CTGTGTTCCCT GCTTAGTTTA
 TTCAGTTTAG TTGCCCTAAT TGCTGCATGT ACAAATCAGC CGCAAAAAGA AACAGTTTCA
 ACAAAAAAAG AAGAAATAAC CCTTGCGGCA GCAGCTAGCT TAGAATCAGT CATGGAGAAG
 AAAATTATTC CAGCCTTTGA AAAAGAGCAT CCAGATATTC AGGTAAGTGG AACCTATGAT
 AGTTCTGGAA AATTACAGAT GCAAATTGAA AAAGGCCTAA AAGCCGATGT ATTTTCTCA
 GCTTCGACAA AACAAATGAA TGCATTGGTT GCAGAAAAAC TAATTAATAA AAAAAGTGTC
 GTTCCTTTAT TGGAAAACCA GTCGTTCTT ATTGTGCCTA ACCAAGATCA AGCAAAGTGG
 CATGATTTTT CTGATTTAAA AAAAGCCCAA ATGATAGCAA TTGGTGATCC TGCAAGTGTT
 CCAGCTGGTC AATATGCCGA AGAAGGCTTA AAAGCTTTAG GCGCTTGGTC TTATGTAGAA
 AAACACGCAA GCTTTGGCAC GAATGTAACA GAAGTCCTTG AATGGGTAGC TAATGCAAGT
 GCAGAAGCTG GCTTAGTTTA TGCGACAGAT GCAGCAACCA ATTCAAAAGT AGCGATTGTT
 GCGGCCATGC CTGAAGCTGT TTTGAAAAAG CCAATTATCT ATCCAGTTGG TAAAGTTGCC
 GCCTCTAAGA AACAAAAATC AGCAGATGCT TTTTAAATT TTTTACAGAG TCAACAATGC
 AGAAAATATT TTGANAATAT TGGCTTTAAG TTAACAAAGT AG

EF051-2 (SEQ ID NO:190)

MSKQ KKAFFLLSLF SLVALIACT NQPQKETVST KKEEITLAAA ASLESVMEKK
 IIPAFEKEHP DIQVTGTYDS SGKLQMIEK GLKADVFFSA STKQMNALVA EKLINKKSVV
 PLENQLVLI VPNQDQAKWH DFSDLKKAQM IAIGDPASVP ACQYAEGLK ALGAWSYVEK
 HASFGTNVTE VLEWVANASA EAGLVYATDA ATNSKVAIVA AMPEAVLKKP IIYPVGKVAA
 SKKQKSADAF LNFLSQQCR KYFXNIGFKL TK

EF051-3 (SEQ ID NO:191)

ATGT ACAAATCAGC CGCAAAAAGA AACAGTTTCA
 ACAAAAAAAG AAGAAATAAC CCTTGCGGCA GCAGCTAGCT TAGAATCAGT CATGGAGAAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAATTATTC CAGCCTTTGA AAAAGAGCAT CCAGATATTC AGGTAACTGG AACCTATGAT
 AGTTCTGSA AATTADAGAT GCAAATTGAA AAAGSCTTAA AAGDCGATGT ATTTTCTCA
 GCTTCBACAA AACAAATGAA TGCATTGGTT GCAGAAAAAC TAATTAATAA AAAAAGTGTC
 GTTCCTTTAT TGGAAAACCA GCTCGTTCTT ATTBIGCCTA ACCAAGATCA AGCAAAGTGG
 CATGATTTTT CTGATTTTAA AAAAGSCTTAA ATGATAGCAA TTGGTGATCC TGCAAGTGTT
 CCAGCTGGTC AATATSCCGA AGAAGSCTTA AAASCTTTAG GCGCTTGGTC TTATGTAGAA
 AAACACGCAA GCTTTGGCAC GAATGTAACA GAATGCTTG AATGGGTAGC TAATGCAAGT
 GCAGAAGCTG GCTTAGTTTA TGCGACAGAT GCAGCAACCA ATTCAAAAGT AGCGATTGTT
 GCGGCCATGC CTGAAGCTGT TTTGAAAAAG CCAATTATCT ATCCAGTTGG TAAAGTTGCC
 GCCTCTAAGA AACAAAAATC AGCAGATGCT TTTTAAATT TTTTACAGAG TCAACAATGC
 AGAAAAATATT TTGANAATAT TGGCTTTAAG TTAACAAAGT AG

EF051-4 (SEQ ID NO:192)

CT NCPQKETVST KKEEITLAAA ASLESVMEKK
 IIPAFEKEHP DIQVTGYDS SGKLQMIEK GLKADVFSA STKQMNALVA EKLINKKSVV
 PLEENQLVLI VPNQDQAKWH DSELKKAQM IAIGDPASVP AGQYAEGLK ALGAWSYVEK
 HASFGTNVTE VLEWVANASA EAGLVYATDA ATNSKVAIVA AMPEAVLKKP IIPVGVKVA
 SKKQKSADAF LNFLQSQQCR KYFXNIGFKL TK

EF052-1 (SEQ ID NO:193)

TAAAGTAGGA GAAGCGCAAG CGAAAAAAGT GAATCAATCG GCAGCGTATC AAGTAGTGAT
 CCCACAAATGG GTACCATGGG TAGCATTATC TTTGACAGTA GCACTTGCTG GATTGATTGC
 TTACTTAGTT CGTCGTGGAG AGAAGTGGA AAACGAAGGG GAAGTGACAT AATGAGANGA
 NGAAATCTTC NGTTTTTATT ATTGTTGGTT CTATTAATTT ATATTCCTCA AACAACTTAT
 GCAGAAAATA GGGAGACCAC AGAAGTCGGA ATCGGGTTTA CAAAAACTTC AGACATACCA
 TCAAAAAAAA ATCCAGTTGT GAATGTATTG CCGCAAACAA CCATTCAATC GCTATCAATC
 GTTCGTAGCA GAACGCAAAT AAAAAGATTA CCTAAAACTG GTGACAATCG AATAACTTGG
 CTAAGCTGGT TTGGCATATT GTTTTAAATA AGTAGTTTTT GGCTGTTTCT ATTTAGACAA
 TTATGTAGAA AAGGAGAATA A

EF052-2 (SEQ ID NO:194)

MRXX
 NLXFLLLLVL LIYIPQTTYA ENRETTEVGI GFTKTSIPS KKNPVNVLP QTTIQSLSIV
 RSRTQIKRLP KTGDNRIITWL SWFGILFLIS SFWLFLRQL CRKGE

EF052-3 (SEQ ID NO:195)

AGAAAAATA GGGAGACCAC AGAAGTCGGA ATCGGGTTTA CAAAACTTC AGACATACCA
 TCAAAAAAAA ATCCAGTTGT GAATGTATTG CCGCAAACAA CCATTCAATC GCTATCAATC
 GTTCGTAGCA GAACGCAAAT AAAAAGAT

EF052-4 (SEQ ID NO:196)

ENRETTEVGI GFTKTSIPS KKNPVNVLP QTTIQSLSIV
 RSRTQIKR

EF053-1 (SEQ ID NO:197)

TAGTCATGGC ACCATAACAA GGAGGAGAGA AGTGAGATGA AAAAATACCT TTTGCTTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TGTTTTTTAG GTCTTTTCAG CTTCTGTCA T CAGACACTG CGTTTGGAGA AGCAGCTTAT
 GAAAATAGTG GTGTTGTCTC CTTTTATGGA ACGTATGAAT ATCCACAGA AGAGTCGACA
 ACAGCGACTA GTAATTCTTC CACAACGACC GAACCCACCA AGCCAGCTGA CGGAGGCGCT
 TCATCCGTCC TTTCTTCTGG CGTATATGGA TCGCGACAAG GAAGATTACC AGCGACAGGT
 ACCACCAATC AAGCACCATT TATTTATTTG GGAATCAGCC TTATCACTAT AGGCATATTA
 TTTATTAAAA GGAGAAGAGA AGATGAAAAA AACAGTATTA GCAGTAGTAG GGATTGTAGG
 ATTTAG

EF053-2 (SEQ ID NO:198)

MKKYLLLS SC FLGLFSFCHS DTAFGEAA YE NSGVVSFYGT YEYPTEESTT
 ATSNSSTTTE PTKPADGGAS SVLSSGVYGS RQGRLPATGT TNQAPFIYLG ISLITIGILF
 IKRRREDEKN SSSSRDCRI

EF053-3 (SEQ ID NO:199)

TTTGGAGA AGCAGCTTAT
 GAAAATAGTG GTGTTGTCTC CTTTTATGGA ACGTATGAAT ATCCACAGA AGAGTCGACA
 ACAGCGACTA GTAATTCTTC CACAACGACC GAACCCACCA AGCCAGCTGA CGGAGGCGCT
 TCATCCGTCC TTTCTTCTGG CGTATATGGA TCGCGACAAG GAAGA

EF053-4 (SEQ ID NO:200)

FGEEA YE NSGVVSFYGT YEYPTEESTT
 ATSNSSTTTE PTKPADGGAS SVLSSGVYGS RQGR

EF054-1 (SEQ ID NO:201)

TAAATAAAAA ATTATTTGGA GGAAATTACA ATGAAAAAAA TTATTTTATC AAGCTTGTTT
 AGTGCACTAC TAGTATTCGG TGGCGGAAGT ATAACAGCAT TCGCTGACGA TTTAGGACCA
 ACAGATCCAG CAACTCCACC AATTACCGAA CCAACTGATT CTAGTGAACC TACGAATCCT
 ACTGAGCCGG TGGATCCTGC AGAACCGCCA GTAATACCAA CTGATCCAAC AGAACCAAGC
 AAGCCAACCG AGCCTACAAC ACCGAGTGAG CCAGAAAAGC CAACAGAACC AACAACGCCA
 ATTGATCCTG GAACGCCGGT TGAACCGACT GAACCAAGCG AGCCAACAGA ACCTAGTCAA
 CCAACCGAGC CTACAACACC AAGCGAACCA GAAAAACCTG TTACTCCAGA ACAACCGAAA
 GAACCAACTC AACCAGTGAT TCCAGAAAAA CCAGCAGAAC CAGAAACACC AAAAACTCCT
 GAACAGCCCA CTAAACCAAT AGACGTAGTC GTTACACCTA GTGGAGAAAT TGATAAAACG
 AATCAATCGG CAGGAACACA ACCAAGTATT CCTATTGAAA CAAGCAACTT AGCGGAGGTA
 ACACATGTAC CAAGTGAAAC TACTCCAATT ACAACAGAAG CTGGGGAAGA AATTGTAGCA
 GTAGATAAAG GTGTTCCGTT AACCAAAACA CCAGAAGGAT TAAAACCAAT TAGCAGCTCG
 TATAAGGTTT TACCTAGCGG AAACGTTGAG GTAAAAGCAA GTGATGGAAA AATGAAAGTA
 TTGCCACATA CAGGAGAGAA ATTCACTCTC CTTTCTCTCTG TATTGGGAAG CTTCTTTGTA
 TTAATTTTCA GATTCTTTTT CTTTAAAAAG AATAAGAAAA AAGCTTAA

EF054-2 (SEQ ID NO:202)

M KKIILSSLFS AVLVFGGGSI TAFADDLGPT DPATPPITEP TDSSEPTNPT
 EPVDPAEPPV IPTDPTEPSK PTEPTTPSEP EKPTPTPI DPGTPVEPTE PSEPTEPSQP
 TEPTTPSEPE KPVTPPEQKE PTQPIVEKP AEPETPKTPE QPTKPIDVVV TPSGEIDKTN
 QSAGTQPSIP IETSNLAEVT HVPSETTPI T EAGEEIVAV DKGVP LTKTP EGLKPISSSY
 KVLPSGNVEV KASDGKMKVL PHTGEKFTLL FSVLGSFFVL ISGFFFFKKN KKKA

EF054-3 (SEQ ID NO:203)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

A

ACAGATCCAG CAACTCCACC AATTACCGAA CCAACTGATT CTAGTGAACC TACGAATCCT
 ACTGAGCCGG TGGATCCTGC AGAACCBCCA GTAATACCAA CTGATCCAAC AGAACCAAGC
 AAGCCAAACG AGCCTACAAC ACCGAGTBAG CCAGAAAAGC CAACAGAACC AACCAACGCCA
 ATTSATCCTG GAACGCCGGT TGAACCGACT GAACCAAGCG AGCCCAACAGA ACCTAGTCAA
 CCAACCGAGC CTACAACACC AAGCGAACCA GAAAAACCTG TTAATCCAGA ACAACCGAAA
 GAACCAACTC AACCAAGTAT TCCAGAAAAA CCAGCABAAC CAGAAACACC AAAAATCCTT
 GAACAGCCCA CTAAACCAAT AGACGTAGTC GTTACACCTA CTGCAGAAAT TGATAAAACG
 AATCAATCGG CAGGAACACA ACCAAGTATT CCTATTBAAA CAAGCAACTT AGCGGAGGTA
 ACACATGTAC CAAGTGAAAC TACTCCAATT ACAACABAAG CTGGGGAAGA AATTGTAGCA
 GTAGATAAAG GTGTTCCGTT AACCAAAACA CCAGAA33AT TAAAACCAAT TAGCAGCTCG
 TATAAGGTTT TACCTAGCGG AAACGTTGAG GTAAAA33AA GTGATGGAAA AATGAAAGTA
 T

EF054-4 (SEQ ID NO:204)

DDLGPT DPATPPITEP TDSSEPTNPT
 EPVDPAEPPV IPTDPTEPSK PTEPTTPSEP EKPTEFTTPI DPGTPVEPTE PSEPTEPSQP
 TEPTTPSEPE KPVTPSEQPK PTQPVIEKP AEPETPKTPE QPTKPIDVVV TPSGEIDKTN
 CSAGTQPSIP IETSNLAEVT HVPSETTPIIT TEAGEEIVAV DKGVPLTKTP EGLKPISSSY
 KVLPSGNVEV KASDGKMKV

EF055-1 (SEQ ID NO:205)

TAACAAAAGG TTGTTTTGTC TTTCTTGTGT AAAAGGGCAA GAAAGGCTAG CGAGTTAAAA
 GGAGGTTTTT CAATGAAAAA AAAGCGTTAT TTAATGATTG TGTGTCTACT ATCTTCTCCT
 AGTTTTTTTA TAAATGTTGA AGCGTCTGAT GGTGGTTCTA GTTCGGTGGG GATTGAATTT
 TACCAAAATC CGAGAACACC CGCTCCTAAA GATCCCCCAC CGAAAACAGA TGCGCCAGCT
 GCTGATCCCA AGGAACCAGC TGGTCCTCCG CAAGGAGATC AACGAAGTGG TGGTTCGACA
 CAGACCACCA CAACTGGCTC AACGCTCCCT CGTACAGGGA GCAAGAGTCA GGCAAATTTG
 AGCATTCTCN GNTTCGCCCTT AATCGGTTTG CCGGGAATCG TACATAGAAA GAAGGGACGA
 CATGAAGCAA ACTAA

EF055-2 (SEQ ID NO:206)

MKKKRYL MIVCLLSSPS FFINVEASDG GSSSVGIEFY
 QNPRTPAPKD PPPKTDAPAA DPKEPAGPPQ GDQRSGGSTQ TTTTGSTLPR TGSKSQANLS
 ILXFALIGLA GIVHRKKGRH EAN

EF055-3 (SEQ ID NO:207)

AGCGTCTGAT GGTGGTTCTA GTTCGGTGGG GATTGAATTT
 TACCAAAATC CGAGAACACC CGCTCCTAAA GATCCCCCAC CGAAAACAGA TGCGCCAGCT
 GCTGATCCCA AGGAACCAGC TGGTCCTCCG CAAGGAGATC AACGAAGTGG TGGTTCGACA
 CAGACCACCA CAACTGGCTC AACG

EF055-4 (SEQ ID NO:208)

SDG GSSSVGIEFY
 QNPRTPAPKD PPPKTDAPAA DPKEPAGPPQ GDQRSGGSTQ TTTTGST

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF056-1 (SEQ ID NO:209)

TAAATGAAAA AAAAGCGTTA TTTAATAATT GCGTGTTCAC TATTTTCCCC TAGTTTTTTT
ATAAATGTTG AAGCATCTGA GGGTGGTTCT AGTTCGGTGG GAATTGAATT TTACCAAAAT
CCGGCAACAC CCGCTCCTAA AGATGCCCCA CCGAAAACAG ATGAGCCAGC TCGGGATCCC
AAGGAACCAG CTGGTCCTCT GCAAGGAGAT CAACGAAGTG GTGGTTCGAC ACAGACCACC
ACAGCTGGCT CGCAGCTCCC TCGTACAGGA AGCAAGAGTC AGGCAAACCT GAGCATTCTT
GGTCTTGTCT TGATTGGTCT TGTCGGAATG GTCCAGAGAA AGAAGGGACG ACATGAAGCA
AACTAA

EF056-2 (SEQ ID NO:210)

MKKKRYLIIA CLLFSPFFI NVEASEGGSS SVGIEFYQNP ATPAPKDAPP KTDEPAADPK
EPAGPLQGDQ RSGGSTQTTT AGSQLPRTGS KSQLNLSILG LVLIGLVGMV QRKKGRHEAN

EF056-3 (SEQ ID NO:211)

ATCTGA GGGTGGTTCT AGTTCGGTGG GAATTGAATT TTACCAAAAT
CCGGCAACAC CCGCTCCTAA AGATGCCCCA CCGAAAACAG ATGAGCCAGC TCGGGATCCC
AAGGAACCAG CTGGTCCTCT GCAAGGAGAT CAACGAAGTG GTGGTTCGAC ACAGACCACC
ACAGCTGGCT CGCAG

EF056-4 (SEQ ID NO:212)

SEGGSS SVGIEFYQNP ATPAPKDAPP KTDEPAADPK
EPAGPLQGDQ RSGGSTQTTT AGSQ

EF057-1 (SEQ ID NO:213)

TAATGTTTAT TGGCTGGGCC AGTCAATGTT GAAAATGGGG AAGGAGGAAT TCAGATGAAA
ATCATAAAAA GGTTTAGTTT GGTATGTTTA GGGCTATTGA TCATTGGGTT GCNAACAAAA
AGCGNTATGG CTGAAGAAAA TAATTATGAA TCAAATGGTC AAGCGAGCTT CTATGGTACC
TACGTTTATG AGAATGAAAA AGAGTCAAAT GACGTAGCGT ATACCCAACA ATCAGAAGAA
CAGGGAAGAA ACAATTTAGC TGCTTCTGGA CAAGCAGTTT TACCTAAAAC AGGCGAGTCT
GAAAATCCGC TGTATTCCTT GATAGGAGTT AGTTTGTGG GGATAGTCAT TTATTTAATT
AATAAAATGA AACGAGAGAA GGAGTTTATT TAA

EF057-2 (SEQ ID NO:214)

MKI IKRFSLVCLG LLIIGLXTKS XMAEENNYES NGQASFYGTY
VYENEKESND VAYTQQSEEQ GRNNLAASGQ AVLPKTGESE NPLYSLIGVS LLGIVIIYLIN
KMKREKEFI

EF057-3 (SEQ ID NO:215)

AAA TAATTATGAA TCAAATGGTC AAGCGAGCTT CTATGGTACC
TACGTTTATG AGAATGAAAA AGAGTCAAAT GACGTAGCGT ATACCCAACA ATCAGAAGAA
CAGGGAAGAA ACAATTTAGC TGCTTCTGGA CAAGCAGTTT

EF057-4 (SEQ ID NO:216)

EENNYES NGQASFYGTY
VYENEKESND VAYTQQSEEQ GRNNLAASGQ AV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF058-1 (SEQ ID NO:217)

TGAAGAACGT TCTATTTGGT TGACGATTGC AGGCCTGCTA ATCATTGGGA TGGTAGTCAT
 TTGGCTATTT TATCAAAAAC AAAAAAGAGG AGAGAGAAAA TGAAGCAATT AAAAAAGTTT
 TGGTACACCG TTAGTACCTT GTTACTAATT TTGCCACTTT TCACAAGTGT ATTAGGGACA
 ACAACTGCAT TTGCAGAAGA AAATGGGGAG AGC3CACAGC TCGTGATTCA CAAAAAGAAA
 ATGACGGATT TACCAGATCC GCTTATTCAA AATAGCGGGA AAGAAATGAG CGAGTTTGAT
 AAATATCAAG GACTGGCAGA TGTGACGTTT AGTATTTATA ACGTGACGAA CGAATTTTAC
 GAGCAACGAG CGGCAGGCGC AAGCGTTGAT 3CAGCTAAAC AAGCTGTCCA AAGTTTAACT
 CCTGGGAAAC CTGTTGCTCA AGGAACCACC 3ATGCAAATG GGAATGTCAC TGTTCAGTTA
 CCTAAAAAAC AAAATGGTAA AGATGCAGTG TATACCATTA AAGAAGAACC AAAAGAGGGT
 GTAGTTGCTG CTACGAATAT GGTGGTGGCG TTCCCACTTT ACGAAATGAT CAAGCAAACA
 GATGGTTCCCT ATAAATATGG AACAGAAGAA TTAGCGGTTG TTCATATTTA TCCTAAAAAT
 GTGGTAGCCA ATGATGGTAG TTTACATGTG AAAAAAGTAG GAACTGCTGA AAATGAAGGA
 TTAAATGGCG CAGAATTTGT TATTTCTAAA AGCGAAGGCT CACCAGGCAC AGTAAAAATAT
 ATCCAAGGAG TCAAAGATGG ATTATATACA TGGACAACGG ATAAAGAACA AGCAAAACGC
 TTTATTACTG GGAAAAGTTA TGAATTTGGC GAAAATGATT TCACAGAAGC AGAGAATGGA
 ACGGGAGAAT TAACAGTTAA AAATCTTGAG GTTGGTTTCT ATATTTTAGA AGAAGTAAAA
 GCTCCAAATA ATGCAGAATT AATTGAAAAT CAAACAAAAA CACCATTTAC AATTGAAGCA
 AACAATCAAA CACCTGTTGA AAAAACAGTC AAAAATGATA CCTCTAAAGT TGATAAAACA
 ACACCAAGCT TAGATGGTAA AGATGTGGCA ATTGGCGAAA AAATTAAATA TCAAATTTCT
 GTAAATATTC CATTGGGGAT TGCAGACAAA GAAGGCGACG CTAATAAATA CGTCAAATTC
 AATTTAGTTG ATAAACATGA TGCAGCCTTA ACTTTTGATA ACGTGACTTC TGGAGAGTAT
 GCTTATGCGT TATATGATGG GGATACAGTG ATTGCTCCTG AAAATTATCA AGTGACTGAA
 CAAGCAAATG GCTTCACTGT CGCCGTTAAT CCAGCGTATA TTCTACGCT AACACCAGGC
 GGCACACTAA AATTTCGTTA CTTTATGCAT TTAAATGAAA AAGCAGATCC TACGAAAGGC
 TTTAAAAATG AGGCGAATGT TGATAACGGT CATACCGACG ACCAAACACC ACCAATGTT
 GAAGTTGTGA CAGGTGGGAA ACGTTTCATT AAAGTCGATG GCGATGTGAC AGCGACACAA
 GCCTTGGCGG GAGCTTCCTT TGTGCTCCGT GATCAAAAACA GCGACACAGC AAATTATTTG
 AAAATCGATG AAACAACGAA AGCAGCAACT TGGGTGAAAA CAAAAGCTGA AGCAACTACT
 TTTACAACAA CGGCTGATGG ATTAGTTGAT ATCACAGGGC TTAAATACGG TACCTATTAT
 TTAGAAGAAA CTGTAGCTCC TGATGATTAT GTCTTGTTAA CAAATCGGAT TGAATTTGTG
 GTCAATGAAC AATCATATGG CACAACAGAA AACCTAGTTT CACCAGAAAA AGTACCAAAC
 AAACACAAAG GTACCTTACC TTCAACAGGT GGCAAAGGAA TCTACGTTTA CTTAGGAAGT
 GGGCGAGTCT TGCTACTTAT TGCAGGAGTC TACTTTGCTA GACGTAGAAA AGAAAAATGCT
 TAA

EF058-2 (SEQ ID NO:218)

MKQLKKVW YTVSTLLLLI PLFTSVLGTT
 TAFAEENGES AQLVIHKKKM TDLPDPLIQN SGKEMSEFDK YQGLADVTFS IYNVTNEFYE
 QRAAGASVDA AKQAVQSLTP GKPVAQGTDD ANGNVTVQLP KKQNGKDAVY TIKEEPKEGV
 VAATNMVAVF PVYEMIKQTD GSYKYGTEEL AVVHIYPKNV VANDGSLHVK KVGTAENEGL
 NGAEFVSKS EGSPGTVKYI QGVKDGLYTW TTDKEQAKRF ITGKSYEIGE NDFTEAENGT
 GELTVKNLEV GSYILEEVKA PNNAELIENQ TKTPFTIEAN NQTPVEKTVK NDTSKVDKTT
 PSLDGKDVAI GEKIKYQISV NIPLGIADKE GDANKYVKFN LVDKHDAAIT FDNVTSGEYA
 YALYDGDVI APENYQVTEQ ANGFTVAVNP AYIPTLTGGG TLKFVYFMHL NEKADPTKGF
 KNEANVDNGH TDDQTPPTVE VVTGGKRFIK VDGDTVATQA LAGASFVVRD QNSDTANYLK
 IDETTKAATW VKTKAEATTF TTTADGLVDI TGLKYGTYYL EETVAPDDYV LLTNRIEFVY
 NEQSYGTEN LVSPEKVPNK HKGTLPTSTGG KGIYVYLGSG AVLLLIAGVY FARRRKENA

EF058-3 (SEQ ID NO:219)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AGAAGA AAATGGGGAG AGCGCACAGC TCGTGATTCA CAAAAAGAAA
 ATGACGGATT TACCAGATCC GCTTATTCAA AATAGCGGGA AAGAAATGAG CGAGTTTGAT
 AAATATCAAG GACTGGCAGA TGTGACGTTT AGTATTTATA ACGTGACGAA CGAATTTTAC
 GAGCAACGAG CGGCAGGCGC AAGCGTTGAT GCAGCTAAAC AAGCTGTCCA AAGTTTAACT
 CCTGGGAAAC CTGTTGCTCA AGGAACCACC GATGCAATG GGAATGTCAC TGTTCAGTTA
 CCTAAAAAAC AAAATGGTAA AGATGCAGTG TATACCATTA AAGAAGAACC AAAAGAGGGT
 GTAGTTGCTG CTACGAATAT GGTGGTGGCG TTCCCAGTTT ACGAAATGAT CAAGCAAACA
 GATGGTTCCCT ATAAATATGG AACAGAAGAA TTAGCGGTTG TTCAATTTTA TCCTAAAAAT
 GTGGTAGCCA ATGATGGTAG TTTACATGTG AAAAAAGTAG GAACTGCTGA AAATGAAGGA
 TTAAATGGCG CAGAATTTGT TATTTCTAAA AGCGAAGGCT CACCAGGCAC AGTAAAAATAT
 ATCCAAGGAG TCAAAGATGG ATTATATACA TGGACAACGG ATAAAGAACA AGCAAAACGC
 TTTATTACTG GGAAAAGTTA TGAAATTGGC GAAAATGATT TCACAGAAGC AGAGAATGGA
 ACGGGAGAAT TAACAGTTAA AAATCCTTGAG GTTGGTTCGT ATATTTTAGA AGAAGTAAAA
 GCTCCAAATA ATGCAGAATT AATTGAAAAT CAAACAAAAA CACCATTTAC AATTGAAGCA
 AACAATCAAA CACCTGTGTA AAAAACAGTC AAAAATGATA CCTCTAAAGT TGATAAAACA
 ACACCAAGCT TAGATGGTAA AGATGTGGCA ATTGGCGAAA AAATTAAATA TCAAATTTCT
 GTAAATATTC CATTGGGGAT TGCAGACAAA GAAGGCGACG CTAATAAATA CGTCAAATTC
 AATTTAGTTG ATAAACATGA TGCAGCCTTA ACTTTTGATA ACGTGACTTC TGGAGAGTAT
 GCTTATGCGT TATATGATGG GGATACAGTG ATTGCTCCTG AAAATTATCA AGTGACTGAA
 CAAGCAAATG GCTTCACTGT CGCCGTTAAT CCAGCGTATA TTCCTACGCT AACACCAGGC
 GGCACACTAA AATTCGTTTA CTTTATGCAT TTAAATGAAA AAGCAGATCC TACGAAAGGC
 TTTAAAAATG AGGCGAATGT TGATAACGGT CATACCGACG ACCAAACACC ACCCAACTGTT
 GAAGTTGTGA CAGGTGGGAA ACGTTTCATT AAAGTCGATG GCGATGTGAC AGCGACACAA
 GCCTTGGCGG GAGCTTCCTT TGTCGTCCGT GATCAAAACA GCGACACAGC AAATTATTTG
 AAAATCGATG AAACAACGAA AGCAGCAACT TGGGTGAAAA CAAAAGCTGA AGCAACTACT
 TTTACAACAA CGGCTGATGG ATTAGTTGAT ATCACAGGCG TTAAATACGG TACCTATTAT
 TTAGAAGAAA CTGTAGCTCC TGATGATTAT GTCTTGTTAA CAAATCGGAT TGAATTTGTG
 GTCAATGAAC AATCATATGG CACAACAGAA AACCTAGTTT CACCAGAAAA AGTACCAAAC
 AACACAAAG GTACCTTACC T

EF058-4 (SEQ ID NO:220)

EENGES AQLVIHKKKM TDLDPDPLIQN SGKEMSEFDK YQGLADVTFIS IYNVTNEFYE
 QRAAGASVDA AKQAVQSLTP GKPVAQGTDD ANGNVTVQLP KKQNGKDAVY TIKEEPKEGV
 VAAATNMVAF PVYEMIKQTD GSYKYGTEEL AVVHIYPKNV VANDGSLHVK KVGTAENEGL
 NGAEFVSKS EGPSTGVKYI QGVKDGLYTW TTDKEQAKRF ITGKSYEIGE NDFTEAENGT
 GELTVKNLEV GSYILEEVKA PNNAELIENQ TKTPFTIEAN NQTPVEKTVK NDTSKVDKTT
 PSLDGDVAI GEKIYQISV NIPLGIADKE GDANKYVKFN LVDKHDAAIT FDNVTSGEYA
 YALYDGDVI APENYQVTEQ ANGFTVAVNP AYIPTLTPGG TLKFVYFMHL NEKADPTKGF
 KNEANVDNGH TDDQTPPTVE VVTGGKRFIK VDGDTVATQA LAGASFVVRD QNSDTANYLK
 IDETTKAATW VKTKAEATTF TTTADGLVDI TGLKYGTYYL EETVAPDDYV LLTNRIEFVV
 NEQSYGTEN LVSPEKVPNK HKGT

EF059-1 (SEQ ID NO:221)

TAGATTGGAA GAATGAAAAT GAAAAAATG ATTATTATTG CCTTATTCAG TACAAGCCTT
 TTAGCAGGGG GAAGCAGTGT TTCTGCTTAT GCGCAAGAAT CAGAAGGAAA TCTTGGTGAA
 ACAACAGGGA GTGTTTACC AGATGAACCG AATGTACCAA CTGACCCAAT AACGCCAAGT
 GAGCCAGAGC AACCAACAGA GCCAAGTACA CCAGAGCAAC CATCGGAACC GTCAACACCA
 ACCGAACCTA GTGAGCCTTC AAAACCGACG GATCCTTCGT TACCAGACGA ACCGAGCGTA
 CCAACAGAGC CAACAACGCC AAGTAAGCCA GAGCAACCAA CAGAGCCAAC AACGCCAAGT
 GTACCAGAGC AACCAACAGA GCCAAGTGTA CCAGAAAAAC CAGTAGAACC AAATAAACCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCGAGCCAG AAAAGCCTGT GGCAGTTGTT CCTGAAAAAC CAGTTGTACC ACAACAACCA
 GAGCAACCAA CAGATGTGST GGTAAAGCCA AATGAGAGAA TTGCAACAGG AGAATCTACA
 CAACAGCCAA CTGTTCCAAT TGAAACGAAT AACCTTTCAG AAGTAACACA TGTCCCAACT
 GTGACGACAC CGATTGAAAC AGCAAGCGGA GAAGCAATTG TCGCAGTGGA TAAGGGCGTT
 CCTTTAACAC AAACGCTGTA TGGATTAAAA CCGATTAAAA GTGAATATAA AGTATTACCA
 AGTGGCAATG TACAAGTGAA AAGTGCTGAC GGAAAAATGA AAGTACTTCC TTACACTGGT
 GAAAAAATGG GCATAATTGG GTCAATCGGT GGTGTATGTT TACTGTGTTT ATCAGGAATC
 TTAATTTATA AAAAACGTAA AGTGTAG

EF059-2 (SEQ ID NO:222)

MKKMI IIALFSTSL AGGSSVSAYA QSEGNLGET TGSVLPDEPN VPTDPITPSE
 PEQPTPSTP EQPSEPSTPT EPSEPSKPTD PSLPDEPSVP TEPTTPSKPE QPTEPTPSV
 PEQPTPSVP EKPVEPNKPT EPEKVPVVP EKPVPVQPE QPTDVVVKPN GEIATGESTQ
 QPTVPIETNN LSEVTHVPTV TTPIETASGE AIVAVDKGVP LTQTADGLKP IKSEYKVLPS
 GNVQVKSADG KMKVLPYTGE KMGIGSIAG VCLTVLSSIL IYKKRKV

EF059-3 (SEQ ID NO:223)

AGAAGGAAA TCTTGCTGAA
 ACAACAGGGA GTGTTTACC AGATGAACCG AATGTACCAA CTGACCCAAT AACGCCAAGT
 GAGCCAGAGC AACCAACAGA GCCAAGTACA CCAGAGCAAC CATCGGAACC GTCAACACCA
 ACCGAACCTA GTGAGCCTTC AAAACCGACG GATCCTTCGT TACCAGACGA ACCGAGCGTA
 CCAACAGAGC CAACAACGCC AAGTAAGCCA GAGCAACCAA CAGAGCCAAC AACGCCAAGT
 GTACCAGAGC AACCAACAGA GCCAAGTGTG CCAGAAAAAC CAGTAGAACC AAATAAACCA
 ACCGAGCCAG AAAAGCCTGT GCCAGTTGTT CCTGAAAAAC CAGTTGTACC ACAACAACCA
 GAGCAACCAA CAGATGTGGT GGTAAAGCCA AATGGAGAAA TTGCAACAGG AGAATCTACA
 CAACAGCCAA CTGTTCCAAT TGAAACGAAT AACCTTTCAG AAGTAACACA TGTCCCAACT
 GTGACGACAC CGATTGAAAC AGCAAGCGGA GAAGCAATTG TCGCAGTGGA TAAGGGCGTT
 CCTTTAACAC AAACGCTGTA TGGATTAAAA CCGATTAAAA GTGAATATAA AGTATTACCA
 AGTGGCAATG TACAAGTGAA AAGTGCTGAC GGAAAAATGA AAGTAC

EF059-4 (SEQ ID NO:224)

EGNLGET TGSVLPDEPN VPTDPITPSE
 PEQPTPSTP EQPSEPSTPT EPSEPSKPTD PSLPDEPSVP TEPTTPSKPE QPTEPTPSV
 PEQPTPSVP EKPVEPNKPT EPEKVPVVP EKPVPVQPE QPTDVVVKPN GEIATGESTQ
 QPTVPIETNN LSEVTHVPTV TTPIETASGE AIVAVDKGVP LTQTADGLKP IKSEYKVLPS
 GNVQVKSADG KMKV

EF060-1 (SEQ ID NO:225)

TGAAAAATAG ACAAGGAGCA CGCGATGATG ACAATGAAAA GTAAAGGGTC ACTTCTGGTG
 ACGTTGGGAA TACTTTTAAC CGTTGGCATT GCGAGTCTAA TTGTTTCTTC TGAGAGTTTT
 GCAGAAGAAG TAGGGCAAAC GAATATCGGT GTAACGTTCT ATGGAGGAAA AGAGCCACTA
 AAAACCGAAG GTGTCATTAA GCCAATAGAG CAACCAAGTCA CTGATAAAGA TAAAAAACG
 TCACAACAAC AAGACAAAGT GAGCAGAAAA ACCACTGCTA AAACGAATCC GACTAATGCA
 CAGACGTCAT TACCAAGGAC AGGTGAACGA AATAGCACGT GGCTTTACAG CCTTGGTATT
 GCCTGTTTAC TCGTAGTACT AACAAGTTTC TATTATTGTA ATAAAAAAG GAAAAAGGAA
 AAATAA

EF060-2 (SEQ ID NO:226)

MMT MKSKGSLVLT LGILLTVGIA SLIVSSESFA EEVGQTNIGV TFYGGKEPLK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TEGVIKPIEQ PVTDKDKKTS QQQDKVSRKT TAKTNPTNAQ TSLPRTGERN STWLYSLGIA
CLLVVLTsfY YLNKKRRKKEK

EF060-3 (SEQ ID NO:227)

AGAAGAAG TAGGGCAAAC GAATATCGGT GTAACGTTCT ATGGAGGAAA AGAGCCACTA
AAAACGGAAG GTGTCATTAA GCCAATAGAG CAACCAGTCA CTGATAAAGA TAAAAAACG
TCACAACAAC AAGACAAAGT GAGCAGAAAA ACCACTGCTA AAACGAATCC GACTAATGCA
CAGACGTCAT

EF060-4 (SEQ ID NO:228)

EEVGQTNIGV TFYGGKEPLK
TEGVIKPIEQ PVTDKDKKTS QQQDKVSRKT TAKTNPTNAQ TS

EF061-1 (SEQ ID NO:229)

TAATGGAACG ACCGACAGAA GAAGATTTTG AACTTACAAA TTAAAATTAA AATGGAGGAA
ATAATGATGA AAAAAATTCT TTTTGCTAGT TTATTAGTG CCACACTACT ATTTGGGGGA
AGTGAAATTT CTGCTTTTGC ACAAGAAATT ATCCCTGATG ATACTACGAC ACCGCCATT
GAAGTACCAA CAGAACCAAG TACACCAGAA AAGCCAACAG ATCCAACACC GCCAATTGAG
CCACCTGTAG ACCCTGTAGA GCCACCTATT ACACCAACGG AGCCAACAGA ACCGACAGAG
CCGACAACAC CAACAGAACC TACAACCTCT ACAGAGCCAA GTGAACCAGA ACAACCAACG
GAGCCAAGTA AACCAGTAGA ACCTGAAAAA CCAGTTACAC CAAGCAAACC AGCAGAACCC
GAAAAAATCT TGACACCAAC TAAACCAACA GAATCTGAAA AACCAGTACA ACCAGCAGAA
CCAAGCAAGC CAATCGACGT TGTGTAAACG CCAACAGGGG AATTAAATCA CGCTGGAAAT
GGTACACAAC AGCCAACAGT CCCTATTGAA ACAAGTAATT TGGCAGAAAT CACGCACGTG
CCTAGTGTAA CAACACCTAT TACAACCTACA GACGGAGAAA ACATTGTAGC TGTAGAAAAA
GGTGTTCAC TTACACAAAC AGCAGAAGGG TTAAAACCTA TTCAATCNAG TTACAAAGTA
TTGCCTAGCG GAAATGTAGA AGTAAAAGGT AAGGACGGTA AAATGAAGGT TTTACCATAC
ACAGGTGAAG AAATGAATAT CTTTTTATCT GCCGTAGCGG TATCTTGCTCT GTAG

EF061-2 (SEQ ID NO:230)

MMKILFASL FSATLLFGGS EISAFQEI PDDTTTPPIE
VPTPESTPEK PTDPTPIEP PVDPVEPPIT PTEPTEPTEP TTPTEPTTPT EPSEPEQPTE
PSKPVEPEKP VTPSKPAEPE KVTPTPKPTE SEKPVQPAEP SKPIDVVVTP TGELNHAGNG
TQQPTVPIET SNLAEITHVP SVTTPITTTD GENIVAVEKG VPLTQTAEGL KPIQSSYKVL
PSGNVEVKGK DGKMKVLPYT GEEMNIFLSA VAVSCL

EF061-3 (SEQ ID NO:231)

GAAATTT CTGCTTTTGC ACAAGAAATT ATCCCTGATG ATACTACGAC ACCGCCATT
GAAGTACCAA CAGAACCAAG TACACCAGAA AAGCCAACAG ATCCAACACC GCCAATTGAG
CCACCTGTAG ACCCTGTAGA GCCACCTATT ACACCAACGG AGCCAACAGA ACCGACAGAG
CCGACAACAC CAACAGAACC TACAACCTCT ACAGAGCCAA GTGAACCAGA ACAACCAACG
GAGCCAAGTA AACCAGTAGA ACCTGAAAAA CCAGTTACAC CAAGCAAACC AGCAGAACCC
GAAAAAATCT TGACACCAAC TAAACCAACA GAATCTGAAA AACCAGTACA ACCAGCAGAA
CCAAGCAAGC CAATCGACGT TGTGTAAACG CCAACAGGGG AATTAAATCA CGCTGGAAAT
GGTACACAAC AGCCAACAGT CCCTATTGAA ACAAGTAATT TGGCAGAAAT CACGCACGTG
CCTAGTGTAA CAACACCTAT TACAACCTACA GACGGAGAAA ACATTGTAGC TGTAGAAAAA
GGTGTTCAC TTACACAAAC AGCAGAAGGG TTAAAACCTA TTCAATCNAG TTACAAAGTA
TTGCCTAGCG GAAATGTAGA AGTAAAAGGT AAGGACGGTA AAATGAAGGT TT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF061-4 (SEQ ID NO:232)

QEII PDDTTTPPIE

VPTPESTPEK PTDPTFPIEF PVDPEVPPIT PTEPTPTPEP TTEPTPTPT EPSEPEQPTE
 PSKPVEPEKP VTPSKPAEPE KTVPTKPTF SEKPVFAEP SKPIDVVVTP TGELNHAGNG
 TQOPTVPIET SNLAEITHVP SVTTPITTTD GENIVAVKES VPLTQTAEGL KPIQSSYKVL
 PSGNVEVKGK DGKMKV

EF062-1 (SEQ ID NO:233)

TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
 DACTGGGTAA CTGTCCCTAT TCTTTTCTTA AGTGTTTAA GAGCCGTAGG ATTAGCTACT
 GATAATGTAC AAGCCGCGGA ATTAGATACG CAACCAGAAA CAACGACGGT TCAACCCCAAT
 AACCCCGACC TGCACTCAGA AAAGGAAACA CCTAAACGGG CAGTATCTGA AGAAGCAACA
 GTACAAAAAG ACACTACTTC TDAACCGACC AAAGTAGAAB AAGTAGCGCC AGAAAATAAA
 GGTACTGAAC AAAGTTCAGC TACCCCAAAT SATACACAA ACCGCGAACA ACCAACAGTA
 GGAGCTGAAA AATCAGCACA AGAACAACCA TAGTAAGCC CTGAAACAAC CAATGAACCT
 CTAGGGCAGC CAACAGAAGT TGCACCAGCT GAAAATGAAB TGAATAAATC AACGTCCATT
 CCTAAAGAAT TTGAAACACC ABACGTTGAT AAAGCAGTBB ATGAAGTAAA AAAAGATCCA
 AACATTACCG TTGTGAAAA ACCAGCAGAA GACTTAGGCA ACGTTTCTTC TAAAGATTTA
 GCTGCAAAAG AAAAAGAACT AGACCAACTA CAAAAGAAAC AAGCGAAAAA GATTGCCCAA
 CAAGCAGCTG AATTAAAGC CAAAATGAA AAAATTGCCA AAGAAAATGC AGAAATTGCC
 GCAAAAAACA AAGCNGAAAA AGAGCNGTAN GANAAAGAA TCCGNGAATA CAACAAGCAT
 AAGAACGAAA ACAGCTATGT CAATGAAGCG ATTAGTAAAA ACCTAGTGTT CGATCAATCT
 GTCGTGACGA AAGACACTAA AATTCGTCC ATTAAGGCC GAAAATTTAT CAAAGCAACT
 GATTTTAAATA AAGTAAATGC AAGGATTCA AAAGATATCT TTACAAAATT ACGGAAAGAT
 ATGGGNGGGA AAGNTACTGG CAACTTCCAG AATTCCTTTG TAAAAGAGGC AAATCTTGGG
 TCTAATGGTG GGTATGCGGT TCTTTTAGAA AAAAAATAAC CAGTGACAGT GACCTATACA
 GGAATAACG CTAGTTATTT AGGACGTAAA ATTACAAAAG CAGAATTTGT TTATGAACTA
 CAATCCTCAC CAAGCCAAAG TGGAACGTTA AATGCAGTAT TTCAAACGA TCCGATTATC
 ACNGCTTTTA TTGGTACAAA CAGAGTCAAT GGTAAAGATB TTAACACAG CTTAACGATT
 AAGTTCTTTG ATGCGTCAGG TAAAGAAAGTA CTACCAGATA AAGATAGTCC ATTTGCGTAT
 GCGCTGTCTT CTTTAAATTC AAGTTTAAAC AATAAAGGTG GCCATGCGGA ATTTGTTTCT
 GATTTTGGGG CNAACAATGC GTTCAAATAC ATTAATGGNT CNTATGTGAA AAAACAAGCG
 GATGGGAAAT TTTACTCACC GGAAGATATT GACTATGGCA CAGGACCTTC TGGATTGAAA
 AATAGTGATT GGGACGCTGT AGGTCAACAAG AATGCCTACT TTGGTTCAGG TGTAGGTCTA
 GCNAATGGNC GTATTTCTCT TCTTTTGGT ATGACAACAA AAGGAAAAAG TAATGTGCCT
 GTATCTAGTG CGCAATGGTT TGCCTTTAGN ACTAACTTAA ATGCGCAATC AGTGAAGCCT
 ATTTTCAATT ATGGGAATCC AAAAGAACCA GAAAAAGCAA CGATTGAATT CAATNGATAC
 AAAGCCAATG TCGTTCCTGT NCTTGTCN CNATAAAGAAG TCACTGATGG NCAGAAAAAT
 NTCAATGATT TAAATGTGAA NCGTGGCGAT TCTTTACAAT ACATTGTGAC AGGGGATACG
 ACAGAAGTTG CCAAAGTAGA TCCAAAAACA GTAACNAAAC AAGGGATTCC AGATACNTTT
 GATGCAGAAA AAGTGACGAT TGATTTATCC AAAGTGAAAG TTTATCAAGC AGACGCAAGT
 CTNAACGANA AAGACTNAAA AGCTGTTGCT GCAGCNATTA ATTCAGGAAN AGCTAAAGAC
 GTGACTGCTT CTTATGANCT CAATTTAGAT CAAAAACCG TCACAGCAAT GATGAAAACC
 AACGNGACG GNTCNGTTGT TTTAGCAATG GGGTATAAAT ATTTACTTGT CTTGCCGTTT
 GTAGTGAAAA ATGTAGAAGG CGATTTTGAA AATACAGCTG TTCAGCTGAC AAANGATGGN
 GAAACGGTAA CAAATACAGT GATTAACCAT GTGCCAGGTA GTAATCCTTC CAAAGATGTA
 AAAGCAGATA AAAACGGTAC AGTTGGCAGT GTTCTCTTAC ATGATAAAGA TATTCCGTTA
 CAAACAAAAA TTTATTATGA AGTGAATCT TCCGAACGTC CAGCNAACTA TGGCGGAATN
 ACNGAAGAAT GGGGCATGAA TGATGTCCTG GACACGACCC ATGATCGTTT CACAGGNAAA
 TGGCAGGCTA TTACNAANTA TGACCTTAAA GTAGGCGANA AAACGTTAAA AGCAGGAACA
 GATATTTCTG CCTACATTCT TTTAGAAAAC AAAGACAATA AAGACTTGAC GTTTACNATG
 AATCAAGCAT TATTGGCNGC NTTAAATGAA GGAAGCAATA AAGTAGGCAA ACAAGCTTGG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCTGTGTATC TGGAAGTCGA ACGGATNAAA ACAGGTGAGG TAGAAAAACAC GCAAACAGAA
 AACTACAACA AAGAGCTTGT NCGTTCTAAT ACNGTGGTGA CGCATAACNC TGATGATCCA
 AAACCAACCA AAGCCGTTC AACAAGAAA GGGGAAGANA TTAANCATGG AAAAGTNGCT
 CGTGGTGATG TTCTTTCTTA TGAAATGACN TGGGACTTAA AAGGCTACGA TAAAGACTTT
 GCCTTTGATA CAGTCGATCT TGCGACAGGC GTTCTTTCT TCGATGATTA CGATGAAACG
 AANGTGACAC CAATCAAAGA CTTACTTCGT GTCAAAGATT CTAAAGGGGN AGACATTACG
 AACCAGTTCA CGATCTCNTG GGACGATGCC AAAGGCAGGG TGACNATNTC TGCCAAAGAC
 CCACAAGCCT TTATTCTAGC GNATGGTGGG CAAGAATTGC GTGTAAACNCT CCCTACAAAA
 GTCAAAGCCG ATGTTTCTGG NGATGTTTAT AATTCAAGGG AACAAAATAC ATTTGGNCAA
 CGAATTAAAA CCAATACNGT TGTCAACCAT ATTCCAAAAG TGAANCCTAA AAAAGACGTG
 GTTATTAAAG TNGGTGACAA ACAAAGTCAA AATGGNAGCA CAATCAAATT AGGGGAGAA
 TTCTTCTATG AATTTACAAG TAGTGACATT CCTGCAGAA ACCTGGNGT TGTGGAGAA
 TGGTCGATTA GCGATAAACT AGACGTCAA CATGACAAAT TTAGTGCCCA ATGGTCTGTG
 TTTGCCAATT CTAATTTTGT TTTAGCAGAC GGAACCAAAG TGAATAAAGG GGACGACATT
 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
 TTTTNGATG CGATGAATCT AAAAGAAAAC AAAACSTTG CACACTCATG GAAAGCGTTC
 ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAACA CAATCGAAGA ATCTTTCAAC
 AATGAGAAGA TAAAAACNAA TACGGTAGTG ACNCATAGGC CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAACAG CGCAAGCACC AGTAGAGCCA
 TTAGTGGTAG AAAAGGCAAG TGTNGTGCCA GAATTGGTGC AAACAGGCGA AAAACAAAAT
 GTCTTATTAA CGGTAGCTGG TAGTTTAGCC GCAATGCTTB GCTTAGCAGG CTTAGCCTTT
 AAACGTAGAA AAGAAACAAA ATAA

EF062-2 (SEQ ID NO:234)

MKAKK QYKTYKAKNH WVTVPILFLS VLGAVGLATD NVQAAELETTQ PETTTVQPNN
 PDLQSEKETP KTAVSEETV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAQEQPV VSPETTNEPL GQPTVEVAPAE NEVNKSTPIP KEFETPDVVK AVDEVKKDPN
 ITVVKEPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK IAKENAEIAA
 KNKAERKXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGKFIKATD
 FNKVNAGDSK DFTKLRKDM GKGXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAEFVYELQ SSQSQSGTLN AVFSNDPIIT AFIGTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGANNAFKYI NGSYVKKQAD
 GKFPSPEDID YGTGPSGLKN SDWDVAVGHKN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAXT NLNAQSVKPI FNYGNPKPEP KATIEFINYK ANVVPVLVPN KEVTDGQKNX
 NDLNVXRGDS LQYIVTGDIT ELAKVDPKTV TKQGIRDFED AEKVTIDLSK VKVYQADASL
 NXKDXKAVAA AINSGXAKDV TASYXLNLDQ NVTAMAKTN ADGSVVLAMG YKYLVLPLFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLQ
 TKIYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGEW HAITYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGFVAR GDVLSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDET XVTPIKDLLRV KDSKGXDTN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFQQR IFNTNTVNHV PKVXPVKDVV
 IKVGDQKQSN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNGGDDIS KLEFMTFEQG VVKITASQAF XDMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPTTP EKTIVVPPTP KTPQAPVEPL
 VVEKASVVE LPQTGEKQNV LLTVAGSLAA MLGLAGLGFK RKKETK

EF062-3 (SEQ ID NO:235)

TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
 CACTGGGTAA CTGTCCCTAT TCTTTTCTTA AGTGTGTTAG GAGCGTAGG ATTAGCTACT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GATAATGTAC	AAGCCGCGGA	ATTAGATACG	CAACCAGAAA	CAACGACGGT	TCAACCCAAT
AACCCCGACC	TGCAGTCAGA	AAAGGAAAACA	CCTAAAACGG	CAGTATCTGA	AGAAGCAACA
GTACAAAAAG	ACACTACTTC	TCAACCGACC	AAASTASAA	AASTAGCGGG	AGAAAATAAA
GGTACTGAAC	AAAGTTCCAG	TACGCCAAAT	GATACCAGAA	ACGTCGAACA	ACCAACAGTA
GGAGCTGAAA	AATCAGCACA	AGAACAACCA	GTASTAAGCT	CTGAACCAAD	CAATGAACCT
DTAGGGCAGC	CAACAGAAGT	TGCACCAGCT	GAAAATGAAT	TGAATAAATC	AACGTCCATT
CCTAAGAAT	TTGAAACACC	AGAGCTTGAT	AAAGCAGTTT	ATGAAGTAAA	AAAAGATCCA
AACATTACCG	TTGTTGAAAA	ACCAGCAGAA	GACTTAGGCA	ACGTTCTCTC	TAAAGATTTA
GCTGCAAAAG	AAAAAGAAGT	AGACCAACTA	CAAAAAAAT	AAGCGAAAAA	GATTGCCCAA
GTAGCAGCTG	AATTAAGAAG	CAAAAAATGAA	AAAAATTGCA	AAGAAAATGC	AGAAATTGCG
GCAAAAAACA	AAGCNGAAAA	AGAGCGNTAN	GAAAAAATA	TGBCNGAATA	CAACAAGCAT
AAGAACGAAA	ACAGCTATGT	CAATGAAGCG	ATTAGTAAAA	ACCTAGTGTT	CGATCAATCT
STCGTGACGA	AAGACACTAA	AATTTCTGTC	ATTAAAGGGB	GAAAATTTAT	CAAAGCAACT
GATTTTAATA	AAGTAAATGC	AGGGGATTCA	AAAGATATCT	TTACAAAAAT	ACGGAAAGAT
ATGGGNGGGA	AAGNTACTGG	CAACTTCCAG	AATTCCTTTC	TAAAAGAGGC	AAATCTTGGG
TCTAATGGTG	GSTATGCGGT	TCTTTTAGAA	AAAAATAAA	CAGTGACAGT	GACCTATACA
GGACTAAACG	CTAGTTATTT	AGGACGTAAA	ATTACAAAA	CABAATTTGT	TTATGAACTA
CAATCCTCAC	CAAGCCAAAG	TGGACGGTTA	AATGCATAT	TTTCAAACGA	TCCGATTATC
ACNGCTTTTA	TTGGTACAAA	CAGAGTCAAT	GGTAAGGATG	TTAAAACACG	CTTAACGATT
AAGTTCTTTG	ATGCGTCAGG	TAAAGAAGTA	CTACCAATA	AAGATAGTCC	ATTTGCGTAT
GCGCTGTCTT	CTTTAAATTC	AAGTTTAACG	AATAAABSTB	GCCATGCGGA	ATTTGTTTCT
GATTTTGGGG	CNAACAATGC	GTTCAAATAC	ATTAATBENT	CNTATGTGAA	AAAACAAGCG
GATGGAATA	TTTACTCACC	GGAAGATATT	GACTATGSEA	CAGGACCTTC	TGGATTGAAA
AATAGTGATT	GGGACGCTGT	AGGTCACAAG	AATGCCTACT	TTGTTTCAGG	TGTAGGTCTA
GCNAATGGNC	GTATTTCCCTT	TTCTTTTGGT	ATGACAAAA	AAGBAAAAAG	TAATGTGCCT
GTATCTAGTG	CGCAATGGTT	TGCCTTTAGN	ACTAATTAA	ATGTCGAATC	AGTGAAGCCT
ATTTTCAATT	ATGGGAATCC	AAAAGAACCA	GAAAAAGCAA	CGATTGAATT	CAATNGATAC
AAAGCCAATG	TCGTTCTCTG	NCTGTGCCN	AATAAAGAA	TCACTGATGG	NCAGAAAAAT
NTCAATGATT	TAAATGTGAA	NCGTGGCGAT	TCTTTAGAA	ACATTGTGAC	AGGGGATACG
ACAGAACTTG	CCAAAGTAGA	TCCAAAAACA	GTAACNAAA	AAGGGATTCC	AGATACNTTT
GATGCAGAAA	AAGTGACGAT	TGATTTATCC	AAAGTGAAA	TTTATCAAGC	AGACGCAAGT
CTNAACGANA	AAGACTNAAA	AGCTGTTGCT	GCAGCNATTA	ATTCAGGAAN	AGCTAAAGAC
GTGACTGCTT	CTTATGANCT	CAATTTAGAT	CAAAACACCG	TCACAGCAAT	GATGAAAACC
AACGCNGACG	GNTCNGTTGT	TTTAGCAATG	GGGTATTAAT	ATTTACTTGT	CTTGCCGTTT
GTAGTGAAAA	ATGTAGAAGG	CGATTTTGAA	AATACAGCTG	TTACAGTGAC	AAANGATGNN
GAAACCGTAA	CAAAATACAGT	GATTAACCAT	GTGCCAGGTA	GTAATCCTTC	CAAAGATGTA
AAAGCAGATA	AAAACGGTAC	AGTTGGCAGT	GTTTCTCTAC	ATGATAAAGA	TATTCCGTTA
CAAAACAAAA	TTTATTATGA	AGTGAAATCT	TCCGAACGTC	CAGCNAACTA	TGGCGGAATN
ACNGAAGAAT	GGGGCATGAA	TGATGTCTTG	GACACGACCC	ATGATCGTTT	CACAGGNAAA
TGGCACGCTA	TTACNAANTA	TGACCTTAAA	GTAGGGGANA	AAACGTTAAA	AGCAGGAACA
GATATTTCTG	CCTACATTCT	TTTAGAAAAC	AAAGACAATA	AAGACTTGAC	GTTTACNATG
AATCAAGCAT	TATTGGCNGC	NTTAAATGAA	GGAAGCAATA	AATAGGCAA	ACAAGCTTGG
TCTGTGTATC	TGGAAGTCGA	ACGGATNAAA	ACAGGTGACG	TAGAAAAACAC	GCAAAACAGAA
AACTACAACA	AAGAGCTTGT	NCGTTCTAAT	ACNGTGCTGA	CGCATACNCC	TGATGATCCA
AAACCAACCA	AAGCCGTTCA	TAACAAGAAA	GGGGAAGANA	TTAANCATGG	AAAAGTNGCT
CGTGGTGATG	TTCTTTCTTA	TGAAATGACN	TGGGACTTAA	AAGGGTACGA	TAAAGACTTT
GCCTTTGATA	CAGTCGATCT	TGCGACAGGC	GTTTCTTTCT	TGATGATTA	CGATGAAACG
AANGTGACAC	CAATCAAAGA	CTTACTTCGT	GTCAAAGATT	CTAAAGGGGN	AGACATTACG
AACCAAGTTCA	CGATCTCNTG	GGACGATGCC	AAAGGCACCG	TGACNATNTC	TGCCAAAGAC
CCACAAGCCT	TTATTCTAGC	GNATGGTGGG	CAAGAATTGG	GTGTAACNCT	CCCTACAAAA
GTCAAAGCCG	ATGTTTCTGG	NGATGTTTAT	AATTCAGCGG	AAADAAATAC	ATTTGGNCAA
CGAATTAAAA	CCAATACNGT	TGTCAACCAT	ATTCCAAAAG	TGAANCCTAA	AAAAGACGTG
GTTATTAAAG	TNGGTGACAA	ACAAAGTCAA	AATGGNGGCA	CAATCAAATT	AGGGGAGAAN
TTCTTCTATG	AATTTACAAG	TAGTGACATT	CCTGCAGAA	ACGCTGGNGT	TGTGGAAGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TGGTCGATTA GCGATAAACT AGACGTCAAA CATGACAAAT TTAGTGGCCA ATGGTCTGTG
 TTTGCCAATT CTAATTTTGT TTTAGCAGAC GGAACCAAAG TGAATAAAGG GGACGACATT
 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
 TTTTITNGATG CGATGAATCT AAAAGAAAAC AAAAACGTTG CACACTCATG GAAAGCGTTC
 ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAACA CAATCGAAGA ATCTTTCAAC
 AATGAGAAAGA TTAAAAACNA TACGGTAGTG ACNCATACGC CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAAAC CGCAAGCACC AGTAGAGCCA
 TTAGTGGTAG AAAAGGCAAG TG

EF062-4 (SEQ ID NO:236)

AELDTQ PETTTVPNN
 PDLQSEKETP KTAVSEETV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAQEOPV VSPETTNEPL GQPTVEVAPAE NEVNKSTSIP KEFETPDVVK AVDEVKKDPN
 ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK IAKENAEIAA
 KNKAERKRX KEVAEYNKHK NENSYVNEAI SKNLVFIQSV VTKDTKISSI KGGKFIKATD
 FNKVNAGDSK DIFTKLKRDG GGGXTGNFQD SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAFFVYELQ SSPSQSGTLN AVFSNDFIIT AFICTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGAINNAFKYI NGSYVKKQAD
 GKFYSPEDID YGTGSPGLKN SDWDVAGHKN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAXFT LNAQSVKPI FNYGNPKPEE KATIEFHXK ANVVPVLVPN KEVTDGQKNX
 NDLNVXRGDG LQYIVTGDIT ELAKVDPKTV TKQGITRFTD AEKVTIDLSK VKVYQADASL
 NXKDXKAVAA AINSXAKDV TASYXLNLDQ NTVTAMETTH ADGSVVLAMG YKYLVLVLPFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSFDVH AEKNGTVGSV SLHDKDIPLO
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGFVAF GDVLSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDETX VTPIKDLRLV KDSKXEDITH QFTISWDDAK GTVTVXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQE IKTNTVNNHI PKVXPBKDVV
 IKVGDQKQSN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISKDLVKH DKFSGQWSVF
 ANSNFVLADG TKNVKGDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
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EF063-1 (SEQ ID NO:237)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

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```


TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 FNKVNAGDSK DIFTKLRLKDM GKKXTGNFQH SFVKEANLGE NGDYAVLLEK NKPVTVTYTG
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 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPTQEP EKTIVVPTTP KTPQAPVEPL
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EF063-3 (SEQ ID NO:239)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF063-4 (SEQ ID NO:240)

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 FNFVNAGDSK DIFTKLKMD GOKXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
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EF064-1 (SEQ ID NO:241)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF064-2 (SEQ ID NO:242)

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 ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AELKAKNEK IAKENAEIAA
 KNKAERKEXX KEVAEYNKHK NENSYVNEAI SKNLVFLQSV VTFDTKISSI KGGKFIKATD
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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF064-3 (SEQ ID NO:243)

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 GTCAAAGCCG ATGTTTCTGG NGATGTTTAT AATTCAGGCG AACAAAATAC ATTTGGNCAA
 CGAATTA AAA CCAATACNGT TGTCAACCAT ATTCCAAAAG TBAANCCTAA AAAAGACGTG
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 TTCTTCTATG AATTTACAAG TAGTGACATT CCTGCAGAA ATGCTGGNGT TGTGGAAGAA
 TGGTCGATTA GCGATAAACT AGACGTCAAA CATGACAAAT TTAGTGGCCA ATGGTCTGTG
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 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTBA AAATACGGC CAGTCAAGCC
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 AAACGTAGAA AAGAAACAAA ATAA

EF064-4 (SEQ ID NO:244)

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 NXKDXKAVAA AINSXKADV TASYXLNLDQ NTVTAMMKTN ADGSV/LAMG YKYLVLVLPFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLQ
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTSKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS WYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GCVLSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKSGXDTN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFQQR IKTNVTVNHI PKVXPBKDVV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IKVGDQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNGGDDIS KLFMTTFEQG VVKITASQAF XIAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EMTVIVPPTP KTPQAPVEPL
 VVEKASV

EF065-1 (SEQ ID NO:245)

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 GAAACGGAAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
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 GTGATGCTGG CTTTCATATCG CGGCGGAAAA CAATTTATGT TTCCTGATGG AAAGACAAAA
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 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
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TABLE 1 Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAACCTAAAC AACCGGTAAA ACCGAAAAAA CGGTGAGCTT CTACAAATCA TCAAGCACCA
 ACGAACCCAG TCAATTTTGG AAAATCAGCA ASTAAAGGAA TTGATTTTACC AATGACTAAT
 ACAACASTAA ATCCACTTTA CATGATCGCA GGTTTAATTT TCGTTATAGT GGTATTAGC
 TTTTCCATAA CAAAAAATAA AAAAAGAAAA AATTAG

EF065-2 (SEQ ID NO:246)

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 LKALDVTYNQ THGELTNRKT YFLLVTDGVA NTELDGYLEH TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLF SVNSYFDYK TEVGPFEVKQE
 LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTIDAAT LNESGTMNQG TIAKEFPEAT
 IPKNDNAHAC DVTPEPTIT KDIENTEHLN LTNRDSFDW HVTAFGNET STWTQASMVD
 DINKVLDDID VEVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLSG HTYTMITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHSEKPT VTPPPVDFNI AKDVEGQEH
 DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDDIT DVEVTDENGK DVTANGKV
 ENNKVTFEMN XQADSYDYLS GHTYTMITTT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHSEKPT TVTPPAPTPE DPTITKDEG QEHLDLTNRD QEFKWNVKT FGNSTSTWTQ
 ASMVDDINKV LDITDVKVXX ENKDVTDNG IVTQENNKVT FENKKNDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
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 GITKNKKRKN

EF065-3 (SEQ ID NO:247)

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 GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATST TTCTGATGG AAAGACAAAA
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 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTCAATAGT ATACAATGAC TATCACCCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGAGG TGTACATTC CAACAAACCA
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TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAAGG TAAAAACAGC TTTCGGTAAC
GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAANCAAG CAGACAGCTA TGACTATTTA
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GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAAGG AAGCCGACTT GAACCTTGGC
AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
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GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
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EF065-4 (SEQ ID NO:248)

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VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFPVKQE
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DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTPEMIR QADSYDYLSE HTYMTITTK
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EF066-1 (SEQ ID NO:249)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAAATTACTA ACCAAGGCTA TGAATGATT AATCGGTATT GGGAAAGTST TGAATCTTTA
 AGTTCAGTGA ATTCATACTT TGATAAATAT AAAACAGAAAG TGGGTCCTTT TGTAAAACAA
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 ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
 TTTGGCATAA CAAAAATAA AAAAAGAAAA AATTAG

EF066-2 (SEQ ID NO:250)

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 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PKQPLPKPKP LTPTNHQAPT NPVNFGKSAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
GITKNKKRKN

EF066-3 (SEQ ID NO:251)

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GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
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EF066-4 (SEQ ID NO:252)

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LKLALDTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFPVKQE
LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHVEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
IPKNDNAHAC DVTPEPTIT KDIENTEHLN LTNREDSFDW HVKTAFGNET STWTQASMVD
DINKVLDIID VKVT

EF067-1 (SEQ ID NO:253)

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GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATGT TTCCTGATGG AAAGACAAAA
ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACC GCCCCA
GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGTCAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
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 GAGTTGCAAC AAGGCTCTAG CACACAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
 TTTACAACCC AATTAAACA AATTGTCAAA GATCGTGTGG CGCAATCGAG ACCAGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTGAT ATTCAATCTG CGACCGCTAG GGACGATGCT
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 ACAAAGATA TCGAAAATCA AGAACACTTA GATTTAACA ATCGTGAAGA TAGTTTCGAT
 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCAAGC CAGCATGGTG
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EF067-2 (SEQ ID NO:254)

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 LKLALDYNQ THGDLNKRKT YFLLVTDGVA NTFLDGYLHK TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDEYK TEVGPFFVKQE
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 NDVPVQINGQ TISATSTEGY VGNITIHVEY KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
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 DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLGS HTYTMITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHNSKPT VTPPPVLPNI AKDVEGQEHL
 DLTNRDQEFH WNVKTAFGNE TSTWTQASMV DDINKVLDT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSYDYL GHTYTMITTT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHNSKP TVTPPAPTPE DPTITKDIEG QEHLDTNDRD QEFKWNKETA FNETSTWTQ

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFCKSAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF067-3 (SEQ ID NO:255)

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 GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACTTT TGAAATGAAC
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 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTCATTTC CAACAAACCA
 ACCGTAAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAAATT AAATGGAACG TCAAAACAGC TTTCGGTAAC
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EF067-4 (SEQ ID NO:256)

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 DLNTRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKVTQ
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 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFCKSAS KGIH

EF068-1 (SEQ ID NO:257)

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 GCCGCAAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCTCTCTGA GTTAAGAGGA
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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 ATTACCAAGTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTBAC GGAAGTGAAT
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 GGTGTTTACG GCSTAAATGA GTTAGTGGAT GCTTCCTTAC TAGGCACAAE CACGGTTACT
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 ATTGGTGACA TTAAGTGAGA TTCAACAAC TGTATGAAA TCACTGGGAC GGCGGACCCT
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 ACTGATGGCA AATACACAGT GACTTTAGAG CCAGGGAAGG CCTCAGSTAA CGAAACAATA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTTACTTTTT	TGACTGCCGT	TTTGAATGCA	GCCAATGATT	TAACCAATGT	GATTACTCAA
ATTACCACTG	GGGCGTTAGG	GAATTTAACT	GGTGTGATA	TTGATTGAC	GGAAGTGAAT
CGTCAATTGG	AATTAGTTAA	TAACATTGAA	AACTTAGGTG	CTGCTTCATT	TACAGCTCCG
GAAACGTTAG	CAGCTGACGG	CTCATACATT	AGTGCACCGA	TTAGTGATGG	TTTAGGGTTA
GTTTTAGCCC	AAAATGTTTC	AAACATCTTA	CAAGATTGGA	ATGCGGCAGT	TCAAGCTTTG
GAGGCAAAAG	GTACCAGTAT	CCCAAGTAAT	CTTGTCCCGG	CAGCTATAAA	TGCAGCCTTG
CTTCCTGTCA	AAGGCACGGT	AAACGTGGCT	GTTTCAGGTG	CTTTGCCTTT	ATTAGCGGTT
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GGAACAGTCG	TTCAAACAGA	TCTTTTAGAC	GTTAATTTAT	TAGCAACAGC	AGACCGTGTA
TCCAACATTT	ATTTTGCTGC	AGGCACTACT	AGTGAAGTAA	CCGCACCAAC	AATCACAGGA
GTAACAGGTA	ATTC AACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
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GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA	GCAGGCGCCA	ATGAAACGTT	AACCGCCGTA
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GGTACAACAG	TTGAGGTGCG	TGACGCCGAT	GGCACAGTCC	TTGGCATGGC	AACTACTGGA
ACTGATGGCA	AATACACAGT	GACTTTAGAG	CCAGGGAAGG	CCTCAGCTAA	CGAAACAATA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

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ACTGTGGTAG CGAAAAATGC AACAGGAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA
GTGGACTTAG CCATACCAAC CATTCATTCT ATTATCGGAA ATTCTABTAA AGGTTACGAA
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EF068-2 (SEQ ID NO:258)

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SIAVTSGTIS ASAAVLDIEL LSNVTSNNDG GTSTSNFWTA ANQNQPVNFT VSGGALADAS
AVFSGQKQAV LVPPELRGN VAAAGSAAIN TNVTIDLSKV TFLTAVLNAA NDLTNVITQI
TSGALGNLTG VDIDLTEVNR QLELVNHIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTVNVAV SGALPLLA VG
GSGVNELVDA SLLGTTTVTL PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADEA TVTAPTITGV TGNSTAGYEV
KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
VKGTAEVGTI IEVRDAAGTV LGTATTGTDG KYTVTLDSGT ATANQTLNVV AKNASGTESQ
PATATTPADV TAPTVDNITG HSGSGYEITG TADPNTTIEV RDPGSAVIGT GTSDANGDFT
VTLPTGTTNP GDTLTVIGKD MAGNESQPTL VLVPADATVT APTVTGVTGN SVAGYQVTGT
ADPNATIEIR DADGNVIATG TADGTGSFAV NLPAGTANAN ETLTALAKDP AGNTSTPTTF
QTPADEVVAP PSVDKVTGNT TQGYQVTGTA ELGTTIEVRA TDGTVLGTAT TGPTGQYTVT
LASGKATAKQ TVNVVAKNDT GLESQPTTAM TPADVTTPTI GDITGDSITG YEITGTADPN
TTIEVRNPDG TIIGTTTDD QGNFTVDLPA GAANPGDILT VVGKDGDSNE SQPTEVTVPE
DATVAAPTIVT TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTTTGA GAFTITLPTG
TATANEALTA IAKDAAGKES NPTAFKTPAD PDAPVATPTV DKITGSTTNG YQVVGAAEVG
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TPGETITII KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGYTVT GTADPNVTQ
FYNSSSQLLA SGNTTTGCTF SVHIAAGLAT EKETLTALIT DTQGNVSPKT TFMTPADITG
EPEIKIAAPT VSSVLGTSKA GYLIKTAEP NRIQISNRL LRSVIAVGAT DAEGNFAIQL
TAGQATAQQS LLATATDGAG HYSTATTFMT PADPTNPGGG NGNTGGNNGN TGGNTGNNGA
TGGNNGNSN TGSNPNCGSG LGTTGSGLGS LGNGLGTNGS GYHPKLSTIS YGTGNHGKGT
YLPSTGEKES SAVTTSLFGA FVALLASMI IKRKRKN

```

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF068-3 (SEQ ID NO:259)

CTC TGGCACAATC AGTGCATCAG CAGCGGTCTT GGATATCGAA
 CTATTATCAA ATGTTACGTC AAATAATGAC AGTGGCACTT CAACGAGTAA TCGTTGGACA
 GCGGCAAACC AAAATCAACC AGTTAATTTC ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCCTCCTGA GTTAAGAGGA
 AATGTAGCTG CAGCAGGCAG CGCAGCAATC AATACCAATG TCACGATTGA TCTTTCAAAA
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 ATTACAGTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTGAC GGAAGTGAAT
 CGTCAATTGG AATTAGTTAA TAACATTGAA AACTTAGGTG CTGCTTCATT TACAGCTCCG
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 GTAACAGGTA ATTCACAGC AGGTACGAA GTTAAAGGAA CTGCCGATGC CAATGCCACG
 GTTGAAATCC GAAATGCAGG AGGCACCGTA ATAGGCACAG GTACCGCTGA TGGGACAGGA
 GCGTTTACAG TTACCGTTCC CGCAGGTGAA GCAGGCGCCA ATGAAACGTT AACC GCCGTA
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 CCAACAACGT TCCAAACACC AGCGGATGAA GCAACCGTAA CCGCACCAAC AATCACAGGA
 GTGACAGGTA ATTCACAGC AGGTACGAA GTTAAAGGAA CTGCCGATGC CAATGCCACG
 GTTGAGATCC GAAATGCAGG AGGTGCCGTG ATAGGTACAG GTACTGCTGA TGGGACAGGG
 GCATTTACAG TTACATTCC CGCAGGTGAA GCAGGTGCGA ATGAAACGTT AACC GCCGTA
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EF068-4 (SEQ ID NO:260)

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 TSGALGNLTG VDIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTNVNAV SGALPLLA VG
 GSGVNELVDA SLLGTTFTVL PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTEXTP TTFQTP

EF069-1 (SEQ ID NO:261)

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 GTAAGTATAG CTGTTACCTC TGGCACAATC AGTGCATCAG CAGCGGTCTT GGATATCGAA
 CTATTATCAA ATGTTACGTC AAATAATGAC AGTGGCACTT CAACGAGTAA TCGTTGGACA
 GCGGCAAAACC AAAATCAACC AGTTAATTTC ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCCTCCTGA GTTAAGAGGA
 AATGTAGCTG CAGCAGGCAG CGCAGCAATC AATACCAATG TCACGATTGA TCTTTCAAAA
 GTTACTTTTT TGA CTG CCGT TTTGAATGCA GCCAATGATT TAACCAATGT GATTACTCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATTACCAGTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TGGATTTCAG GGAAGTGAAT
 CGTCAATTG AATTAGTTAA TAACATTGAA AACTTATGTG CTGCTTCAAT TACAGCTCCG
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 GTTTTAGCCG AAAATGTTTC AAACATCTTA CAASATTTGA ATGCGGATGT TCAAGCTTTG
 GAGGCAAAA GATCCAGTAT CCGAAGTAAT GTTGTGCGCG CAGCTATAAA TGCAGCCTTG
 GTTCTGTGCA AAGGACCGGT AAACGTGGCT GTTTCAGGTG CTTTGCGTAT ATTAGCGGTT
 GGTGTTTACG GCCTAAATGA GTTAGTGGAT GCTTCTTTAC TAGGCACAA CACGGTTACT
 TTACCAACTA CCCTTTCAAC ACCTCAAAAT TTATCCAATA ATTTAGATBT TCGTTTTGTA
 GGAACAGTCG TTCAAACAGA TCTTTTAGAC GTTAATTTAT TAGCAACAG AGACGGTGTA
 TCCAACATTT ATTTTGCTGC AGGCCTACT AGTGAAGTAA CCGCACCAAC AATCACAGGA
 GTAACAGGTA ATTCAACAGC AGGTACGAA GTTAAAGGAA CTGCCGATGC CAATGCCACG
 GTTGAAATCC GAAATGCAGG AGGCACCGTA ATAGGCACAG GTACCGGTGA TGGGACAGGA
 GCGTTTACAG TTACCGTTCC CGCAGGTGAA GCAGGCGCCA ATGAAAGCTT AACC GCCGTG
 GCGAAAAACG CCAGCGGNAC AGAAAGNAC CCAACAACGT TCCAAATGTC AGCGGATGAA
 GCAACCGTAA CCGCACCAAC AATCACAGGA GTGACAGGTA ATTCAATGTC AGGTACGAA
 GTTAAAGGAA CTGCCGATGC CAATGCCACG GTTGAAATCC GAAATGTAAG AGGCACCGTA
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 GTGACAGGTA ATTCAACAGC AGGTACGAA GTTAAAGGAA CTGCCGATGC CAATGCCACG
 GTTGAGATCC GAAATGCAGG AGGTGCCGTG ATAGGTACAG GTACTGCTGA TGGGACAGGG
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 CAACCAGCAA CCGCGACAAC ACCAGCTGAT GTCCTGTCAC CAACAGTGA TAACATCACA
 GGCAACTCTG GTTCGGGTTA TGAAATTACA GGAACAGCAC ACCCTAATAC AACAATCGAA
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 TTAGTTATTG CTACGGGAAC GACTGATGGT GCTGGCGCAT TTACAATCAC TCTTCCGACG
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 GGTACAACAG TTGAGGTGCG TGACGCCGAT GGCACAGTCC TTGGCATGGC AACTACTGGA
 ACTGATGGCA AATACACACT GACTTTAGAG CCAGGGAAGG CCTCAGCTAA CGAAACAATA
 ACTGTCGTAG CGAAAAATGC AACAGSAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTCTGACTTAG CCACACCAAC CATTGATTCT ATTACCGGAA ATTCTAGTAA AGGTTACGAA
 ATCACTGGAA CGGCGGAGCC AAAAACCCTT ATTGATGTCC GTGACGCAAA CGGAACCATC
 ATTTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGACTCTAAG AGCTGGCGTA
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 CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAACCTAT TACGAAGGTT
 GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAACTG CTGATCCAAA TGTCACGGTT
 CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGGCA ATACAACCTA TGGAGGTACC
 TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAAG CGCACTAACC
 ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAAG CGATATTACG
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 GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACCTAGGCA ATGGCCTCAG TACAAATGGT
 AGTGGCTACC ACCCTAAACT AAGTACCATC AGTTATGGCA CTGGAAATCA CGGGAAAACA
 GGCTACTTAC CTAGCACAGG TGAAAAAGAG TCTTCAGCCG TGACAACAAG TTTGTTTGCG
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EF069-2 (SEQ ID NO:262)

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 AVFSGQKQAV LVVPPELRGN VAAAGSAAIN TNNVTLDSKV TFLTAVLHMA NDLTNVITQI
 TSGALGNLTG VDIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTNVNAY SGALPLLAVG
 GSGVNELVDA SLLGTTTIVTL PTTVSTPQNL SNNLDARFVG TVVQTDLLIV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
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 KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
 TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
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 TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGDTLT VVGKDGDSNE SQPTEVTVPE
 DATVAAPTIV TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTEDSA GAFTITLPTG
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 TAGQATAQQS LLATATDGAG HYSTATTFMT PADPTNPGGG NGNTGGNNGN TGGNTGNNGA
 TGGNNGNSN TGSNPNGGSG LGTTGSGGLS LGNGLGTNGS GYHPKLTIS YGTGNHGKTG
 YLPSTGEKES SAVTTSLFGA FVALLASMI IKRKRKN

EF069-3 (SEQ ID NO:263)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 GUGAAAAACG CCAGCGGTAC AGAAAGTACC CCAACAAAGT TCCAAACGCG ACAGGATCCT
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 GAGGTCAAAG GGAAGTCTGA AATTGGGACC ACCATTGAGG TTCGCGATGC AGCTGGCACG
 GTCTTTGGTA CTGCAACAAC TGGAACTGAC GAAAAATATA CAGTGATTTT AGATTTCAGGA
 ACAGCAATAG CAAATCAAAC GGTGAGCGTT CTAGCGAAAA ACCGCTAGTGG CACGGAAAGT
 CAACCAGCAA CGGCGACAAC ACCAGCTGAT CTCACTGCAC CAACAGTTGA TAACATCACA
 GCAACTCTG GTTCGGGTTA TBAATTTACA GBAACAGCAG ACCCTAACGC AACAATCGAA
 GTTCGTGATC CATCTGGGGT AGTCATTGGT ACAGGTATCT CTGATGCGAA TGGTGATTTT
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 GCGACTGCCG ATGGGACTGG TTCTTTTGCT GTGAACCTTC CAGCTGCGAC GCAAAATGCG
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EF069-4 (SEQ ID NO:264)

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 VKGTAEVGTT IEVRDAAGTV LGTATTGTDG KYTVTLDSGT ATANQTLSEV AKNASGTESQ
 PATATTPADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDPGAVIGT GTSDANGDFT
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 LASGKATAKQ TVNVVAKNDT GLESTPTTAM TPADVTTPTI GDITGDSITG YEITGTADPN
 TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGDTLT VVGKDGDCNE SQPTEVTVPE
 DATVAAPTPTV TVTGT

EF070-1 (SEQ ID NO:265)

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 GTAAGTATAG CTGTTACCTC TGGCACAATC AGTGCAATCAG CAGCGGTCTT GGATATCGAA
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 GCCGCAAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
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 ATTACCAGTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTGAC GGAAGTGAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGTCAATTGG	AATTAGTTAA	TAACATTGAA	AACTTAGGTG	CTGCTTCATT	TACAGCTCCG
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GTTTTAGCCC	AAAATGTTTC	AAACATCTTA	CAAGATTTGA	ATGCGGCAST	TCAAGCTTTG
GAGGCAAAAG	GTACCAGTAT	CCCAAGTAAT	CTTGTCGCCG	CAGCTATAAA	TGCAGCCTTG
CTTCCTGTCA	AAGGCACGGT	AAACGTGGCT	GTTTCAGGTG	CTTTGCGCTT	ATTAGCGGTT
GGTGGTTCAG	GCGTAAATGA	GTTAGTGGAT	GCTTCTTTAC	TAGGCACAAC	CACGGTTACT
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GGAACAGTCG	TTCAAACAGA	TCTTTTAGAC	GTTAATTTAT	TAGCAACAGC	AGACGGTGTA
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GTAACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
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GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA	GCAGGCGCCA	ATGAAACGTT	AACCGCCGTA
GCGAAAAACG	CCAGCGGNAC	AGAAAGNACG	CCAACAACGT	TCCAAACNED	AGCGGATGAA
GCAACCGTAA	CCGCACCAAC	AATCACAGGA	GTGACAGGTA	ATTCAACGBC	AGGTTACGAA
GTTAAAGGAA	GTGCCGATGC	CAATGCCACG	GTTGAAATCC	GAAATGCABG	AGGCACCGTA
ATAGGCACAG	GTACCGCTGA	TGGGACAGGA	GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA
GCAGGTGCCA	ATGAAACGTT	AACCGCCGTA	GCGAAAAACG	CCAGCGGCAC	AGAAAGTACG
CCAACAACGT	TCCAACACC	AGCGGATGAA	GCAACCGTAA	CCGCACCAAC	AATCACAGGA
GTGACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
GTTGAGATCC	GAAATGCAGG	AGGTGCCGTG	ATAGGTACAG	GTACTGCTGA	TGGGACAGGG
GCATTTACAG	TTACCATTC	CGCAGGTGAA	GCAGGTGCGA	ATGAAACGTT	AACCGCCGTA
GCGAAAAACG	CCAGCGGTAC	AGAAAGTACG	CCAACAACGT	TCCAAACGBC	AGCGGATGAA
AATACGCCCC	TGGCGACGCC	AATTGTTGAG	ACTGTAACAG	GTAGTACAAC	AAAAGGCTAT
GAGGTCAAAG	GGACTGCTGA	AGTTGGCACC	ACCATTGAGG	TTCCGCGATGC	AGCTGGCACG
GTCTTTGGTA	CTGCAACAAC	TGGAACGTAC	GGAAAATATA	CAGTGACTTT	AGATTCAGGA
ACAGCAACAG	CAAATCAAAC	GCTGAGCGTT	GTAGCGAAAA	ACGCTAGTGG	CACGGAAAGT
CAACCAGCAA	CGGCGACAAC	ACCAGCTGAT	GTCACGTCAC	CAACAGTTGA	TAACATCACA
GGCAACTCTG	GTTCCGGGTTA	TGAAATTACA	GGAACAGCAG	ACCCTAACAC	AACAATCGAA
GTTTCGTGATC	CATCTGGGGC	AGTCATTGGT	ACAGGTACCT	CTGATGCGAA	TGGTGATTTT
ACTGTAACGC	TACCAACGGG	AACGACCAAT	CCTGGGGATA	CGTTAACAGT	GATTGGAAAG
GATAACGCGG	GAAATGAAAG	TCAACCGACT	GAAGTCCTTG	TTCCCTGCTGA	TGCCACGGTT
ACAGCACCAA	CTGTAACAGG	AGTAACAGGT	AATTACAGTTG	CTGGTTATCA	GGTGACAGGC
ACCGCTGATC	CGAATGCTAC	CATCGAAATT	CGTGATGCAG	ATGGGAACT	GATTGCAACA
GGGACTGCCG	ATGGGACTGG	TTCTTTTGCT	GTGAACCTTC	CAGCTGGGAC	GGCAAATGCG
AATGAAACAT	TGACAGCGTT	AGCCAAAGAT	CCTGCTGGCA	ATACAAGTAC	ACCGACAACC
TTCCAAACAC	CAGCAGATGA	AGTAGTGGCA	CCGCCAAGTG	TCGACAAAGT	TACTGGGAAT
ACAACACAAG	GATATCAAGT	GACAGGTACC	GCTGAACCTG	GCACCACAT	TGAAGTTCGT
GCAACAGACG	GAACAGTTTT	AGGCACCGCA	ACAACCTGGAC	CGACTGGGCA	ATATACTGTG
ACGTTAGCTT	CAGGAAAAGC	AACAGCTAAA	CAAACAGTGA	ATGTAGTTGC	TAAAAATGAT
ACTGGACTTG	AGAGTCAACC	AACTACAGCT	ATGACACCCG	CTGATGTTAC	CACACCAACA
ATTGGTGACA	TTACTGGAGA	TTCAACAAC	GTTTATGAAA	TCACTGGGAC	GGCGGACCCCT
AATACCACCA	TTGAAGTACG	GAACCCAGAT	GGAACAATTA	TTGGTACAC	GACAACGGAT
GATCAAGGAA	ACTTTACTGT	GGACCTTCCA	GCGGGAGCCG	CTAATCCTGG	TGATACATTA
ACAGTTGTTG	GAAAAGACGG	TGACGGCAAT	GAAAGTCAAC	CAACGGAAAT	GACGGTCCCT
GAAGATGCAA	CCGTAGCAGC	ACCAACTGTG	ACGACTGTTA	CAGGAACAAC	TGCCACTGGG
TATCAAGTAA	CCGGCACGGC	AGAGCCAAAT	GTCACCATTG	AGATTCAACA	TGAAGCAGGT
TTAGTTATTG	CTACGGGAAC	GACTGATGGT	GCTGGCGCAT	TTACAATCAC	TCTTCCGACG
GGCACAGCAA	CAGCTAACGA	AGCCTTAAC	GCCATTGCGA	AAGATGCTGC	TGGGAAAGAA
AGTAATCCGA	CTGCTTTCAA	AACACCTGCT	GATCCAGATG	CACCACTGTC	GACACCTACT
GTTTACAAAA	TGCTGGTAG	CACGACAAAC	GGCTATCAAG	TAGTAGGABC	AGCAGAAGTT
GGTACAACAG	TTGAGGTGCG	TGACGCCGAT	GGCACAGTCC	TTGGCATGTC	AACTACTGGA
ACTGATGGCA	AATACACAGT	GACTTTAGAG	CCAGGGAAGG	CCTCAGCTAA	CGAAACAATA
ACTGTCTGTG	CGAAAAATGC	AACAGGAAAA	GAAAGTCAGC	CAGCTACAGC	AACTACACCA
GTCGACTTAG	CCACACCAAC	CATTGATTCT	ATTACCGGAA	ATTCTAGTAA	AGGTTACGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATCACTG3AA CGGCGGAGCC AAAAACCACCT ATTGATGTCC GTGACB3AA3 CGGAACCATC
 ATTGCTG3TA CAACTGCTAA CGAAACCGGC CAATATAAGG TGACTGTAA3 AGCTGGCGTA
 GTGACAC3AG GAGAAACGAT TACGATTATT AGCAAGATG GCGCAG3TAA TGAAGTCAA
 CCAB3TA3AG CGGTATTTC3 ABCGGATGTT GTTTTAGCGG CGCCAA3TAT TACGAAGGTT
 BAAB3AAACA AAG3CAAT33 CTATACAGTC ACTGGAACTG CTGATC3AAA T3TCACGGTT
 CAATTTTACA ATAGCAGTGA ACAATTATTG GTAAGTGGCA ATACAABTAC T33AGGTACC
 TTCTCCCTTC ATATTGCA3C A3G3TTAGCA A3AGAAAAAG AAACGT3AA3 C3C3ACTAACCC
 AC3ATACAC AAG3AAAT3T GASTCCTAAA ACCACATTTA TGACGCG3AG C3ATATTACG
 G3AGAACCA3 AGATTAAAA3 T3CG3CACCA3 ACTGTTTCTT CAGTTT3AG3 AACGTCTAAA
 G3CGGCTACC TCATCAA33G AACAGCTGAA C3AAAC3GAA TCATTCAAA3 TAGTAACCGA
 CTATTAGAA GTGTGATT3C T3TAG3TGCC A3CGAT3CTG AAGGCAACTT C3CTATCCAA
 TTAACAGCGG GACAAGCGAC T3CTCAACAA A3TTTACTTG CGACAG3TAC C3ATGGCGCA
 G3ACATTACA GTACGGCTAC AACCTTCATG A3CCCA3CCG ACCCAAG3AA T3CTGGAGGA
 G3CAATG3TA ACATGGC33 AATAACGGC AATACA3CG GCAATADAG3 AAACAATGGC
 GCAACTGGCG GGAATAAT33 GAATG3TTCA AACACA3GTT CAAATC3AAA T3GAGGTTCT
 G3TTTAGGCA CAACAGGTTT T3GCTTAGGT T3ACTAG3CA ATGGCCTCG3 TACAAATGGT
 A3TGGCTACC ACC3TAA3T AAGTACCATC A3TTAT3GCA CTGGAAT3CA C3GGAAAACA
 G3CTACTTAC CTAGCACAG3 T3AAAAGAG T3TTCA3CCG TGACAACA33 TTTGTTTGGC
 GCCTTTGTCC CACTCCTT3C GAGCATGGGA ATCATCAAAC G3AAAC3TAA AAAC3TAG

EF070-2 (SEQ ID NO:266)

M KKKIVEDFNE FSQHKKWTKF FMLNLAISSG LLFTSLAIPV
 SIAVTSGTIS ASAAVLDEL LSNVTSNNDS GTSTSNRWA ANQNQPVNFT VSGGALADAS
 AVFSGQKQAV LVVPPELRCN VAAAGSAAIN TNVTIELSKV TFLTAVLNAA NLTNVITQI
 TSGALGNLTG VEDIDLTEVNR QLELVNNIEN L3AASFTAPE TLAADG3T33 AFISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTNVNAV SGALPLLAVG
 GSGVNELVDA SLLGTTTTL FTTVSTPQNL SNNLDARFVG TVVQTDLL33 NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV K3TADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA FNASGTEXTF TTFQTPADEA TVTAPTITGV TGNSTAGYEV
 FGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA FNASGTESTP
 TTFQTPADEA TVTAPTITGV TGNSTAGYEV K3TADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA FNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
 VKGTAEVGTI IEVRDAAGTV LGTATTGTDG FYTVTLDSGT ATANQTL33V AKNASGTESQ
 PATATTPADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDP3GAVIGT GTSDANGDFT
 VTLPTGT3NP GDTLTVIGKD NAGNESQ3TE VLVPADATVT APTVTGVTGN SVAGYQVTGT
 ADPNATIEIR DADGNVIATG TADGTGSFAV NLPAGTANAN ETLTALAKDP AGNTSTPTTF
 QTPADEVVAP PSVDKVTGNT TQGYQVTGTA ELGTTIEVRA TDGTVLGTAT TGPTGQYTVT
 LASGKATAKQ TVNVVAKNDT GLE3QPTTAM TPADVTTPTI GDITGDSTT3 YEITGTADPN
 TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGD3LT VVGKDG33NE SQ3TEVTVPE
 DATVAAPT3T TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTT33A GAFTITLPTG
 TATANEALTA IAKDAAGKES NP3AFKTPAD PDAPVATPTV DKITG3STT3 YQVVGAAEVG
 TTVEVRDADG TVLGMATTGT DGKYTVTLEP CKASANETIT VVAKNAT33E SQPATATTPV
 DLATPTID3I TGNSSKGYEI T3TAEPKTTI D3RDADGTII AATTANET3Q YTVTL3AGVV
 TPGETIT3IS KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGY3TV GTADPNVTVQ
 FYN3SEQLLA SGNTTTGGTF SVHIAAGLAT EKETLTALT3 DTQGNV33PT TFMTPADITG
 EPEIKIAAPT VSSVLGTSKA GYLIK3TAEP NRII3ISNRL LRSVIAVGAT DAEGNFAIQL
 TAGQATAQQ3 LLATATDGAG H3STATTFMT PADPTNPGGG NGNTGGN33N T3GNTGNNGA
 TGGNNGN33N TGSNPN33SG LGTTG3GLG3 LGNGLG3NGS GYHPKL3TIS YGTGNH3K3TG
 YLPSTGEKES SAVTTS3LFGA FVALLAS3GI IKRKRKN

EF070-3 (SEQ ID NO:267)

CGG TGACGGCAAT GAAAGTCAAC CAACGGAAGT GACGGTCCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAAGATGCAA CCGTAGCAGC ACCAACTGTG ACGACTGTTA CAGGAACAAC TGCCACTGGG
TATCAAGTAA CCGGCACGGC AGAGCCAAAT GTCACCATIG AGATTCACAA TGAAGCAGGT
TTAGTTATTG CTACGGGAAC GACTGATGGT GCTGGCGCAT TTACAATCAE TCCTCCGACG
GGCACAGCAA CAGCTAACGA AGCCTTAACT GCCATTGCGA AAGATGCTGC TGGGAAAGAA
AGTAATCCGA CTGCTTTCAA AACACCTGCT GATCCAGATG CACCAGTCGC GACACCTACT
GTTGACAAAA TCACTGGTAG CACGACAAAC GGCTATCAAG TAGTAGGAGC AGCAGAAGTT
GGTACAACAG TTGAGGTGCG TGACGCCGAT GGCACAGTCC TTGGCATGBC AACTACTGGA
ACTGATGGCA AATACACAGT GACTTTAGAG CCAGGGAAGG CCTCAGCTAA CGAAACAATA
ACTGTCGTAG CGAAAAATGC AACAGGAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA
GTCGACTTAG CCACACCAAC CATTGATTCT ATTACCGGAA ATTCTAGTAA AGGTTACGAA
ATCACTGGAA CGGCGGAGCC AAAAACCCTT ATTGATGTCC GTGACGCABA CGGAACCATC
ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGA CTCTACG AGCTGGCGTA
GTGACACCAG GAGAAACGAT TACGATTATT AGCAAAGATG GCGCAGGTAA TGAAGTCAA
CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTT TAGCGG CGCCAAC TAT TACGAAGGTT
GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAAGTG CTGATCCAAA TGTCACGGTT
CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGGCA ATACAAC TAC TGGAGGTACC
TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAC CGCACTAACC
ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAGC CGATATTACG
GGAGAACCAG AGATTAAAAT TGCGGCACCA ACTGTTCTTT CAGTTT TABG AACGTCTAAA
GCCGGCTACC TCATCAAAGG AACAGCTGAA CCAAACCGAA TCATTCAAAT TAGTAACCGA
CTATTAAGAA GTGTGATTGC TG TAGGTGCC ACCGATGCTG AAGGCAACTT CGTATCCAA
TTAACAGCGG GACAAGCGAC TGCTCAACAA AGTTTACTTG CGACAGCTAC CGATGGCGCA
GGACATTACA CTACGGCTAC AACCTTCATG ACGCCAGCCG ACCCAACGAA TCCTGGAGGA
GGCAATGGTA ACACTGGCGG AAATAACGGC AATACAGGCG GCAATACAGG AAACAATGGC
GCAACTGGCG GGAATAATGG GAATGGTTCA AACACAGGTT CAAATCCAAA TGGAGGTCTT
GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACTAGGCA ATGGCCTCGG TACAAATGGT
AGTGGCTACC ACCCTAAACT AAGTACCATC AGTTATGGCA CTGGAAATCA CGGGAACAACA
GGCTACT

EF70-4 (SEQ ID NO:268)

DGDGNE SQPTEVTVP

DATVAAPTPT TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTTDBA GAFTITLPTG
TATANEALTA IAKDAAGKES NPFAFKTPAD PDAPVATPTV DKITGSTTHB YQVVGAAEVG
TTVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNATGKE SQPATATTPV
DLATPTIDSI TGNSSKGYEI TGTAEPKTTI DVRDADGTII AATTANETBQ YTVTLPAQVV
TPGETITIIIS KDGAGNESQP ATAVIPADV V LAAPTITKVE GNKANGYTTF GTADPNVTVQ
FYNSSQQLLA SGNTTTGTF SVHIAAGLAT EKETLTALT DTQGNVSPRT TFMTPADITG
EPEIKIAAPT VSSVLGTSKA GYLIKGTAEF NRIIQISNRL LRSVIAVGAT DAEGNFIAQL
TAGQATAQQS LLATATDGAG HYSTATTFMT PADPTNPGGG NGNTGGNNEN TGGNTGNNGA
TGGNNGNGSN TGSNPNNGSG LGTTGSGLGS LGNGLGTNGS GYHPKLSTIS YGTGNHGKTG
YL

EF071-1 (SEQ ID NO:269)

TAAGTAGAAG TGGTCGGGAC AAACGTAGAA CTTTCGCTGA TTGCCGAA3A AATTACTTCT
GTCCCGCCAT TTATCTGCAG GTTTAAGCCG TGGAAAGGGAA GTTATTTTBA CTTTCCTTTC
ATGGCTTTTT TAAGAAAGGA GCATGCTATG TTTAAAAAAT TAATGATTCA ACTTGCTTTA
GTGATTGGTT TAAGTTTAAAC GATTCCGATG ACGGCTTNCG CTTACACCAT CGAAGCGGAT
CCAATCAACT TTACTTATTT TCCCGGCTCT GCAAGCAATG AATTAATBET TTTACATGAA
TCTGGAAACG AGCGGAACCT AGGACCACAC AGTTTAGACA ATGAAGTBBC CTATATGAAA
CGAAATTGGT CAAATGCTTA TGCTCATAT TTTGTCGGAT CTGGTGAGC AGTGAAACAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTAGCTCCTG CTGGCCAAAT TCAATATGGC GCAGGTTCTT TAGCTAATCA AAAAGCCTAT
 GCGCAAATCG AATTGGCTCG AACGAATAAT GCGCGACAT TTAATAAACA TTATGCTGCC
 TATGTTAATT TGGCCCGTGA TTGGGCTCAG AACATTGGTG CTGATTTTTC TCTGGACGAT
 GSAACA33TT ATGGCATACT CACTCATGAT TGGATTACAA AAAATTGGTG GGGAGATCAT
 ACAGATCCTT ATGGTTATTT AGCGCGTGGG GATTATGTA AGCGCATTTG CACNAGATTT
 APAACG33CG TTTCNGNAAC AGGTGAGACT GGTCAATTATT CAGCCAGGTA A

EF071-2 (SEQ ID NO:270)

MF KKLMQLALV

IGLSLTIPMT AXAYTIEADP INFYTFPGSA SNELIVLHES GNERNLGPHE LDNEVAYMKR
 NWSNAYVSFY VGSGGRVKQL APA3QIQYGA GSLANQKAYA QIELARTENA ATFKKDYAAY
 VNLRDLAQN IGADPSLDDG TGYGIVTHDW ITKNWWDHT DPYGYLARG LVKRIGTRFT
 TGVSTGETG HYSAR

EF071-3 (SEQ ID NO:271)

G TTTAAAAAAT TAATGATTCA ACTTGCTTTA

GTGATTGGTT TAAGTTTAAC GATTCCGATG ACGGCTTNCG CTTACACCAT CGAAGCGGAT
 CCAATCAACT TTACTTATTT TCCCGGCTCT GCAAGCAATG AATTAATTCT TTTACATGAA
 TCTGGAAACG AGCGGAACCT AGGACCACAC ACTTTAGACA ATGAAGTGGC CTATATGAAA
 CGAAATGGT CAAATGCTTA TGTCTCATAT TTTGTCGGAT CTGGTGGAGC AGTGAAACAA
 TTAGCTCCTG CTGGCCAAAT TCAATATGGC GCAGGTTCTT TAGCTAATCA AAAAGCCTAT
 GCGCAAATCG AATTGGCTCG AACGAATAAT GCGGCGACAT TTAATAAACA TTATGCTGCC
 TATGTTAATT TGGCCCGTGA TTGGGCTCAG AACATTGGTG CTGATTTTTC TCTGGACGAT
 GGAACAGGTT ATGGCATACT CACTCATGAT TGGATTACAA AAAATTGGTG GGGAGATCAT
 ACAGATCCTT ATGGTTATTT AGCGCGTGGG GATTATGTA AGCGCATTTG CACNAGATTT
 ACAACGGGCG TTTCNGNAAC AGGTGAGACT GGTCAATTATT CAGCCAGGT

EF071-4 (SEQ ID NO:272)

F KKLMQLALV

IGLSLTIPMT AXAYTIEADP INFYTFPGSA SNELIVLHES GNERNLGPHE LDNEVAYMKR
 NWSNAYVSFY VGSGGRVKQL APAGQIQYGA GSLANQKAYA QIELARTENA ATFKKDYAAY
 VNLRDLAQN IGADPSLDDG TGYGIVTHDW ITKNWWDHT DPYGYLARG LVKRIGTRFT
 TGVSTGETG HYSAR

EF072-1 (SEQ ID NO:273)

TAATCAATGA AAAACGCACG TTGGTTAAGT ATTTGCGTCA TGCTACTGCG TCTTTTCGGG
 TTTTCACAGC AAGCATTAGC AGAGGCATCG CAAGCAAGCG TTCAAGTTAC GTTGACACAA
 TTATTGTTCC CTGATGGTCA ATTACCAGAA CAGCAGCAAA ACACAGGGGA AGAGGGAACG
 CTGCTTCAAA ATTATCGGGG CTTAAATGAC GTCACTTATC AAGTCTATGA TGTGACGGAT
 CCGTTTTATC AGCTTCGTTT TGAAGGAAAA ACGGTCCAAG AGGCACAGCG TCAATTAGCA
 GAAACCGGTG CAACAAATAG AAAACCGATC GCAGAAGATA AAACACAGAC AATAAATGGA
 GAAGATGGAG TGGTTTCTTT TTCAATTAGCT AGCAAAGATT CGCAGCAACG AGATAAAGCC
 TATTTATTTG TTGAAGCGGA AGCACCAGAA GTGGTAAAGG AAAAAGCTAG CAACCTAGTA
 GTGATTTTGC CTGTTCAAGA TCCACAAGGG CAATCGTTAA CGCATATTCA TTATATCCA
 AAAAATGAAG AAAATGCCTA TGACTTACCA CCACTTGAAA AAACGGTACT CGATAAGCAA
 CAAGGCTTTA ATCAAGGAGA GCACATTAAC TATCAGTTAA CGACTCAGAT TCCAGCGAAT
 ATTTTAGGAT ATCAGGAATT CCGTTTGTC GATAAGGCGG ATACAACGTT GACACTTTTA
 CCAGAATCAA TTGAGGTAAA AGTGGCTGGA AAAACAGTTA CTACAGGTTA CACTGACG
 ACGCAAAAGC ATGGATTTAC GCTTGATTTT TCAATTAAAG ACTTACAAA CTTTGCAAAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAAACAATGA CTGTGTCGTA TCAAATGCGT TTAGAAAAGA CCGCTGAACC TGACACTGCG
 ATTAACAACG AAGGACAATT AGTCACGGAC AAACATACCT TGACTAAAAG AGCCACAGTT
 CGTACAGGCG GCAAGTCTTT TGTCAAAGTT GATAGTGAAA ATGCGAAAAT CACCTTGCCA
 GAGGCTGTTT TTATCGTCAA AAATCAAGCG GGGAAATACC TCAATGAAC AGCAAACGGG
 TATCGTTGGC AAAAAGAAAA AGCATTAGCT AAAAAATTCA CGTCTAATCA AGCCGGTGAA
 TTTTCAGTTA AAGGNNTTAA AAGATGGCCA GTACTTCTTG GAAGAAATCT CTGCACCAAA
 AGGTTATCTT CTGAATCAAA CAGAAATTCC TTTTACGGTG GGAAAAAATT CTTATGCAAC
 GAACGGACAA CGAACAGCAC CGTTACATGT AATCAATAA

EF072-2 (SEQ ID NO:274)

MKNARWLSI CVMLLALFGF SQQALAEASQ ASVQVTLHLK LFPDQQLPEQ QQNTGEEGTL
 LQNYRGLNDV TYQVYDVTDP FYQLRSEGKT VQEAQRQLAE TGATNRKPIA EDKTQTINGE
 DGVVSFSLAS KDSQQRDKAY LFVEAEAPEV VKEKASNLVV ILPVQDPQQQ SLTHIHLYPK
 NEENAYDLPP LEKTVLDKQQ GFNQGEHINY QLTTQIPANI LGYQEFRLSD KADTTLTLLP
 ESIEVKVAGK TVTTGYTLTT QKHGFTLDFS IKDLQNFANQ TMTVSYQMLL EKTAEPDTAI
 NNEGQLVTDK HTLTKRATVR TGGKSFVKVD SENAKITLPE AVFIVKNQAG EYLNETANGY
 RWQKEKALAK KFTSNQAGEF SVKGXKRWPV LLGRNLCTKR LSSESNNNSF YGGKKFLCNE
 RTTNSTVTCN Q

EF072-3 (SEQ ID NO:275)

ATTACCAGAA CAGCAGCAAA ACACAGGGGA AGAGGGAACG
 CTGCTTCAAA ATTATCGGGG CTTAAATGAC GTCACTTATC AAGTCTATGA TGTGACGGAT
 CCGTTTTATC AGCTTCGTTT TGAAGGAAAA ACGGTCCAAG AGGCACASBG TCAATTAGCA
 GAAACCGGTG CAACAAATAG AAAACCGATC GCAGAAGATA AAACACABAC AATAAATGGA
 GAAGATGGAG TGGTTTCTTT TTCATTAGCT AGCAAAGATT CGCAGCAACG AGATAAAGCC
 TATTTATTTG TTGAAGCGGA AGCACCAGAA GTGGTAAAGG AAAAAGCTAG CAACCTAGTA
 GTGATTTTGC CTGTTCAAGA TCCACAAGGG CAATCGTTAA CGCATATTC A TTTATATCCA
 AAAAATGAAG AAAATGCCTA TGACTTACCA CCACTTGAAA AAACGGTACT CGATAAGCAA
 CAAGGCTTTA ATCAAGGAGA GCACATTAAC TATCAGTTAA CGACTCAGAT TCCAGCGAAT
 ATTTTAGGAT ATCAGGAATT CCGTTTGTCA GATAAGGCGG ATACAACBT GACACTTTTA
 CCAGAATCAA TTGAGGTAA AGTGGCTGGA AAAACAGTTA CTACAGSTEA CACACTGACG
 ACGCAAAAGC ATGGATTTAC GCTTGATTTT TCAATTAAAG ACTTACAAAA CTTTGCAAAAT
 CAAACAATGA CTGTGTCGTA TCAAATGCGT TTAGAAAAGA CCGCTGAACC TGACACTGCG
 ATTAACAACG AAGGACAATT AGTCACGGAC AAACATACCT TGACTAAAAG AGCCACAGTT
 CGTACAGGCG GCAAGTCTTT TGTCAAAGTT GATAGTGAAA ATGCGAAAAT CACCTTGCCA
 GAGGCTGTTT TTATCGTCAA AAATCAAGCG GGGGAATACC TCAATGAAC AGCAAACGGG
 TATCGTTGGC AAAAAGAAAA AGCATTAGCT AAAAAATTCA CGTCTAATCA AGCCGGTGAA
 TTTTCAGTTA AAGGNNTTAA AAGATGGCCA GTACTTCTTG GAAGAAATCT CTGCACCAAA
 AGGTTATCTT CTGAATCAAA CAGAAATTCC TTTTACGGTG GGAAAAAATT CTTATGCAAC
 GAACGGACAA CGAACAGCAC CGTTACATGT A

EF072-4 (SEQ ID NO:276)

QLPEQ QQNTGEEGTL
 LQNYRGLNDV TYQVYDVTDP FYQLRSEGKT VQEAQRQLAE TGATNRKPIA EDKTQTINGE
 DGVVSFSLAS KDSQQRDKAY LFVEAEAPEV VKEKASNLVV ILPVQDPQQQ SLTHIHLYPK
 NEENAYDLPP LEKTVLDKQQ GFNQGEHINY QLTTQIPANI LGYQEFRLSD KADTTLTLLP
 ESIEVKVAGK TVTTGYTLTT QKHGFTLDFS IKDLQNFANQ TMTVSYQMLL EKTAEPDTAI
 NNEGQLVTDK HTLTKRATVR TGGKSFVKVD SENAKITLPE AVFIVKNQAG EYLNETANGY
 RWQKEKALAK KFTSNQAGEF SVKGXKRWPV LLGRNLCTKR LSSESNNNSF YGGKKFLCNE
 RTTNSTVTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF073-1 (SEQ ID NO:277)

TAAATGAACA AATTAAATAC AAAATTACTG ATTGGCTATA TTCTTTTAA GGCCTTAATC
 ATTGCTGTCTG CTAGAGAATA TGGCTTCTTC GCTTTTSTGA TTCTGCTAGG CTTTTTAGTA
 TTGCTTCTCT ATCGAAAAAA GAAAAATGCC GCGACAAAA GCGATCAAAT GCCTTACTTA
 ACGAAAGATA AAGAAGCCCA TTATCGTGAG TTGGGGTTAT CTCCACAAA AATTGATTTT
 TTCAGAAGTA CAATGAGCAC AGCCAAAAAA CAAATCATAC AATTGCABA AAACATGAAT
 CGTTCAACTA AATTACGGGC GATTGACTTA CGTAATGATA CTACGAAGGT TTCTAAAGCT
 CTSTTTAAAG AGTTAGTGAA AGAACCTAAA AAGTTACACT TAGCCAATCA CTTTCTCTAT
 ACACATTTAC CAAATATCGT TGACTTAACA AGTAAACATT TAGAAATCGA ACAACACGAA
 GTAAAAAACA AACAAACGTA TGAAAAATTA GAAGAAAGCG CACAAATCAT TGACCAATTG
 TCAAAATTAG TTA AAAATGA TTATGAGGAA ATCGTTTCCG ATGACTTAGA CGATTTAGAT
 GTCGAAATGT CGATCGCTAA AAGCAGCTTG TCGCAAAAAG CTGCAACTGA GGAATCACCT
 CAAGTAAACG AAGACCAGCA ATAA

EF073-2 (SEQ ID NO:278)

MNKLNTKLLI GYILLGALII AVAREYGFFA FVILVGFVLF VLYRKKKNAA DKSDQMPYLT
 KDKEAHYREL GLSPQEIDFF RSTMSTAKKQ IIQLQENMNR STKLRAIDLR NDTTKVSKAL
 FKELVKEPKK LHLANHFLYT HLPNIVDLTS KHELEIEQHEV KNKQTYENLE ESAQIIDQLS
 KLVKNDYEEI VSDDLDDLDV EMSIAKSSLS QKAATEESPQ VNEDQQ

EF073-3 (SEQ ID NO:279)

CT ATCGAAAAAA GAAAAATGCC GCGACAAAA GCGATCAAAT GCCTTACTTA
 ACGAAAGATA AAGAAGCCCA TTATCGTGAG TTGGGGTTAT CTCCACAAA AATTGATTTT
 TTCAGAAGTA CAATGAGCAC AGCCAAAAAA CAAATCATAC AATTGCABA AAACATGAAT
 CGTTCAACTA AATTACGGGC GATTGACTTA CGTAATGATA CTACGAAGGT TTCTAAAGCT
 CTGTTTAAAG AGTTAGTGAA AGAACCTAAA AAGTTACACT TAGCCAATCA CTTTCTCTAT
 ACACATTTAC CAAATATCGT TGACTTAACA AGTAAACATT TAGAAATCGA ACAACACGAA
 GTAAAAAACA AACAAACGTA TGAAAAATTA GAAGAAAGCG CACAAATCAT TGACCAATTG
 TCAAAATTAG TTA AAAATGA TTATGAGGAA ATCGTTTCCG ATGACTTAGA CGATTTAGAT
 GTCGAAATGT CGATCGCTAA AAGCAGCTTG TCGCAAAAAG CTGCAACTGA GGAATCACCT
 CAAGTAAACG AAGACCAGCA AT

EF073-4 (SEQ ID NO:280)

YRKKKNAA DKSDQMPYLT
 KDKEAHYREL GLSPQEIDFF RSTMSTAKKQ IIQLQENMNR STKLRAIDLR NDTTKVSKAL
 FKELVKEPKK LHLANHFLYT HLPNIVDLTS KHELEIEQHEV KNKQTYENLE ESAQIIDQLS
 KLVKNDYEEI VSDDLDDLDV EMSIAKSSLS QKAATEESPQ VNEDQQ

EF074-1 (SEQ ID NO:281)

TAAAGGAGTT CTCAAAAAAT GAAGCTAAAA AAAATAATTC CTGCTTTTCC CTTTCTTTCA
 ACCGTTGCAG TTGCTTGTG GTTAACGCCT ACTCAAGCTT CTGCAGATGC TGCGGATACG
 ATGGTAGATA TCTCTGGCAA AAAAGTGTG GTTGGATATT GGCATAASTG GGCCTCAAAA
 GGACGCGATG GTTACAAACA AGGAACATCA GCATCACTAA ACCTTTTCTA AGTAAATCAA
 GCCTACAATG TCGTACCGGT TTCCTTCATG AAAAGCGATG GCACGACAG GATTCTACG
 TTCAAGCCTT ATAACCAAAC GGACACTGCC TTCCGACAAG AAGTCGCACA ATTAAATAGT
 CAAGGTCGCG CAGTTTATT GGCCTTGGT GGAGCAGATG CACATATTCA ATTAGTCAAA
 GCGGATGAAC AAGCCTTTGC GAATGAAATC ATTCTGCAAG TGGAACATA CGGCTTTGAT
 GGTTTAGACA TCGACTTAGA GCAATTGGCG ATTACTGCTG GCGACAAAAC AACCGTCATC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCTGCTACGT TGAAAATAGT CAAAGACCAT TATCGAGCAC AAGGAAAAAA TTTCATCATT
 ACGATGGCAC CAGAATTCCC TTATTTAAAA CCTGGTGCCG CTTATGAAAC ATACATTACT
 TCCCTAAATG GTTATTATGA TTACATTGCC CCACAATTAT ATAACCAAGG CGGCGACGGT
 GTCTGGGTTG ATGAAGTTAT GACTTGGGTT GCTCAAAGCA ACGATGCTCT AAAATACGAG
 TTCCTCTATN ATATT

EF074-2 (SEQ ID NO:282)

MKLKK IIPAFPLLST VAVGLWLTP T QASADAADTM VDISGKKVLV GYWHNWASKG
 RDGYKQGTSA SLNLSEVNQA YNVVPVSFMK SDGTTRIPTF KPYNQTD TAF RQEV AQLNSQ
 GRAVLLALGG ADAHIQLVKG DEQAFANEII RQVETYGFDG LDIDLEQLAI TAGDNQTVIP
 ATLKIVKDHY RAQGKNFIIT MAPEFPYLKP GAAYETYITS LNGYYDYIAP QLYNQGGDGV
 WVDEVMTWVA QSNDAKLYEF LYXI

EF074-3 (SEQ ID NO:283)

TGC TCGGATACG
 ATGGTAGATA TCTCTGGCAA AAAAGTGTG GTTGGATATT GGCATAACTG GGCCTCAAAA
 GGACGCGATG GTTACAAACA AGGAACATCA GCATCACTAA ACCTTTCGGA AGTAAATCAA
 GCCTACAATG TCGTACCGGT TTCCTTCATG AAAAGCGATG GCACGACACG GATTTCCTACG
 TTCAAGCCTT ATAACCAAAC GGACACTGCC TTCCGACAAG AAGTCGCACA ATTAAATAGT
 CAAGGTCGCG CAGTTTTATT GGCAC TTGGT GGAGCAGATG CACATATTC AATTAGTCAAA
 GGCGATGAAC AAGCCTTTGC GAATGAAATC ATTCTGCAAG TGGAAACATA CGGCTTTGAT
 GGTTTAGACA TCGACTTAGA GCAATTGGCG ATTACTGCTG GCGACAACCA AACCGTCATC
 CCTGCTACGT TGAAAATAGT CAAAGACCAT TATCGAGCAC AAGGAAAAAA TTTCATCATT
 ACGATGGCAC CAGAATTCCC TTATTTAAAA CCTGGTGCCG CTTATGAAAC ATACATTACT
 TCCCTAAATG GTTATTATGA TTACATTGCC CCACAATTAT ATAACCAAGG CGGCGACGGT
 GTCTGGGTTG ATGAAGTTAT GACTTGGGTT GCTCAAAGCA ACGATGCTCT AAAATACGAG
 TTCCTCT

EF074-4 (SEQ ID NO:284)

AADTM VDISGKKVLV GYWHNWASKG
 RDGYKQGTSA SLNLSEVNQA YNVVPVSFMK SDGTTRIPTF KPYNQTD TAF RQEV AQLNSQ
 GRAVLLALGG ADAHIQLVKG DEQAFANEII RQVETYGFDG LDIDLEQLAI TAGDNQTVIP
 ATLKIVKDHY RAQGKNFIIT MAPEFPYLKP GAAYETYITS LNGYYDYIAP QLYNQGGDGV
 WVDEVMTWVA QSNDAKLYEF LY

EF075-1 (SEQ ID NO:285)

TAACCTATAA GAAAAAATC ACAACCTGTG ATAAATTATT GGAGGNAAAA TATGTCAAAA
 GGAAGAAAA TTTTGGCCAT TATCNTTGA ATTATCTTGG NTCTATTCT TGCAGTTGTT
 GGAATGGGAG CAAAACCTTA TTGGGATGTT TCTAAATCAA TGGATAAAAC CTATGAAACA
 GTAGAACGAT CTAAAAAAG TCAGGTCAAT TTAAACAATA AGGAGCCTTT TTCTGTTTTA
 TTATTAGGGA TTGATACAGG CGATGATGGG CGTGTGAGC AAGGTCGTTG GGATACAACA
 ATTGTTGCAA CAGTTAATCC TCGTGACAAG CAAACAACCT TAGTCAGTCT TGCTCGCGAT
 ACCTATGTTG ATATTCCAGG TCAAGGAAAA CAAGATAAAT TGAATCAGGC CTATGCTTTT
 GGTGGCGCAT CTTTAGCAAT GGACACAGTT GAAAACTATT TAAACATACC TATTAATCAT
 TATGTTTCAA TTAATATGGC TGGTTTAAAA GAATTAGTCA ACGCGGTTGG CGGAATCGAA
 GTGAACAATA ATCTGACTTT TTCTCAAGAC GGATATGATT TTACGATTGG TAAAATTTC A
 TTGGATGGTG AACAAGCACT CTCCTATTCA AGAATGCGTT ACGAAGACCC TAATGGTGAC
 TACGGCCGCC AAGAACGTCA AAGAAAAGTG ATTGAAGGCA TCGTCCAAAA AGTCTTAAGT
 CTTAACAGCG TAAGCAACTA TCAAGAAATT TTAACAGCTG TTTCTGATAA TATGAAGACA
 GATTTAAGTT TTGATGACAT GAAAAAATT GCCTTAGATT ATCGCAGTGC CTTTGGTAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGAAACAAG ACCAACTTCA AGGTACTGGT TTTATGCAAG ATGGTGTTCG CTATCAACGT
GTGGATGAAC AAGAATTAAC TCGTGTCCAA CAAGAGTTGA AAAATCAATT GAATACAAA
TAA

EF075-2 (SEQ ID NO:286)

MSKG KKIFATIXGI IIXHFLAVVG MGAKLYWDVS KSMKTYETV
ERSKKSQVNL NNKEPFSVLL LGIDTGDDGR VEQGRSDTTI VATVNPREDQ TTLVSLARDT
YVDIPGQKQ DKLNHAYAFG GASLAMDTVE NYLNIPINHY VSINMAGLKE LVNAVGGIEV
NNNLTFSDG YDFTIGKISL DGEQALSYSR MRYEDPNGDY GRQERQREVI EGIVQKVLSL
NSVSNYQEIL TAVSDNMKTD LSFDDMKKIA LDYRSAPGKV KQDQLQGTGF MQDGVSYQRV
DEQELTRVQQ ELKNQLNNTK

EF075-3 (SEQ ID NO:287)

ACTTTA TTGGGATGTT TCTAAATCAA TGGATAAAAC CTATGAAACA
GTAGAACGAT CTAAAAAAG TCAGGTCAAT TTAACAATA AGGAGCCTTT TTCTGTTTTA
TTATTAGGGA TTGATACAGG CGATGATGGG CGTCTCGAGC AAGGTGCTTC GBATACAACA
ATTGTGTCAA CAGTTAATCC TCGTGACAAG CAAACAACCT TAGTCAGTCT TCGTCGCGAT
ACCTATGTTG ATATTCCAGG TCAAGGAAAA CAABATAAAT TGAATCAGGC CTATGCTTTT
GGTGGCGCAT CTTTAGCAAT GSACACAGTT GAAAACTATT TAAACATACC TATTAATCAT
TATGTTTCAA TTAATATGGC TGGTTTAAAA GAATTAGTCA ACGCGGTTGG GBSAATCGAA
GTGAACAATA ATCTGACTTT TTCTCAAGAC GGATATGATT TTACGATTGG TAAAATTTCA
TTGGATGGTG AACAAGCACT CTCCTATTCA AGAATGCGTT ACGAAGACCC TAATGGTGAC
TACGGCCGCC AAGAACGTCA AAGAAAAGTG ATTGAAGGCA TCGTCCAAAA AGTCTTAAGT
CTTAACAGCG TAAGCAACTA TCAAGAAATT TTAACAGCTG TTTCTGATAA TATGAAGACA
GATTTAAGTT TTGATGACAT GAAAAAATT GCCTTAGATT ATCGCAGTGC CTTTGGTAAA
GTGAAACAAG ACCAACTTCA AGGTACTGGT TTTATGCAAG ATGGTGTTCG CTATCAACGT
GTGGATGAAC AAGAATTAAC TCGTGTCCAA CAAGAGTTGA AAAATCAATT GAATACAAA

EF075-4 (SEQ ID NO:288)

KLYWDVS KSMKTYETV
ERSKKSQVNL NNKEPFSVLL LGIDTGDDGR VEQGRSDTTI VATVNPREDQ TTLVSLARDT
YVDIPGQKQ DKLNHAYAFG GASLAMDTVE NYLNIPINHY VSINMAGLKE LVNAVGGIEV
NNNLTFSDG YDFTIGKISL DGEQALSYSR MRYEDPNGDY GRQERQREVI EGIVQKVLSL
NSVSNYQEIL TAVSDNMKTD LSFDDMKKIA LDYRSAPGKV KQDQLQGTGF MQDGVSYQRV
DEQELTRVQQ ELKNQLNNTK

EF076-1 (SEQ ID NO:289)

TAGAAAATAA CAGAGGAGCT GAAGGAAATG AAAGCATCAA CAAAAATTGG TATCGGTTTTA
AGCATTGCTG CAGTTGCAAG TGTCTCTGTT GCAGTCATCG CTTCTGAAAA AATTATTAAG
AAGGTATCTC ATGTTTCCAA TCGTTATAAA GTTAAAAAGT TTGTAGACGA TAAATTTGAT
GGAAACCAAA AATTATTATC GATTGTGAT GATTATCCG ATGATGAATT AGATTCTGTT
TTAAATGTTG TGGATCGTGT GAAAGATGGC GGTTCAAAAT TAGCTGAATA TGGCGAAAAA
GTTAAAGACA ATACAGATTC TTTAAAGAA CGCTTTTCA CATTATTGA AGATGCAATG
AAGTTAAAA AGTGGCCTAG GCCATCTTTT TTTTATAAAA ATAATTCCTT TSTTTCAACA
TAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF076-2 (SEQ ID NO:290)

MK ASTKIGIGLS IAAVASVSVA VIASEKIIKK VSHVSNRYKV KKFVDDDFDG
 NQKLLSIVDD LSDDELDVL NVVDRVKDGG SKLAEYGEKV KDNTDSLKER FFTFIEDAMK
 LKKWPRPSFF YKNSFVST

EF076-3 (SEQ ID NO:291)

CATCG CTTCTGAAAA AATTATTAAG
 AAGGTATCTC ATGTTTCCAA TCGTTATAAA GTTAAAAACT TTGTAGACGA TAAATTTGAT
 GGAAACCAAA AATTATTATC GATTGTCGAT GATTATCCG ATGATCAATT AGATTCTGTT
 TTAAATGTTG TGGATCGTGT GAAAGATGGC GGTTCAAAAT TAGCTGAATA TGGCGAAAAA
 GTTAAAGACA ATACAGATTC TTTAAAAGAA CGCTTTTTC AATTTAATTGA AGATGCAATG
 AAGTTAAAAA AGTGGCCTAG GCCATCTTTT TTTTATAAAA ATAATTCTT

EF076-4 (SEQ ID NO:292)

VIASEKIIKK VSHVSNRYKV KKFVDDKFDG
 NQKLLSIVDD LSDDELDVL NVVDRVKDGG SKLAEYGEKV KDNTDSLKER FFTFIEDAMK
 LKKWPRPSFF YKNS

EF077-1 (SEQ ID NO:293)

TAATGTAAAG TGAATGATGG GAGAGAAAAA GAGATGAAGC ATGTAACAAA ATTGGGGATT
 ACAATTATAA CAGGAGTTTT GGCATTATTA TTTGAATTTA TTTTACATCA GCCGAATTGG
 GCGTATGGCA TTATTTTAAT AACAGGTTCT GTAATGGCGT TAATGATGTT CTGGGAAATG
 ATTCAAACCT TACGTGAAGG AAAATATGGT GTCGATATTT TAGCGATTAC CGCTATCGTT
 GCAACCTTAG CTGTGGGAGA ATACTGGGCC AGTTTGATGA TTTTAATTAT GTTGACTGGT
 CGTGATTCAT TAGAAGACTA TGCCGCTGGA AAAGCTAACC AAGAGCTGAA GTCATTATG
 GATAACTCGC CACAAAAAGC TCATCGCTTG AATGGCGAAA ATTTAGAAGA TGTTTCTGTT
 GAGGAAATCA ATGTTGGCGA TGAATTAGTA GTAAAACCAG GGGAACTAGT TCCAGTTGAT
 GGCTTGGTAA AAACCGGGAC ATCAACAGTC GATGAATCTT CATTACAGG AGAATCAAAA
 CCAATTGAAA AAAATCCTGG GGATGAATTA ATGTCGGGTT CCGTGAATGG TGACGGCTCT
 TTGAAAATGG TTGCTGAAAA AACTGTAGCA GACAGTCAAT ATCAAACAAT TGTGAACCTA
 GTGAAAAGAT CTGCGGCGCG TCCAGCTCAT TTTGTACGTT TAGCAGATCG CTATGCGGTA
 CCTTTTACAC TAGTTGCCCTA CCTAATTGCA GGTGTTGCTT GGTGTTGTTT CAAAAGTCCG
 ACACGTTTTG CGGAAGTCTT AGTTGTTGCT TCGCCGTGTC CTTTAATTCT ATCTGCCCCA
 ATTGCTTTAG TGGCAGGCAT GGGTCGTTCA AGTCGTCATG GGGTCGTTAT TAAATCGGGA
 ACGATGGTCC AAAAAATTAGC TTCTGCAAAA ACGATTGCGT TTGATAAAAC AGGCACGATT
 ACGCAAGGAC AACTTTCTGT TGATCAAGTC CAACCAATCA ATGCTGGAAT AACTGCTGCT
 GAATTAGTGG GATTGGCAGC AAGCGTGGAA CAAGAATCAA GTCATATTTT AGCTAGATCA
 ATTGTTGCTT ATGCCAGAAA GCAAGATGTC CCATTAAGAA ATATTACAGA TCTAGCGGAA
 GTTTCTGGTG CTGGCGTGAA GGCATTGTG GATGGTGCTG AGATACGGGT AGGTAAAAAG
 AATTTTGTGA CACAAGAGTC TCAAGAAACT GAAAAAATTG ATAAAACGAC TATTCATATT
 TCACGTAATG GCACATATTT AGGCCGAATT ACTTTTACAG AACTGTACG CCCAGAAGCA
 AAAGAGACTA TGGAAAAATT ACACCAATTA CATCTTCAAC GAATTTTAAT GCTGACGGGG
 GATCAAGAAAT CCGTTGCAGA AACGATTGCT GCAGAAGTAG GAATTACCGA AGTACATGGG
 GAATGTTTAC CACAAGATAA ATTAACATATT CTAAAAGAAT TGCTTAAAGA AAATCATCCA
 GTCATCATGG TAGGAGATGG TGTAATGAT GCACCTTCGC TTGCTGCTGC AGACGTAGGT
 ATTGCTATGG GTGCTCATGG AGCTACTGCG GCTAGTAAA CTGCTBACGT TGTATTTTTA
 AAAGATGACT TAAGTAAAGT CAGCCAAGCG GTCGAAATTG CCCAABATAC CATGAAAATT
 GCCAAACAAT CTGTATTAAT CGGAATTTT ATCTGCGTTT TACTAATGTT AATTGCTAGT
 ACCGGGATCA TTCCGGCGCT AATCGGGGCT ATGCTACAAG AAGTCTGGGA CACTGTGTCA
 ATCTTATCTG CTTTGCGTGC TCGTCGAATT GGCCAGTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF077-2 (SEQ ID NO:294)

MKHVTKLGIT IITGVLLLF EFILHQPWNA YGIILITGSV MALMMFWEMI
 QTLREBKYGV DILAITAIVA TLAVGEYWAS LMILIMLTGG DSLEDYAAGK ANQELKSLLD
 NSPQKAHRLN GENLEDVSV EINVDELVV KPGELVPVDG LVKTGTSTVD ESSLTGESKP
 IEKNPGEDEL SGSVNGDGS KMVAEKTVD SQYQTIIVNLV KESAAEPAPF VRLADRYAVP
 FTLVAYLIAG VAVFVSKSPT RFAEVLVVAS PCPLILSAPI ALVAMSESS RHGVVIKSGT
 MVEKLASAKT IAFDKTGTIT QGQLSVBQVQ PINAGITAAE LVGLAASVEQ ESSHILARSI
 VAYARKQDVP LKNITDLAEV SGAGVKAFVD GAEIRVGKKN FVTIESQETE KIDKTTIHIS
 RNTYLGRIT FTDTVRPEAK ETMEKLHQLH LQRILMLTGD QESVAETIAA EVGITEVHGE
 CLPQDKLTIL KFLPKENHPV IMVGDGVNDA PSLAAADVGI AMGAGATAA SETADVILK
 DDLSKVSQAV EIAQDTMKIA KQSVNLGIFI CVLLMLIAST GIIPALIGAM LQEVVDTVSI
 LSLARRRIG C

EF077-3 (SEQ ID NO:295)

TCA GCCGAATTGG
 GCGTATGGCA TTATTTTAAT AACAGGTTCT GTAATGGCGT TAATGATGTT CTGGGAAATG
 ATTCAAACCT TACGTGAAGG AAAATATGCT GTCGATATTT TAGCGATTAC CGCTATCGTT
 GCAACCTTAG CTGTGGGAGA ATACTGGGCC AGTTTGATGA TTTTAATTAT CTGACTGGT
 GGTGATTCAT TAGAAGACTA TGCCGCTGGA AAAGCTAACC AAGAGGTGAA GTCATTATTG
 GATAACTCGC CACAAAAGC TCATCGCTTG AATGGCGAAA ATTTAGAAGA TGTTTCTGTT
 GAGGAAATCA ATGTTGGCGA TGAATTAGTA GTAAAACCAG GGGAAATAGT TCCAGTTGAT
 GGCTTGGTAA AAACCGGAC ATCAACAGTC GATGAATCTT CATTAACAGG AGAATCAAAA
 CCAATTGAAA AAAATCCTGG GGATGAATTA ATGTCGGGTT CCGTGATGG TGACGGCTCT
 TTGAAAATGG TTGCTGAAA AACTGTAGCA GACAGTCAAT ATCAAAACAT TGTGAACCTA
 GTGAAAGAAT CTGCGGCGCG TCCAGCTCAT TTTGTACGTT TAGCAATCTC CTATGCGGTA
 CCTTTTACAC TAGTTGCCTA CCTAATTGCA GGTGTGCTT GGTTTTCTTC AAAAAGTCCG
 ACACGTTTTG CGGAAGTCTT AGTTGTTGCT TCGCCGTGTC CTTTAATTCT ATCTGCCCCA
 ATTGCTTTAG TGGCAGGGAT GGGTCGTTCA AGTCGTCATG GGGTCCTTAT TAAATCGGGA
 ACGATGGTCG AAAAATTAGC TTCTGCAAAA ACGATTGCGT TTGATAAAAC AGGCACGATT
 ACGCAAGGAC AACTTTCTGT TGATCAAGTC CAACCAATCA ATGCTGGAAT AACTGCTGCT
 GAATTAGTGG GATTGGCAGC AAGCGTGGAA CAAGAATCAA GTCATATTTT AGCTAGATCA
 ATTGTTGCTT ATGCCAGAAA GCAAGATGTC CCATTAAAAA ATATTACAGA TCTAGCGGAA
 GTTTCTGGTG CTGGCGTGAA GGCATTTGTG GATGGTGCTG AGATACGGGT AGGTAAAAAG
 AATTTTGTGA CACAAGAGTC TCAAGAACT GAAAAAATG ATAAAACGAC TATTCATATT
 TCACGTAATG GCACATATTT AGGCCGAATT ACTTTTACAG ACAGTGTACG CCCAGAAGCA
 AAAGAGACTA TGGAAAAATT ACACCAATTA CATCTTCAAC GAATTTTAAT GCTGACGGGG
 GATCAAGAAT CCGTTGCAGA AACGATTGCT GCAGAAGTAG GAATTACGGA AGTACATGGG
 GAATGTTTAC CACAAGATAA ATTAATATT CTAAAAGAAT TGCTTAAAGA AAATCATCCA
 GTCATCATGG TAGGAGATGG TGTAATGAT GCACCTTCGC TTGCTGCTGC AGACGTAGGT
 ATTGCTATGG GTGCTCATGG AGCTACTGCG GCTAGTGAAA CTGCTGCTGC TGTATTTTTA
 AAAGATGACT TAAGTAAAGT CAGCCAAGCG GTCGAAATTG CCCAAGATAC CATGAAAATT
 GCCAAACAAT CTGTATTAAT CGGAATTTTT ATCTGCGTTT TACTAATSTT AATTGCTAGT
 ACCGGGATCA TTCCGGCGCT AATCGGGGCT ATGCTACAAG AAGTCTGGA CACTGTGTCA
 ATCTTATCTG CTTTGCGTGC TCGTCAATT GGCC

EF077-4 (SEQ ID NO:296)

QPNWA YGIILITGSV MALMMFWEMI
 QTLREGKYGV DILAITAIVA TLAVGEYWAS LMILIMLTGG DSLEDYAAGK ANQELKSLLD
 NSPQKAHRLN GENLEDVSV EINVDELVV KPGELVPVDG LVKTGTSTVD ESSLTGESKP
 IEKNPGEDEL SGSVNGDGS KMVAEKTVD SQYQTIIVNLV KESAAEPAPF VRLADRYAVP

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

FTLVAYLIAG VAWFVSKSPT RFAEVLVVAS PCPLILSAPI ALVAGMGRES RHGVVKSQT
 MVEKLASAKT IAFDKTGTIT QQQLSVDQVQ PINAGITAAE LVGLAASVEQ ESSHILARSI
 VAYARKQDVP LKNITDLAEV SGAGVKAFVD GAEIRVGKKN FVTQESQETE KIDKTTIHIS
 RNGTHYLGRT FTDTVRPEAK ETMEKLHQLH LQRILMLTGD QESVAETIAA EVGITEVHGE
 CLPQDKLTIL KELPKENHPV IMVGDGVNDA PSLAAADVGI AMBAGGATAA SETADVILK
 DDLSKVSQAV EIAQDTMKIA KQSVLIGIFI CVLLMLIAST GIIPALIGAM LQEVVDTVSI
 LSLARRRIG

EF079-1 (SEQ ID NO:297)

TAATTTCTAG CATCACCGAA GAAATTTTGA GAAAAACAAA GAGCCTGGGC CAATCACTGT
 CCCAGGCTCT CATGCTTTAT TTTTAAGGAG GAAGCAATGA AGTCAAAAAA GAAACGTCGT
 ATCATTGATG GTTTTATGAT TCTTTTACTG ATTATTGGAA TAGGTGCATT TCGGTATCCT
 TTTGTTAGCG ATGCATTAAA TAACTATCTG GATCAACAAA TTATCGCTCA TTATCAAGCA
 AAAGCAAGCC AAGAAAACAC CAAAGAAATG GCTGAACCTC AAGAAAAAAT GGAAAAGAAA
 AACCAAGAAT TAGCGAAAAA AGGCAGCAAT CCTGGATTAG ATCCTTTTTC TGAAACGCAA
 AAAACAACGA AAAAACCAGA CAAATCCTAT TTTGAAAGTC ATACGATTGG TGTTTTAACC
 ATTCCAAAAA TAAATGTCCG TTTACCAATT TTTGATAAAA CGAATGCATT GCTATTGGAA
 AAAGGAAGCT CCTTGTTAGA AGGAACCTCC TATCCTACAG GTGGTAGGAA TACACATGCG
 GTCATTTTCAG GCCATCGTGG TCTCCCTCAA GCCAAATTAT TTACABATTT GCCAGAAITTA
 AAAAAAGGCG ATGAATTTTA TATCGAAGTC AATGGGAAGA CGCTTCTTTA TCAAGTAGAT
 CAAATAAAAA CCGTTGAACC AACTGATACA AAAGATTAC ACATTAGTC TGGCCAAGAT
 CTCGTCACTT TATTAAGTTG CACACCGTAT ATGATAAACA GTCATCGGTT ATTAGTTTGA
 GGACATCGTA TCCCATATCA ACCAGAAAAA GCAGCAGCGG GGATGAAAAA AGTGGCACAA
 CAACAAAATT TACTATTATG GACATTACTT TTAATTGCCT GTGCGTTAAT TATTAGCGGC
 TTCATTATCT GGTACAAGCG ACGGAAAAAG ACGACCAGAA AACCAAGTA G

EF079-2 (SEQ ID NO:298)

MKSKKKRRI IDGFMJLLLI IGIGAFAYPF
 VSDALNNYLD QQIIAHYQAK ASQENTKEMA ELQEKMEKKN QELAKGSSNP GLDPFSETQK
 TTKKPKDSYF ESHTIGVLT I PKINVRPIF DKTNALLLEK GSSLLESTSY PTGGTNTHAV
 ISGHRGLPQA KLFTDLPELK KGDEFYIEVN GKTLAYQVDQ IKTVETDTK DLHIESGQDL
 VTLLTCTPYM INSHRLVRG HRIPIQPEKA AAGMKKVAQQ QNLLMLTLL IACALIISGF
 IHWYKRRKKT TRPKP

EF079-3 (SEQ ID NO:299)

TCCT
 TTTGTTAGCG ATGCATTAAA TAACTATCTG GATCAACAAA TTATCGCTCA TTATCAAGCA
 AAAGCAAGCC AAGAAAACAC CAAAGAAATG GCTGAACCTC AAGAAAAAAT GGAAAAGAAA
 AACCAAGAAT TAGCGAAAAA AGGCAGCAAT CCTGGATTAG ATCCTTTTTC TGAAACGCAA
 AAAACAACGA AAAAACCAGA CAAATCCTAT TTTGAAAGTC ATACGATTGG TGTTTTAACC
 ATTCCAAAAA TAAATGTCCG TTTACCAATT TTTGATAAAA CGAATGCATT GCTATTGGAA
 AAAGGAAGCT CCTTGTTAGA AGGAACCTCC TATCCTACAG GTGGTAGGAA TACACATGCG
 GTCATTTTCAG GCCATCGTGG TCTCCCTCAA GCCAAATTAT TTACABATTT GCCAGAAITTA
 AAAAAAGGCG ATGAATTTTA TATCGAAGTC AATGGGAAGA CGCTTCTTTA TCAAGTAGAT
 CAAATAAAAA CCGTTGAACC AACTGATACA AAAGATTAC ACATTAGTC TGGCCAAGAT
 CTCGTCACTT TATTAAGTTG CACACCGTAT ATGATAAACA GTCATCGGTT ATTAGTTTGA
 GGACATCGTA TCCCATATCA ACCAGAAAAA GCAGCAGCGG GGATGAAAAA AGTGGCACAA
 CAACAAAATT TACTATTATG GACATTACTT TTAATTGCCT GTGCGTTAAT TATTAGCGGC
 TTCATTATCT GGTACAAGCG ACGGAAAAAG ACGACCAGAA AACCAA

EF079-4 (SEQ ID NO:300)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. histolytica* Genes.

PF

VSDALINWYLD QQIIAHYQAK ASQENTHREMA ELQEKMEKKN QALAHNGSNP GLDPFSETQK
 TTKKPKDKSYF ESHTIGVLTI PKINVRLEPIF DKTNALLLEK GSCLEECTSY PTGGTNTHAV
 ISSHRLPQA ELFTDLPELF KSEDFYIEUN GKTLAYQVDC IFTHEPTDTH DLHIESGQDL
 VTLLTCTPYM INSHRLLVRG HRIPYQPEFA AAGMKKVAQR ENLLWTLLE IACALIISGF
 LIWYKREKKT TRKF

EF080-1 (SEQ ID NO:301)

TAGTTACACT CGTTTAGGBC TAGCAACGTY AGGTATTTTC GGTGCACTCT TAGCACTCTT
 TTTATTAGGA GGTATTTCBC TATGAAAAAA CGATTTTTAC GTTTTTTTTT CCTAATACTT
 CTTACCTTG GCGTTGCCCT ACCCGTTTCG GCGGCTGAAA ATGCAATTGA TGATGGCGCA
 CAATTACTGA CACCTGATCA AATCAACCAA CTAAAGCAAG AGATACAACC TTTAGAAGAA
 AAAACAAAAG CCGTCTGCTT TATTGTAACC ACAAATAATA ATACCTATGG CGATGAACAA
 GAATATGCAG ATCATTATCT TTTAAATAAA GTTGCAAGG AGCAAAATGC GATTCTTTTT
 CTCATTGATA TGGACTTACG GAAAATCTAC ATCTCTACTT CTGAAACAT GATTGATTAT
 ATGACAGATG CACGAATTGA TGATACCTTA GATAAAATAT GGSATAATAT GAGTCAAGGA
 AATTATTTCTG CCGCTGCTCA AACCTTTGTT CAGGAAACTC AAGCATTGT TAATAAAGGG
 GTTCCTGGGG GGCACATCG TGTGGACAGC GAAACAGGTA AATCACTCG TTATAAAGTC
 ATTACCCCGC TGGAAATGGT AATTGCTTTT GCTGCTGCGC TGATACTCAG TTTGGTCTTC
 TTAGGCATTA ATATTCTAA ATATCAATTA AAATTTTCAA GTTATCAATA TCCCTTTAGG
 GAAAAAACAA CTTTAAACTT AACCTCCCGC ACAGATCAGT TAACCAACTC TTTCATCACT
 ACGCGTCGTA TTCCTAAAAA CAATGGCGGC AGTGGCGGAA TGGCGGCTGG TGGTAGCACC
 ACCCACTCAA CTGGCGGCGG CACATTCGGT GCGCGCGGTC GAATTTTTTA G

EF080-2 (SEQ ID NO:302)

MKKR LLPIFFLILL TFGALPVSA AENSIDDGAQ
 LLTPDQINQL KQEIQPLEEK TKASVFIVTT NNNTYGDEQE YADHYLLNKV GKDQNAIFL
 IDMDLRKIYI STSGNMIDYM TDARIDDTLD KIWDNMSQGN YFAAAQTFVQ ETQAFVNKGV
 PGGHYRVDSE TKGITRYKVI TPLEMVIAFA AALILSLVFL GINISKYQLK FSSYQYPFRE
 KTTLNLSRT DQLTNSFITT RRIKNNNGS GGMGGGGSTT HSTGGGTFGG GGRSF

EF080-3 (SEQ ID NO:303)

GGCTGAAA ATTCAATTGA TGATGGCGCA
 CAATTACTGA CACCTGATCA AATCAACCAA CTAAAGCAAG AGATACAACC TTTAGAAGAA
 AAAACAAAAG CCTCTGTCTT TATTGTAACC ACAAATAATA ATACCTATGG CGATGAACAA
 GAATATGCAG ATCATTATCT TTTAAATAAA GTTGCAAGG AGCAAAATGC GATTCTTTTT
 CTCATTGATA TGGACTTACG GAAAATCTAC ATCTCTACTT CTGAAACAT GATTGATTAT
 ATGACAGATG CACGAATTGA TGATACCTTA GATAAAATAT GGSATAATAT GAGTCAAGGA
 AATTATTTCTG CCGCTGCTCA AACCTTTGTT CAGGAAACTC AAGCATTGT TAATAAAGGG
 GTTCCTGGGG GGCACATCG TGTGGACAGC GAAACAGGTA AATCACTCG TTATAAAGTC
 ATTACCCCGC TGGAAATGGT AATTGCTTTT GCTGCTGCGC TGATACTCAG TTTGGTCTTC
 TTAGGCATTA ATATTCTAA ATATCAATTA AAATTTTCAA GTTATCAATA TCCCTTTAGG
 GAAAAAACAA CTTTAAACTT AACCTCCCGC ACAGATCAGT TAACCAACTC TTTCATCACT
 ACGCGTCGTA TTCCTAAAAA CAATGGCGGC AGTGGCGGAA TGGCGGCTGG TGGTAGCACC
 ACCCACTCAA CTGGCGGCGG CACATTCGGT GCGCGCGGTC GAAT

EF080-4 (SEQ ID NO:304)

AENSIDDGAQ
 LLTPDQINQL KQEIQPLEEK TKASVFIVTT NNNTYGDEQE YADHYLLNKV GKDQNAIFL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IDMDLRKIYI STSGNMIDYM TDARIDDTLD KIWDNMSQGN YFAAACTFVQ ETQAFVNKGV
 PGGHYRVDSE TGTKTRYKVI TPLEMVIAFA AALILSLVFL GINISFYQLK ESSYQYPFRE
 KTTLNLTSTRT DQLTNSFITT RRIPKNNNGS GGMGGGGSTT HSTGGCTFGS GGRS

EF081-1 (SEQ ID NO:305)

TGAATGGAAC GAAGCAATCG TAATAAAAAA TCTTCAAAAA AACCACTTAT TCTTGGTGTT
 TCTGCCCTGG TTCTAATCGC TGCTGCCGGT GGCGGGTATT ATGCTTATAG TCAATGGCAA
 GCCAAACAAG AATTAGCCGA AGCGAAGAAA ACAGCTACTA CATTTTAAAG CGTATTGTCA
 AAACAGGAAT TTGATAAGTT ACCGTCCGTT GTTCAAGAAG CTAGCTTAAA GAAAAATGGC
 TATGATACTA AATCTGTTGT TGAAAAATAC CAAGCAATTT ATTCAGGGAT TCAAGCAGAA
 GGAGTCAAAG CTAGTGATGT TCAAGTCAAA AAGGCGAAAG ACAATCAATA CACATTTACC
 TATAAATTAT CGATGAGCAC GCCTTTAGGC GAAATGAAAG ATTTGTCTTA TCAATCAAGT
 ATCGCCAAAA AAGGCGATAC CTACCAATC GCTTGGAAGC CATCTTTAAT TTTTCCAGAT
 ATGTCAGGAA ATGATAAAAT TTCGATTCAA GTAGATAATG CCAAACTGG AGAAATTGTC
 GATCGTAATG GTAGTGGGCT AGCAATTAAC AAAGTGTGTTG ACGAAGTGG CGTAGTGCCT
 GGCAAACTCG GTTCTGGCGC AGAAAAACA GCCAATATCA AAGCTTTAG TGATAAATTC
 GCGGTTTCTG TTGATGAAAT CAATCAAAAG TTAAGCCAAG GATGGGTCCA AGCAGACTCC
 TTTGTACCAA TCACAGTCGC TTCTGAACCA GTGACAGAAT TACCAACAGG GGCTGCGACA
 AAAGATACAG AGTCACGTTA TTATCCGCTG GGGGAAGCAN TCGCAATTA A

EF081-2 (SEQ ID NO:306)

MERSNRNKKK SKKPLILGVS ALVLIAAAGG GYYAYSQWQA KQELAEAKKT ATTFLNVLSK
 QEFDKLPSVQ QEASLKKNY DTKSVVEKYQ AIYSGIQAEG VKASDVQVKK AKDNQYTFTY
 KLSMSTPLGE MKDLSYQSSI AKKGDYQIA WKPSLIFPDM SGNEKISIQV DNAKRGEIVD
 RNSGLAINK VFDEGVVPG KLGSGAEKTA NIKAFSDKFG VSVDEINQKL SQGWVQADSF
 VPITVASEPV TELPTGAATK DTSRYYPGL EAXRN

EF081-3 (SEQ ID NO:307)

T GGCGGGTATT ATGCTTATAG TCAATGGCAA
 GCCAAACAAG AATTAGCCGA AGCGAAGAAA ACAGCTACTA CATTTTAAAG CGTATTGTCA
 AAACAGGAAT TTGATAAGTT ACCGTCCGTT GTTCAAGAAG CTAGCTTAAA GAAAAATGGC
 TATGATACTA AATCTGTTGT TGAAAAATAC CAAGCAATTT ATTCAGGGAT TCAAGCAGAA
 GGAGTCAAAG CTAGTGATGT TCAAGTCAAA AAGGCGAAAG ACAATCAATA CACATTTACC
 TATAAATTAT CGATGAGCAC GCCTTTAGGC GAAATGAAAG ATTTGTCTTA TCAATCAAGT
 ATCGCCAAAA AAGGCGATAC CTACCAATC GCTTGGAAGC CATCTTTAAT TTTTCCAGAT
 ATGTCAGGAA ATGATAAAAT TTCGATTCAA GTAGATAATG CCAAACTGG AGAAATTGTC
 GATCGTAATG GTAGTGGGCT AGCAATTAAC AAAGTGTGTTG ACGAAGTGG CGTAGTGCCT
 GGCAAACTCG GTTCTGGCGC AGAAAAACA GCCAATATCA AAGCTTTAG TGATAAATTC
 GCGGTTTCTG TTGATGAAAT CAATCAAAAG TTAAGCCAAG GATGGGTCCA AGCAGACTCC
 TTGTACCAA TCACAGTCGC TTCTGAACCA GTGACAGAAT TACCAACAGG GGCTGCGACA
 AAAGATACAG AGTCACGTTA TTATCCGCTG GGGG

EF081-4 (SEQ ID NO:308)

G GYYAYSQWQA KQELAEAKKT ATTFLNVLSK
 QEFDKLPSVQ QEASLKKNY DTKSVVEKYQ AIYSGIQAEG VKASDVQVKK AKDNQYTFTY
 KLSMSTPLGE MKDLSYQSSI AKKGDYQIA WKPSLIFPDM SGNEKISIQV DNAKRGEIVD
 RNSGLAINK VFDEGVVPG KLGSGAEKTA NIKAFSDKFG VSVDEINQKL SQGWVQADSF
 VPITVASEPV TELPTGAATK DTSRYYPGL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF082-1 (SEQ ID NO:309)

TAAAAAATGA AAAAGATGCT GCGCATTTCA AGCATTTTGT TGATTCCTAC GCGCTTATG
 CTTTAAATA GTTCAAAAGT TGAAGCAGCT CAAGTGGCTT CTAATGAATC CAACGCTGAT
 ATTACGTTTG CTCTTGATAA TACTGTCACG CCACCTGTCA ATCCGACGAA CCCTTCTCAG
 CCGTGACAC CTAATCCTGC TGATCCTCAT CAACCTGCTA CAGCTGGACC CTTAGTATT
 GACTATGTTT CAAATATCCA TTTTGGATCA AAACAAATTC AAGCTGGAAC AGCGATCTAT
 TCGGCACAAC TGGATCAAGT GCAAAATAGT ACTGGGATT TAAATAGCGT GCCAAACTAT
 GTTCAAGTAA CTGACAAACG TGGTCTAAAT CTTGGCTGGA AATTATCACT TAAACAGAGT
 GCGCAATTTG CTACAAGTGA TTCAACACCC GCTGTTTTGG ATAAATGCATC CTTGACCTTT
 TTAGCAGCAA CACCCAATTC AACACAGTTA CTTTCTTTGG CCGCATTAAC GGTCCCACTA
 ACCTTGGATC CAACTGGTGC CGCCACTTCT CCGTGGCGA CTGGCGCTCT TTCAACAGGA
 ATGGGCACTT GGACATTAGC TTTTGGTAGC GGACGACCG CTGCTCAAGG CATTCAATTA
 ACTGTTCTCG CGACAACGAA AAAAGTTGCA GCTAAACAAT ATAAACAAC GCTTACTTGG
 ATTTTGGATG ATACACCACT TTAA

EF082-2 (SEQ ID NO:310)

MKKIVRISS ILFVATPLML LNSSKVEAAQ VASIQSNADI TFALDNTVTP P'VNPTNPSQP
 VTPNPADPHQ PGTAGPLSID YVSNIHFGSK QIQAGTAIYS AILDQVQNST GDILISVPNYV
 QVTDKRLNL GWKLSVKQSA QFATSDSTPA VLDNASLTFL AATINSTQLL SLAPLTPVPT
 LDPTGAATSP VATAALSTGM GTWTLAFGSG XTAAQGIQLT VVATTKKVAA KQYKTTLTWI
 LDDTPL

EF082-3 (SEQ ID NO:311)

AGCT CAAGTCGCTT CTATTCAATC CAACGCTGAT
 ATTACGTTTG CTCTTGATAA TACTGTCACG CCACCTGTCA ATCCGACGAA CCCTTCTCAG
 CCGTGACAC CTAATCCTGC TGATCCTCAT CAACCTGGTA CAGCTGGACC CTTAGTATT
 GACTATGTTT CAAATATCCA TTTTGGATCA AAACAAATTC AAGCTGGAAC AGCGATCTAT
 TCGGCACAAC TGGATCAAGT GCAAAATAGT ACTGGGATT TAAATAGCGT GCCAAACTAT
 GTTCAAGTAA CTGACAAACG TGGTCTAAAT CTTGGCTGGA AATTATCACT TAAACAGAGT
 GCGCAATTTG CTACAAGTGA TTCAACACCC GCTGTTTTGG ATAAATGCATC CTTGACCTTT
 TTAGCAGCAA CACCCAATTC AACACAGTTA CTTTCTTTGG CCGCATTAAC GGTCCCACTA
 ACCTTGGATC CAACTGGTGC CGCCACTTCT CCGTGGCGA CTGGCGCTCT TTCAACAGGA
 ATGGGCACTT GGACATTAGC TTTTGGTAGC GGACGACCG CTGCTCAAGG CATTCAATTA
 ACTGTTCTCG CGACAACGAA AAAAGTTGCA GCTAAACAAT ATAAACAAC GCTTACTTGG
 ATTTTGGATG ATACACCACT

EF082-4 (SEQ ID NO:312)

AQ VASIQSNADI TFALDNTVTP P'VNPTNPSQP
 VTPNPADPHQ PGTAGPLSID YVSNIHFGSK QIQAGTAIYS AILDQVQNST GDILISVPNYV
 QVTDKRLNL GWKLSVKQSA QFATSDSTPA VLDNASLTFL AATINSTQLL SLAPLTPVPT
 LDPTGAATSP VATAALSTGM GTWTLAFGSG XTAAQGIQLT VVATTKKVAA KQYKTTLTWI
 LDDTP

EF083-1 (SEQ ID NO:313)

TAATTTAAAA GACAAGGAGA AATAAAAATG AAAAAAGAAA TTTTAGCAGG AGCGCTTGTC
 GCTCTGTTT TTATGCCTAC AGCTATGTTT GCGGCAAAAG GAGACCAAGG TGTGGATTGG
 GCGATTTATC AAGGTGAACA AGGTGCGCTTT GGCTATGCAC ATGATAAATT CGCTATTGCC
 CAGATTGGAG GCTACAATGC TAGCGGTATT TATGAACAAT AACATATATA AACGCAAGTG
 GCAAGTGCTA TTGCCCAAGG TAAACGTGCG CATACTATA TTTGCTATGA CACTTGGGGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACATGGACA TTGCGAAAAC AACAAATGGAT TACTTTTTCG CACCTATTCA AACGCCTAAA
 AATTCCATCG TTGCATTAGA TTTTGAACAT GGAGCGTTGG CTAGTGTTC AGATGGATAT
 GGAGGATATG TAAGTTCAGA TGCCGAAAAA GCAGCAAATA CAGAGACAAT TTTGTACGGT
 ATGCGCAGAA TCAAACAGGC TGGCTATACT CCAATGTATT ACAGCTATAA GCCATTTACA
 CTAAATCATG TAAACTATCA ACAAATCATC AAAGAGTTTC CTAACTCTTT ATGGATTGCT
 GCGTATCCTA TCGATGGTGT GTCACCATAT CCATTGTATG CTTATTTCCTC AAGCATGGAT
 GGTATTGGTA TTTGGCAATT CACATCCGCT TATATTGCAG GTGCTTTAGA TGGTAACGTA
 GATTTAACAG GAATTACGGA TAGTGGTTAT ACAGATACCA ATAAACCAGA AACGGATACG
 CCAGCAACAG ATGCAGGCGA AGAAATTGAA AAAATACCTA ATTGTGATGT TAAAGTTGGC
 GATACCGTCA AAGTGAAATT TAATGTAGAT GCTTGGGCAA CTGGGGAAGC TATTCCGCAA
 TGGGTAAAAG GAAACAGCTA CAAAGTGCAA GAAGTAACTG GAAGGAGAGT ATTGCTTGAA
 GGTATCTTGT CATGGATTAG CAAAGGTGAT ATTGAATTAT TGCCAGACGC AACAGTCGTC
 CCTGATAAGC AACCAGAAGC GACTCATGTG GTACAATACG GAGAAACATT ATCAAGTATT
 GCTTATCAAT ATGGAACAGA CTATCAAACG TTGGCGGCAT TAAATGGATT GGCTAATCCA
 AATCTTATTT ATCCTGGTCA AGTTTGTAAA GTCAATGGAT CGGCAACAAG TAATGTCTAC
 ACGGTTAAAT ACGGCGATAA TTTATCTAGT ATTGCAGCAA AACTTGGCAC TACTTATCAA
 GCTTTAGCTG CATTAAACGG ATTAGCAAAT CCTAACTTGA TTTATCCAGG TCAAACATTG
 AATTATTAA

EF083-2 (SEQ ID NO:314)

MK KKILAGALVA LFFMPTAMFA AKGDQGVDA IYQGEQGRFG YAEDEKFAIAQ
 IGGYNASGIY EQYTYKTQVA SAIAQGKRAH TYIWYDTWGN MDIHTTMDY FLPRITPKN
 SIVALDFEHG ALASVPDGYG GYVSSDAEKA ANTEITLYGM RFIHTAGYTP MYYSYKPTFL
 NHVNYQQIHK EFPNSLWIAA YPIDGVSPYP LYAYFPSMDG IGVHTTSAY IAGGLDGNVD
 LTGITDSGYT DTNKPETDTP ATDAGEEIEK IPNSDVKVG D TVNVFNVDA WATGEAIPQW
 VKGNSYKVQE VTGSRVLEGG ILSWISKDI ELLPDATVVP DEDPHATHV VYQETLSSIA
 YQYGTDYQTL AALNGLANPN LIYPGQVLKV NGSATSNVYT VRAHICLLSI AAKLGTITYQA
 LAALNGLANP NLIYPGQTLN Y

EF083-3 (SEQ ID NO:315)

AAAAG CAGACCAAGG TGTGGATTGG
 GCGATTATATC AAGGTGAACA AGGTGCTTTT GGCTATGCAC ATGATAAATT CGCTATTGCC
 CAGATTGGAG GCTACAATGC TAGCGGTATT TATGAACAAT ACATATATAA AACGCAAGTG
 GCAAGTGCTA TTGCCCAAGG TAAACGTGCG CATACCTATA TTTGCTATGA CACTTGGGGA
 AACATGGACA TTGCGAAAAC AACAAATGGAT TACTTTTTCG CACCTATTCA AACGCCTAAA
 AATTCCATCG TTGCATTAGA TTTTGAACAT GGAGCGTTGG CTAGTGTTC AGATGGATAT
 GGAGGATATG TAAGTTCAGA TGCCGAAAAA GCAGCAAATA CAGAGACAAT TTTGTACGGT
 ATGCGCAGAA TCAAACAGGC TGGCTATACT CCAATGTATT ACAGCTATAA GCCATTTACA
 CTAAATCATG TAAACTATCA ACAAATCATC AAAGAGTTTC CTAACTCTTT ATGGATTGCT
 GCGTATCCTA TCGATGGTGT GTCACCATAT CCATTGTATG CTTATTTCCTC AAGCATGGAT
 GGTATTGGTA TTTGGCAATT CACATCCGCT TATATTGCAG GTGCTTTAGA TGGTAACGTA
 GATTTAACAG GAATTACGGA TAGTGGTTAT ACAGATACCA ATAAACCAGA AACGGATACG
 CCAGCAACAG ATGCAGGCGA AGAAATTGAA AAAATACCTA ATTGTGATGT TAAAGTTGGC
 GATACCGTCA AAGTGAAATT TAATGTAGAT GCTTGGGCAA CTGGGGAAGC TATTCCGCAA
 TGGGTAAAAG GAAACAGCTA CAAAGTGCAA GAAGTAACTG GAAGGAGAGT ATTGCTTGAA
 GGTATCTTGT CATGGATTAG CAAAGGTGAT ATTGAATTAT TGCCAGACGC AACAGTCGTC
 CCTGATAAGC AACCAGAAGC GACTCATGTG GTACAATACG GAGAAACATT ATCAAGTATT
 GCTTATCAAT ATGGAACAGA CTATCAAACG TTGGCGGCAT TAAATGGATT GGCTAATCCA
 AATCTTATTT ATCCTGGTCA AGTTTGTAAA GTCAATGGAT CGGCAACAAG TAATGTCTAC
 ACGGTTAAAT ACGGCGATAA TTTATCTAGT ATTGCAGCAA AACTTGGCAC TACTTATCAA
 GCTTTAGCTG CATTAAACGG ATTAGCAAAT CCTAACTTGA TTTATCCAGG TCAAACATTG
 AAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF063-4 (SEQ ID NO:316)

KGDQGVDA IYQGFQGRFG YAHDKFAIAQ
 IGGYNASGIY EQYTYKTQVA SAIAQGHRAH TYIYTDIAGN MDIAKTHMY FLPRIQTPKN
 SIVALDFEHG ALASVFDGYG GYVSSDAEKA ANTETILYGM BKIKCAWCH MYYSYKPFLL
 NHVNYQQIHK EPPNSLWIAA YPIDGVSPYP INAYFPRMGG IGIWQFQAY IAGGLDGNVD
 LTGITDSGYT DTNKPETDTP ATDAGEBIEK IPNSIVKNSD TUKVKFHWIA WATGEAIPQW
 VKGNSYKVE VTGSRVLLEG ILSWISKGDI ELLPDIATVP DKQFENHMY QYGETLSSIA
 YQYGTDYQTL AALNGLANPN LIYPGQVLKV NSSATSNVYT VKYGDNLSSI AAKLGTITYQA
 LAALNGLANP NLIYPGQTLN

EF084-1 (SEQ ID NO:317)

TAGTCAAACG TTTATTTTCT COTTAATCC AGAAAAAATC CCGTAATTAT GSTACACTAC
 CTATTGAATT GGAGGAGAAC TATGAAGAAA TTTGATGTAA TTATTCTCGG TGCTGGGACG
 AGCGGTATGA TGGCCACGAT TGGCGCCGCC GAAGCAGGCG CTCAATATT ATTGATTGAA
 AAAAATCGCC GTGTTGGGAA AAAATTATTA ATGACTGCTG GCGGCGCTG TAATGTAACC
 AATAATCGGC CCGCAGAAGA AATCATTTC TTTATTCCTG GGAATGAAAA ATTTTATATAC
 AGCGCATTTT CACAATTTGA TAACTATGAT ATCATGAACT TTTTGAATC CAATGGTATT
 CACTTAAAAG AAGAAGATCA CGGACGCATG TTCCCTGTTA CAGATAAATC GAAGTCAATT
 GTTGATGCGC TATTTAACCG CATTACGAA TTAGBAGTCA CTGTTTCTAC AAAAACACAG
 GTCACAAAAT TACTACGAAA AGACGATCAA ATAATTGGCG TTGAAGCAGA ACTGGAAAAA
 ATTTATGCAC CGTGTGTTGT ATTAACAAC ATGGGGCATA CCATCAGCCG GCTCTACCCT
 ACTGGTGATG GCTATAAACT AGCCAAAAAA ATGGGGCATA CCATCAGCCG GCTCTACCCT
 ACCGAATCAC CTATTATTTC TGAAGAACCT TTTATCTGCG ATAAACCTTT GAAAGTCTC
 TCTTTACAAG ATGTTAATTT AACTGTTTTG AACCACAAAG GAAAGCTTT AATTAAATCAT
 CAAATGGATA TGCTGTTTAC ACATTTTGCC ATTTACAGAC CTGCTGCTCT CCGCTGTTCT
 AGTTTTATTA ACCAAGAATT AACTCGCAAC GGTAAATCAAC CTGTACCTCT AGCCTTGAT
 GTGTTTCCGA CAAAATCTTT TGAAGAAGTG CCGTCAAAAC AACTAACAGA AAAGCAACGN
 CTTTCCTTTG TGGAACTACT GAAAGACTTT CAGTTCACTT TTACBAAAC ATTGCCTTTG
 GAAAAATCTT TTGTCACAGG CGGTGGGATT TCCCTCAAAG AAGTACCTCC TAAAACAATG
 GAGAGCAAAAT TAGTCAATGG TTTATTTTTT GCTGCTGAAC TTTTATATAT TAATGGCTAT
 ACTGGAGGCT ACAAATGTTAC AGCTGCATTT GTCAGTGCAC ATGTTCTGGG CTCCCATGCC
 GCAGAAATTG CAGAATACAC CTATTTACCA ATTGAAGAAG TCTAA

EF084-2 (SEQ ID NO:318)

MKKF DVIIVGAGTS GMMATIAAAE AGAQVLLIEK
 NRRVGKLLM TGGGRCNVTN NRPAEEIISF IPGNCKFLYS AFSQFDNYDI MNFFESNGIH
 LKEEDHGRMF PVTDKSKSIV DALFNRIHEL GVTVFKTQV TKLLHLEQI IGVETELEKI
 YAPCVVLTG GRTPSTGAT GDGYKLAKKM GHTISPLYPT ESPIISEEPF ILDKTLQGLS
 LQDVNLTVLN QKGKPLVNHQ MDMLFTHFGI SBPAALRCSS FINQELTENG NQPVTVLADV
 FPTKSFEVVP AKQLTEKQRL SFVELLKDFQ FTVTFTLPLE KSFVTGGGIS LKEVTPKTIME
 SKLVNGLFFA GELLDINGYT GGYNVTAAPV TSHVABSHAA EIAHNTYLP I EV

EF084-3 (SEQ ID NO:319)

C GAAGCAGGCG CTCAAGTATT ATTGATTGAA
 AAAAATCGCC GTGTTGGGAA AAAATTATTA ATGACTGCTG GCGGCGCTG TAATGTAACC
 AATAATCGGC CCGCAGAAGA AATCATTTC TTTATTCCTG GGAATGAAAA ATTTTATATAC
 AGCGCATTTT CACAATTTGA TAACTATGAT ATCATGAACT TTTTGAATC CAATGGTATT
 CACTTAAAAG AAGAAGATCA CGGACGCATG TTCCCTGTTA CAGATAAATC GAAGTCAATT
 GTTGATGCGC TATTTAACCG CATTACGAA TTAGBAGTCA CTGTTTCTAC AAAAACACAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTCACAAAAT TACTACGAAA AGACGATCAA ATAATTEGGG TTSAAAACGA ACTGGAAAAA
 ATTTATGCAC CGTGTGTTGT ATTAACAACCT GCGGCGCGCA CTTATCCTTC CACAGGAGCA
 ACTGGTGATG GCTATAAACT AGCCAAAAAA ATGGGCGATA CCATCAGCCC GCTCTACCCCT
 ACCGAATCAC CTATTATTTC TGAAGAACCT TTTATCCTGG ATAAAACGTT GCAAGGTCTC
 TCTTTACAAG ATGTTAATTT AACTGTTTTG AACCAAAAAG GAAAACCTTT AGTTAATCAT
 CAAATGGATA TGCTGTTTAC ACATTTTGGC ATTTCAAGAC CTGCGCGGCT CCGCTGTTCT
 AGTTTTATTA ACCAAGAATT AACTCGCAAC GGTAAATCAA CTGTCAGGCT AGCCTTGGAT
 GTGTTTCCGA CAAAATCTTT TGAAGAAGTG CCTGCGAAAAC AACCAATAGA AAAGCAACGN
 CTTTCCTTTG TGGAACTACT GAAAGACTTT CAGTTCACTG TTATCAAAAC ATTGCCTTTG
 GAAAAATCTT TTGTCACAGG CGGTGGGATT TCCCTCAAAAG AAGTCAACCC TAAACAATG
 GAGAGCAAAT TAGTCAATGG TTTATTTTTT GCTGCTGAAC TTTTACATAT TAATGGCTAT
 ACTGGAGGCT ACAATGTTAC AGCTGCATTG GTCAGTGGAC ATGTTCTGTTG CTCCCATGCC
 GCAGAAATTG CAGAATACAC CTATTTACCA ATTGAAGAAG TC

EF084-4 (SEQ ID NO:320)

E AGAQVLLIEK

NRRVGKKLLM TGGGRCNVN NRPAEEIISF IPGNGKFLYS AFSQFINYDI MNFFESNGIH
 LKEEDHGRMF PVTDKSKSIV DALFNIRINEL GVTIVFTKTQV TKLEKNDQI IGVETELEKI
 YAPCVVLTG GRTYPSTGAT GDGYKLAKKM GHTISPLYPT ESPTESEEPF ILDKTLQGLS
 LQDVNLTVLN QKGKPLVNHQ MDMLFTHFGI SGFAALRCES FINHLTENG NQPVTVALDV
 FPTKSFEFVP AKQLTEKQRL SFVELLKDFQ FTVTFTLPLE KSFVGGGGS LKEVTPKTME
 SKLVNGLFFA GELLDINGYT GGYNVTAFFV TGHVAGSHAA EIAETTYLPI EEV

EF085-1 (SEQ ID NO:321)

TAACCCATGA AATCATTTTG TCCCGCATAT GGGGATATCA CTTTACCGGT GATGGCAGCA
 CAGTCCACAC TCATATCAAA AATCTGCGGG CGAACTGCCG GAAAATATCA TCAAAACCAT
 CCGCGGTGTA GGTTACCGAT TGGAGGAATC ATTATAATCG AAGGAAAAGG GATTTTCATT
 AAGGTTTTTT CCTATACGAT CATTGTCCTG TTACTGCTTG TCGGTCTAAC GGCAACACTG
 TTTGCACAGC AATTTGTGTC TTATTTTCAGA GCGATGGAAG CAGAGCAAAC AGTAAAATCC
 TATCAGCCAT TGGTGGAACT GATTGAGAAT AGCGATAGGC TTGATATGCA AGAGGTGGCA
 GGGCTGTTTC ACTACAATAA CCAATCCTTT GAGTTTTATA TTAAGATAA AGAGGGAAGC
 GTACTCTATG CCACACCGAA TGCCGATACA TCAAATAGTG TTAGTCCCGA CTTTCTTTAT
 GTGGTACATA GAGATGATAA TATTTGATG GTTGTCTCAA GAAAGGCGAGG TGTGGGATTG
 CTTTATCAAG GGCTGACAAT TCGGGGAATT GTTATGATTG CCAATATGGT TGTATTTCAG
 CTTTTATGCG CGTATATCTT TGCGCGGCAA ATGACAACGC CGATCAAGC CTTAGCGGAC
 AGTGCGAATA AAATGGCAAA CCTGAAAGAA GTACCGCCGC CGTTGAGCG AAAGGATGAG
 CTTGGCGCAC TGGCTCACGA CATGCATTCC ATGTATATCA GCTGAAAAGA AACCATCGCA
 AGGCTGGAGG ATGAAATCGC AAGGGAACAT GAGTTGGAGG AAACACAGCG ATATTTCTTT
 GCGGCAGCCT CTCATGAGTT AAAAACGCCC ATCGCGGCTG TAAGCGTTCT GTTGGAGGGA
 ATGCTTGAAA ATATCGGTGA CTACAAAGAC CATTCTAAGT ATCTGCGCA ATGCATCAAA
 ATGATGGACA GGCAGGGCAA AACCATTTCG GAAATACTGG AGCTTCTCAG CCTGAACGAT
 GGGAGAATCG TACCCATAGC CGAACCCTG GACATAGGGC GATCTCTTGC CGAGCTGCTA
 CCCGATTTTC AAACCTTGGC AGAGGCAAAAC AACCAGCGGT TGGTCACAGA TATTCAGCC
 GGACAAATTG TCCTGTCCGA TCCGAAGCTG ATCCAAAAGG CGATATCCAA TGTATATTG
 AATGCGGTTT AGAACACGCC CCAGGAGGT GAGGTACGGA TCTGAGTGA GCCTGGGGCT
 GAAAAATACC GTCTTTCCGT TTTGAACATG GCGGTTTACA TTATGATAC TGCACTTTCA
 AAGCTGTTCA TCCCATTCTA TCGCATTGAT CAGGCGCGAA GCGCAAAAA GTGGCGAAG
 CGGTTTGGGG CTTGCCATCG TACAAAAAAC GCTGGATGCC ATGAGCCTCC AATATGCGCT
 GGAAAAACCC TCAGATGGCG TTTTGTCTG GCTGGATTGA CCGCCACAT CAACACTATA
 AATATTTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF085-2 (SEQ ID NO:322)

MERKGIPIK
VFSYTIIVLL LLNGVTATLF AQCFVSFYFA MEAQQTWSEI QPLVELIQNS DRIDMQEVAG
LFHYNNQSF E FYIEDKEGSV LYATPNADTS NSVRIDFLYV VHFDDNHSIV AQSKAGVGLL
YQGLTIRGIV MIAIMVVPSL LCAYIFARQM TTPIKALADS ANHMANLFEV PPPLERKDEL
GALAHDMHSM YIRLKETIAR LEDEIAREHE LEETQFYFFA AASHLEMTPI AAVSVLLEGM
LENIGDYKDH SKYLRECIKM MDRQGTISE ILELVSLNDS RIVFIAEPLD IGRTVAELLP
DFQTLAEANN QRFVTDIPAG QIVLSDPKLI QKALSNVILN AVQNTPOGGE VRIWSEPGAE
KYRLSVLNMG VHIDTALSK LFIPFYRIDQ ARSSKKWAKE FGACHETENA GCHEPPICAG
KHLRWRFVLA GPTAHINTIN I

EF085-3 (SEQ ID NO:323)

GC AATTTGTGTC TTATTTGAGA GGSATGGAAG CACAGCAAAC ACTAAATCC
TATCAGCCAT TGGTGGAACT GATTCAGAAT AGCGATAGGC TTGATATGCA AGAGSTGGCA
GGGCTGTTTC ACTACAATAA CCAATCCCTT GATTTTATA TTGAAGATAA AGAGGGAAGC
GTACTGTATG CCACACCGAA TGCGATACA TCAATAATG TTAGGCGGA CTCTCTTTAT
GTGTACATA GAGATGATAA TATTTGATT GTTGCTCAA GCAAGGAGG TGTGGGATTG
CTTTATCAAG GGCTGACAAT TGGGGAAAT GTTATGATG GSATAATGAT TGTATTCAGC
CTTTTATGCC CGTATATCTT TGCGCGGAAA ATGACAAAGC GATTAAGAGC CTTAGCGGAC
AGTGCGAATA AAATGGGAAA CCTGAAAGAA GTACCGCGGC CCTGAGAGG AAAGGATGAG
CTTGGCGCAC TGGCTCACGA CATGCATTCC ATGTATATTA CCTTAAGAA AACCATCGCA
AGGCTGGAGG ATGAAATCGC AAGGGAACAT GAGTGGAGG AAGACAGAG ATATTTCTTT
GCGGCAGCCT CTCATGAGTT AAAAAGCGCC ATCGCGGCTG TAAGCTTCT GTTGGAGGGA
ATGCTTGAAA ATATCGGTGA CTACAAAGAC CATTCTAAT ATCTGGGGA ATGCATCAAA
ATGATGGACA GGCAGGGCAA AACCATTTC GAAATACTG AGCTTCTAG CCGAAGCAT
GGGAGAATCG TACCCATAGC CGAACCCTG GACATAGGBC GCAGGCTTC CGAGCTGCTA
CCCGATTTTC AAACCTTGGC AGAGGCAAAC AACCAGCGGT TGCTCAGAGA TATTCAGCC
GGACAAATTG TCCTGTCCSA TCCGAAGCTG ATCCAAAAG CGCTATGAA TGTATATTG
AATGCGGTTG AGAACACGCC CCAGGGAGGT GAGGTAGGA TATGAGTGA GCGTGGGCT
GAAAAATACC GTCTTTCCGT TTTGAACATG GCGGTTACA TTGATGATAC TGCCTTTCA
AAGCTGTTCA TCCCATCTA TCGCATTGAT CAGGCGTGA GCAGCAAAA GTGGGCGAAG
CGGTTTGGGG CTTGCCATCG TACAAAAAC GCTGATGTC ATGAGCTTC AATATGCGCT
GGAAAAACAC TCAGATGGCG TTTTGTCTG GCTGATTTA CCGTCAGAT CAACACTATA
AATATTT

EF085-4 (SEQ ID NO:324)

QFVSFYFA MEAQQTWVSY QPLVELIQNS DRIDMQEVAG
LFHYNNQSF E FYIEDKEGSV LYATPNADTS NSVRIDFLYV VHFDDNHSIV AQSKAGVGLL
YQGLTIRGIV MIAIMVVPSL LCAYIFARQM TTPIKALADS ANHMANLFEV PPPLERKDEL
GALAHDMHSM YIRLKETIAR LEDEIAREHE LEETQFYFFA AASHLEMTPI AAVSVLLEGM
LENIGDYKDH SKYLRECIKM MDRQGTISE ILELVSLNDS RIVFIAEPLD IGRTVAELLP
DFQTLAEANN QRFVTDIPAG QIVLSDPKLI QKALSNVILN AVQNTPOGGE VRIWSEPGAE
KYRLSVLNMG VHIDTALSK LFIPFYRIDQ ARSSKKWAKE FGACHETENA GCHEPPICAG
KHLRWRFVLA GPTAHINTIN I

EF086-1 (SEQ ID NO:325)

TAAGTGGTGG GATTGGCAA TGGTTCCGC GCAGCGCTAA CAGATACATT GATTTTATTA
CATGATGACC TATTGAATAC AGATGCAGAA AAATTAAATA AATTACTGC TCCGCTGATG
CTGTATGCAA AAGATCCAAA CATAAATGG CCAATTTATC GTGCAACAGG AGCTAACTTA
ACAGATATTT CAATCACCGT TTAGGTACT GGAATTTTGT TAGAAGATAA TCAACGCCTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTACAAGTAC AAGAAGCTGT TCCGTCGGTT TTAAAAAGTG TTTGCTGTGG TGATGGCTTA
 TATCCTGATG GTTCCTTGAT TCAACATGGT TATTTTCCGT ACACCGGCAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGGTTGCGA CTGGGAGATG
 AATGACCCTA ACATTAGTAA TTTATTTAAT GTTGTGATA AAGGTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTAGAAATA TTGCGAGAG GCCAGAAACG
 AATCCTTTTA CTACAGAGTT TGAATCGGGT AAAGAAACAA TACCTAATTI AACCTTAATT
 GCAAAAATTTG CACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCATACTA TCATTCTTTT AAAAAGCAAA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGGCTCA CTTGCGCAAG CAGACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCTTA CAGAAAAATA ACATATATSC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGAAAAA TAAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TATAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACGAGGAA CAGACGTTGA CACAAGAGAA
 TTGGCAAAATG GTGCTTATAC AGGGAAACGC ACTGCGCAGT CATGCGTAGG TGGCTCAAAT
 AATGGACAGG TTGCTCTAT AGGAATGTTT TTATATAAAA GTATGGAAGG AATGAACTTA
 GTTGCTAAAA AATCTTGTT CTTATTAGAT GGTCAAAATCA TTAATTTGCG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCTGCGATA ATGCGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCCT GATTAATTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTCNA TCAATAGGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTGTCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TGGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CATTGGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATGCGAG GATCTATGC GTATGATCCA
 ATGTCGGTTA TTTCAGAAAA AATTGATAAC GGTGTITATC GCTTACTCT TGCGAATCCT
 TTACAAAATA ATGCATCCGT TTCTATTGAA TTTGATAAGG GATTTCTTGA AGTAGTCGCA
 GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATATGCG GGGGTAAAT
 GGCAGCTCGC GTTCAATCAT TGTTAAAAACA ACTCTGAAG TAACTAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ATACGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGCGAG ATCAAAACAC AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CTTGCGGCA TGAAGCAATT GGTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAAAGAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAATCATT GAAGCAAGCG
 CAAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAA TGAACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGGAAAATAA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG ACACTTAAAT ACTAGTACAG GAGTTATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCAATTT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGGTC TTCTAETTAT CGCCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF086-2 (SEQ ID NO:326)

LVGLANWFRA ALTDLILLH DDLNNTDAEK INFTAPLML YAEPIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEAQSVL KSVSSGDGLY FEGSLQHG YPYNGSYGNE
 LLKGFGRIQT ILQGSWEMN DPNISNLFNV VDFGYLQLMV NGHPSMVSG RSISRAPETN
 PFTTEFESGK ETIANLTLIA KFAPENLRND IYTSIQTWLQ QSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ FINEYAVGIS MSAQRVGN YFGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDREL ANQAYTGKRS PQSWVGGSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGSGIT GTTDAFIETI LDNRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDVCI EERSGEGYDI NEYFVNDKTY
 TNTFAKISK N YGKTVENGT YLTVVGKTN EEIALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYFLTLANPL QNNASMSIEF DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTHEALEK LIQEQFEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVNP TREVDFTNLL KIIKENEKHQ

TABLE 1. Nucleotide and Amino Acid Sequences of *E. coli* Genes.

EKDYTASSWK VYSEALKQAL TADDTTATC AEUATIAHKL ENUHMLTLK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTR QYKPSQGGF KPAK,PLPST SEPTIALVI IGLLVIASGC
 LLVFRKSKSK E

EF086-3 (SEQ ID NO:327)

ACCAGAAAA TTTAAGAAAT GACATTTATA CATCATCCCA AACGAGGCTT
 CAACAAAGTG GGTGACTACTA TCATTTCTTT AAAAAGCCCA GAGTTTCTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCTGCCAAG CGAATCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGAAAA TAAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACGAGGAA CGAATCTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGC ACTGCTACT CAAGCTTAGG TGGCTCAAAT
 AAT

EF086-4 (SEQ ID NO:328)

PENLRND IYTSIQTWLQ QSGSYHHFFK KPRDFEALIT
 LKNVNSASP AQATPMQSLN VYGMORVLQ KINNEYANGIS MYDNGNYE FGNTENKKGW
 HTAD3MLYLY NQDFAQFDEG YWATIDPYRL PGTNDREEL ANHAYTGKRS PQSWVGGSNN

EF087-1 (SEQ ID NO:329)

TAAGTGGTGG GATTGGCAAA TTGGTTCGGC GCAGGCTTAA CAGATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AATTAAATA AATTACTGC TCCGCTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG CCAATTTATC GCGCAACAGG AGCTAACTTA
 ACAGATATTT CAATCACCGT TTAGGTACTT GCACTTTTGT TAGAAGATAA TCAACGCCTA
 GTACAAGTAC AAGAAGCTGT TCCGTCCGTT TTAAGAAATG TTCTCTGTGG TGATGGCTTA
 TATCTGTATG GTTCCTTGAT TCAACATGGT TATTTTCCGT ACAAAGGCGAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGTTTCCGA CTGGGAGATG
 AATGACCCCTA ACATTAGTAA TTTATTTAAT GTTGTGATA AAGTTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGTTTCT GGTAGAATA TTCCAGAGC GCCAGAAACG
 AATCCTTTTA CTACAGAGTT TGAATCGGTT AAAGAAACAA TAGCTAATTT AACCTTAATT
 GCAAAAATTTG CACCAGAAAA TTTAAGAAAT GACATTTATA CATCATCCCA AACGTGGCTT
 CAACAAAGTG GGTGACTACTA TCATTTCTTT AAAAAGCCCA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCTGCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACGAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGC AGTCCCGAGT CATGCTTAGG TGGCTCAAAT
 AATGGACAGG TTGCCTCTAT AGGAATGTTT TTASATAAAA CTAATGAAGG AATGAACCTTA
 GTTGCTAAAA AATCTTGGTT CTTATTAGAT GGTCAATCA TTAATTTGGG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCTCTGATA AAGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATCTT GATTAGTTT AAGCGCAGCG
 ANTCATTGA ATAACATTGG CTATGTTTTT CCTAATTGNA TCAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTGG CTACGGAGAT ATTAACGAAT AATTGTTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGSCA AACTGTGTA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGGAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCAATGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTCGAG GACTGTATGC GTATGATCCA
 ATGTCCGTTA TTTTCAGAAAA AATTGATAAC GGTSTTTATC GCTTAATCTT TGCGAATCCT
 TTACAAAATA ATGCATCCGT TTCTATTGAA TTGATAAGG CATTCTTGA AGTAGTCGCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATAGTCC GGGGTTAAAT
 GGCAGCTCGC GTTCAATCAT TGTTAAAACA ACTCCTGAAT TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACGCAAG CAGGTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAACCAAG AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TBAAGCAATT GGTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCACCTTG TTGAAATCA TCAAGAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGGAAAAATA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG ACACTTAAAT ACTAGTACAG GAGTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCAATT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGCTC TTCTATTTAT CGCCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF087-2 (SEQ ID NO:330)

LVGLANWFRA ALTDTLILLH DDLNLTDAEK LNKFTAPLML YAKFINIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEAIVPSVL KSVESGDSLY PQGSLIQHGY FPYNGSYGNE
 LLKGFGRIGT ILQGSWEMN DPNISNLFNV VDKSYLQLMV NGFMPSHVBO RSISRAPETN
 PFTTEFESGK ETIANLTLIA KFAPENLRND IYTSIQTNLQ QSGSYHFEK KPRDFEALID
 LKNVNVNSASP AQATPMQSLN VYGSMDRVLO KNNEYAVGIS MYSQRVGNYS FGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDTEEL ANGAYTGKRS PQSWVGGSSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGSGIT GTTDASIEETI LENRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDEVQI EERSGRYGLI NEYFVNDKTY
 TNTFAKISKV YGKTVENGTY EYLTVVGKTN EEIAALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVSIEF DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIIVKTT PEVTKEALEK LIQEPNEQE KEYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVHVP TRENDFTMLL KIIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL ESNVFELEK NSGENKKEQK
 NGGNNHGLNT STGVDQGTGK QVKPSSQGGF RKASQFLPST GEKFSIALVI IGLLVIASGC
 LLVFRKSKSK K

EF087-3 (SEQ ID NO:331)

A ATCGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GGATTAGTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTGNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACCTTCTTAA TGATAAAACC
 TATACAAATA CATTGCTAA AATTAGTAAA AATTATGGCA AGACTCTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCATTGAGGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCAG GACTGTATGC GTATGATCCA
 ATGTCGGTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAATCTT TGCGAATCCT
 TTACAAAATA ATGCATCC

EF087-4 (SEQ ID NO:332)

NRMHHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDEVQI EERSGRYBDI NEYFVNDKTY
 TNTFAKISKV YGKTVENGTY EYLTVVGKTN EEIAALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNAS

EF088-1 (SEQ ID NO:333)

TABLE 1. Nucleotide and Amino Acid Sequences of *A. taeniorhynchus* Genes.

TAACTGGTGG GATTGGCAAA TTGGTTCCGC GCAGAGCTAA CAGATACATG GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AATTTAATAA AATTTACAGC TCGGTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG CCAATTTAAT GTGCAACAGG AGTTAACTTA
 ACAGATATTT CAATCACCGT TTTAGGTACT GGACPTTCTT TAGAATATAA TTAACGCCTA
 GTACAAGTAC AAGAAGCTGT TCCGTCGGTT TTAAGAACTG TTTTCTCTAT TSATSGCTTA
 TATCCTGATG GTTCCCTGAT TCAACATGGT TATTTTCTCT AATACCTGAT TTAACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTGAG ACTATTTTAC AAGSTTCTGA CTGCGAGATG
 AATGACCCTA ACATTAGTAA TTTATTTAAT GTTCTGATAA AAGSTTACCT ACAAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTABAATAA TTTCCACAGC GCGAGAAACG
 AATCCTTTTA CTACAGACTT TGAATCGCGT AAAGAAACAA TAGCTAATTT AATCTTAATT
 GCAAAATTTG CACCAGAAAA TTTAAGAAAT CACATTTATA CATCTATGCA AATCTGGCTT
 CAACAAAGTG GGTCACTATA TCATTTCTTT AAAAAACCAA GAGACTTTGA AGCTTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA TCTGCTCAAG CGACATCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCTTA CAGAAAAATA ACGAATATGC GGTGGGATC
 ACTATGTATT CACAACGTGT CGGAAACTAT CATTTTGGTA ATACGAAAAA TAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAGGAA CGACATTTGA CACAAGAGAA
 TTGGCAAAATG GTGCTTATAC AGGGAAACGC ACTCCCACT CATGGGAGG TGGCTCAAAAT
 AATGGACAGG TTGCCTCTAT AGGAAATGTT TTAGATAAAA GTAACTAAGG AATGAACCTA
 GTTGCTAAAA AATCTTGCTT CTTATTAGAT GGTCAAAATA TTAATTTGAG AATGGCATT
 ACTSGTACGA CAGATGCTTC GATTGAAACA ATCCTCGATA ACGGATCAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GCAATATTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTGNA TCAATACGCT TSATGTTCAA
 ATAGAAGAAC GCTCTGGTGC CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AACTTTTGA AATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAA CCAATTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCA CACTGTATGC GTATGATCCA
 ATGTCGCTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAACTCT TCGGAATCCT
 TTACAAAAATA ATGCATCCGT TTCTATTGAA TTTBATAAGG GCATTCTTGA ACTAGTCGCA
 GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATATGTC GCGGTAAAT
 GGCAGCTCGC GTTCAATCAT TGTTAAAAACA ACTCTGAGAG TAAGGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT AATCCCAAG CAGCTGAAAA
 GTCTACAGCG AAGCATGAA ACAAGCACAA ACTGTGBCAG ATCAAAACAC ACCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGBCAG TGAAGCAATT GCTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAGAAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAAACTGTGG CAGATCAAAC AACAGCAACG CAAGTAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAAATATG CGGAAATATA AAAGGAGCAA
 AAAAAATGGG GGAATAATGG ACACCTAAAT ACTATATAG GATTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCCATTT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGIG ATTATTGCTC TTTATCTTAT CCGCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF088-2 (SEQ ID NO:334)

LVGLANWFRA ALTDTLILLH DDLNNTDAEK LNHFTAPLML YAKDPKQWP IYRATGANLT
 DISITVLGTG LLLLEDNQRLV QVQEAVPSVL KSVSSGGGLY PEGSLICHOY FPYNGSYGNE
 LLKGFGRIFT ILQGSWEMN DPNISNLFNV VDKGYLQLMV NGKMPHNSG RSISRAPETN
 PFTTEFESGK ETIANLTLIA KFAPENLND IYTSIQTLQ CSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ KNNEYAVGIS MYSQRVCHYE FBNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTIVDTREL ANGAVTCHRS PQSWVGGSNN
 GQVASIGMFL DKSNEGMLV AKKSWFLLDG CIIMLGSGIT GTTDASLETI LDNRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMTLEWQI EERSGANGDI NEYFVNDKTY

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TNTFAKISK N YGKTVENGTY EYLTVVGKTN EEIAALSHNK GYTALENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SWISEKIDNG VYRLTLANPL QNNASVWIEP DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTKEALEK LIQEQRHHEQ FDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVHVP TREVDKTNLL HIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAYKELTLK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKKIALVI IGLLVIASGC
 LLVFRKSKSK K

EF088-3 (SEQ ID NO:335)

A ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAACCAAC AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTGGGAG TBAAGCAATT GGTAAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAGAAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA CTBAAGCAAT GAAGCAAGCG
 CAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGAATAATAA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG AACTTTAAAT ACTAATACAG GATTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCABAAAAG CTAGCCATT TTTACCGAGC
 ACAGGAGAAA AGAAA

EF088-4 (SEQ ID NO:336)

T PEVTKEALEK LIQEQRHHEQ KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVHVP TREVDKTNLL HIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAYKELTLK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKK

EF089-1 (SEQ ID NO:337)

TGACAGATAC ACCTGCTAAC ACAGGAAACT AAGAACGACA GCATACACGC AAGATCGGGA
 TATAGGTCAA AAATTTTTTG GCTTATCTTT CGGTCTTTTG GTCTTTATAA TACAACAAAG
 AATGACAGAC ATAGGAGAAT GAATATGAAC AGATGGAAG TATATGCAAC GGTAATCGCT
 TGTATGTTAT TTGGCTGGAT TGGCGTGGAG GCGCAGGCTT CTBAATTTAA TTTTGCGGTC
 ACACCAACAA TTCCCGAAAA TCAAGTGGAT AAATGAAAAA CCTACTTTTA CTAAAAATG
 GCGCCTGGTG CCAAACAAAC CGTAGAAATT CAGTTACGCA ATGATACABA TGAAGACATT
 ACCATTGAAA ATACGGTGAA CTCAGCGACA ACAAATTTAA ATGCGGTAGT AGAATATGGC
 CAAAACGGGA TCAACCTGA CAAAACCTTA CGTTTAACT TAAAAGATTA TGTGGAAGCA
 CCGAAAGAAA TCATCTTGCC GAAGCATTCC CAAAAGACCT TACCTTTAAC CATTACGATG
 CCTAAAGATT CTTTTGATGG CGTGATGGCT GCGGTATAA CACTCAABA GAAAAAGAAA
 GAAACAACGA CTTCTGCGGA TCAATCAAAA GGGTTAGCTA TTAATAATTA ATACTCCTAT
 GTTGTGGCTA TTATTCTTCA GCAAAATGAG ACAAAGGTTT AACCAATTTT AAAATTACTG
 GGGGTTAAAC CAGGCCAAGT CAACGCGCGA AACGTCATCA ATGTTTCTTT ACAAACCCA
 CAAGCGGCCT ATTTAAACCA ATTACATTTA ATCAACACTT TTCAAAAGG AGCGGAAACG
 CTTTACCAAT CCGATACTGA GGATATGCAA GTGGCGGCAA ACTCTAATTT TAGTTACCCA
 ATTTCTTTTAA AAGGGGAACG ATTAACGCCA GGAAATATG TCTTGAAATC AACGGCCTAT
 GGTGTAAAAG ATGAAAAGGG CACCTATCAA GTCAAAGGCG CCAATGCTTA AGAACGGTAC
 CTGTACAAAT GGGAAATTAC AAAAGAATTT ACTATTTCTT GGGACGTCGC TAAAGAATTA
 AATGAAAAAG ACGTAACCAT TAAAGGAACC AATTGGTGGT TGTATCTACT GATTGCATTA
 ATCATTCTAG CGCTGCTCTT ATTGATTTTC TTCTTGTTAT GTAAAAAGAA AAAAGAGGAA
 GAACAACAAT CTGAGCAATA A

EF089-2 (SEQ ID NO:338)

TABLE 1. Nucleotide and Amino Acid Sequences of *A. baumannii* genes.

MEF WKVYATVIAC

MLPGWIGVEA HASEFNFAVT PTIPENQVDF SKTYFDLHMA PGAKQTVEIQ LRNDTDEDIT
IENTVNSATT NLNGVVEYQG NGIKPKDKTLR FNLKDYVEAP KDLILFNSQ KTLPLTITMP
KDSFDGVMAG GITLKEKKKE TTTSADQSKS LAINEHYSUV VAILLIMET KVQPDLLKLG
VKPGQVNARN VINVSLQNPQ AAYLNQLHLI NTVSKGSETL YKSDTEHMQV APNSNFSYPI
SLKGERLTPG KYVLKSTAYG VKDEKGTQV HANGHEBTL YWDEPTWEPT ISSGVAKELN
EKDVTIKGTN WWLYLLIALI ILALLLLIFF LYRKKKKREE QCSQ

EF089-3 (SEQ ID NO:339)

T CTGAATTTAA TTTTGCGGTC

ACACCAACAA TTCCCGAAAA TCAAGTGGAT AAATCAAAAA CTTACTTTGA CTTAAAAATG
GCGCCTGGTG CCAAACAAAC COTAGAAATT CAGTTACGCA ATGATACAGA TGAAGACATT
ACCATTGAAA ATACGGTGAA CTCAGCGACA ACAAATTTAA ATGCGCTACT AGAATATGGC
CAAAACGGGA TCAAACCTGA CAAAACCTTA CTTTTTAAAT TAAAAATTA TGTGGAAGCA
CCGAAAGAAA TCATCTTGCC GAAGCATTCC CAAAAGACTT TACCTTTAAC CATTACGATG
CCTAAAGATT CTTTATATG CGTGATGGGT GCGGTATTA CACTCAAAA GAAAAAGAAA
GAAACAACGA CTTCTGCGCA TCAATCAAAA GSBTTAGCTA TTATTAATBA ATACTCCTAT
GTTGTGGCTA TTATTCTTCA GCAAAATGAG ACAAAGGTTT ACCAATATTP AAAATTACTG
GGGTTTAAAC CAGGCCAAGT CAACGCGGCA AACGTGATCA ATGTTTCTTT ACAAACCCA
CAAGCGGCTT ATTTAAACCA ATTACATTTA ATCAACACTS TTTCAGAGS AGGCGAAACG
CTTTACCAAT CCGATACTGA GGATATGCAA GTGGGSCCAA ACTTAACTT TAGTTACCCA
ATTTCTTTAA AAGGGGAACG AT

EF089-4 (SEQ ID NO:340)

SEFNFAVT PTIPENQVDF SKTYFDLKMA PGAKQTVEIQ LRNDTDEDIT

IENTVNSATT NLNGVVEYQG NGIKPKDKTLR FNLKDYVEAP KDLILFNSQ KTLPLTITMP
KDSFDGVMAG GITLKEKKKE TTTSADQSKS LAINEHYSUV VAILLIMET KVQPDLLKLG
VKPGQVNARN VINVSLQNPQ AAYLNQLHLI NTVSKGSETL YKSDTEHMQV APNSNFSYPI
SLKGER

EF090-1 (SEQ ID NO:341)

TAGTCTCTAA GAAATAAACC TAAAATTAT GTATATAAAG ATGAAACAAAT GAAAAAGAA
GAAATGCAAA TCGCTAATAC ACGTCGTCAA AAATCAGGAA AAAATANTAA AAAGAAAAGTA
ATTATTACTT CTTTGGTTGG ACTAGCTCTG GTTGCTGGCG CCACTATGTG TTATTTTCAA
AGTCACTTTT TNCCAACCAC AAAAGTAAAT GGAGTTTCTG TAGGCTGTTT AAATGTAAAT
GCTGCAGAAG AAAAATTAGC GCAAGTTAAT CAAACCGAAG AAGTTGTGCT TCAAACGGGG
ACAAAAGAAG AAAAATTCA ACTTCCTAAA AAATACCAAT TGBATCAAAA ATTTTIAAAA
GACCATTAC ACAGTAGCAA GGTGAAGCTA CCGTTAAAG AGGCATTCAA AAAAGAACTA
GAAGCCAAAT TAGCAACTTT GAGTTTTCOA GAGGCGAAG CAGCAAAAA TGCGAGTATC
CGTCGAGGCA ATGGCACTTT TGAAATTCTT CCCGAGAAGC AAGGCATAGT AGTGGACACA
CAGCGCTTAA ACCAGCAGAT TATTGCGGAT GTTGAAGCGG CAAAAGGCAA CTATCAATAT
AATGCCAAAG ATTTTTATAA AGCCCTGAA ATTACAAAG AGGATCAAC GTTAAAGGCA
ACATTGACAA CGCTCAATAA CAAGTTAAAT AAAACAATTA CAGTTATAT TAATGGTGAA
AAAGTAGCCT TTGATAAAAC ACAAATTCAA AACGTGCTGA ATGATGATGG CACAATCAAC
AAAGAAAAAC TAACTACTTG GGTGACACAA TTAGAAACAA CATATGCTTC TGCTAATCAA
CCAGTTTAT TTACAGATGT TCACGGCAGC ACACGTCTTT TTAACAAAC CGGAAGTTAT
GGCTGGTGA TTGATGGGGC CAAAACGCAA GAACCTACTAG TAAACGCGCT AATAGCCAA
GAACAAACGA ATGCAATCAC TGCTCCGTTG GTTGCTGATA CCAACAAAA TAGTAAATTT
GCCAATAATT ACATTGAAAT TGATTTAAAA GATCAAAAA TGTATTTTTT CATTGATGGC
AAAAAATAG TCACCACAGA TGTCATTACT GGCAGATATA ACAAACCAAC CGCAACAGTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGGATTCC ATACAATTTT ATATCGGACA ACGATGTTA ATTAAAGC TCAAATGCTT
 GATGTTCTC GATACAGTGT GCCAGTAAAA TATTGGATTC CTTATTAAAG TCAAGGGGGC
 GTTGTCACAC AAATCGGGAT TCATGACTCC GACCATAAAT TCATTAAGTA TGGCGATAAA
 GAAGCCTTTA AAACCGATGC TGGTAGTAAT GCTGTATCA ACAGGATAGG AACAGAAGTT
 TCAAAAATCT TTGATGTATC CTATGACGGA ATGCTGCTAA TTATTATGG ACATATCTAT
 GATGATGCAC CAGGTGAATT TGATAAACCT GTAGATTAGC GCGAAGAAG ATAA

EF090-2 (SEQ ID NO:342)

MRNTRRQK SGKNNKKKVI ITSIVGLALV AGGSYVYFQS
 HFXPTTKVNG VSVGWLVNVA AEEKLAQVNG TEEVVVQTGT FHEKIQLEKE YQLDQKFLKD
 HLHSSKVKLP LNEAFKKELE AKLATLSFPE GKPSHNASIR FNGGTFEIVP EEQGTIVVDQ
 RLNQIIADV EAGKGNVQYN AKDFYKAPEI TKEIQTLKAT LTTLNKLNK TITVDINGEK
 VAFDKTQIQN VLNDDGTINK EKLTTWVTQL ETTYGSANQP VLFTDVHGT FRFKNNGSYG
 WSIDGAKTQE LLVNALNSQE QTNAITAPLV GDTKENSRIA NNYIELDLKD QKMYCFIDGK
 KIVTTDVITG RYNKGTATVP GFHTILYRTT DVNLEGGQLD GSKYSVPVKY WMPLLSQGGV
 VTQIGIHDSH HKLDKYGDKE AFKTDAGSNG CINTPSTENS KIFDVSILGM PVIIYGHYID
 DAPGEFDKPV DYGEV

EF090-3 (SEQ ID NO:343)

CAC AAAAGTAAAT GGAGTTTCTG TAGGCTGGTT AAATGTAAAT
 GCTGCAGAAG AAAAATTAGC GCAAGTTAAT CAAACGGAAG AAGTTGTGGT TCAAACGGGG
 ACAAAGAAG AAAAAATTCA ACTTCCTAAA AAATACCAAT TGGATCAAAA ATTTTAAAAA
 GACCATTAC ACAGTAGCAA GGTGAAGCTA CCGTTAAAGC AAGCATTCAA AAAAGAACTA
 GAAGCCAAAT TAGCAACTTT GAGTTTCCA GAGGGAAGC CAGGCAGAAA TGGGAGTATC
 CGTCGAGGCA ATGGCACTTT TGAAATTGTT CCGAAGAAC AAGGCATGAT AGTGGACACA
 CAGCGCTTAA ACCAGCAGAT TATTGCGGAT GTTCAGTGG GAAAGAGCAA CTATCAATAT
 AATGCCAAAG ATTTTATATA AGCCCTGAA ATTACAAAAG AGATCAAAAC GTTAAAGGCA
 ACATTGACAA CGCTCAATAA CAAGTTAAAT AAAACAATTA CATTGATAT TAATGGTGAA
 AAAGTAGCCT TTGATAAAC ACAAATTCAA AACCTGCTGA ATGATGATGG CACAATCAAC
 AAAGAAAAAC TAACACTTG GGTGACACAA TTAGAAACAA CATATGCTTC TGCTAATCAA
 CCAGTTTTAT TTACAGATGT TCACGGCAGC ACAGTCTTT TTAAAGACAA CGGAAGTTAT
 GGCTGGTCGA TTGATGGGGC CAAAACGCAA GAAGTCTAG TAAAGGCTT GAATAGCCAA
 GAACAAACGA ATGCAATCAC TGCTCCGTTG GTTGTGATA CCAAGGAAA TAGTAAATTT
 GCCAATAATT ACATTGAAAT TGATTTAAAA GATCAAAAA TGTATTSTTT CATTGATGGC
 AAAAAAATAG TCACCACAGA TGTCATTACT GGCAGATATA ACAAAGGAAC CGCAACAGTA
 CCAGGATTCC ATACAATTTT ATATCGGACA ACCGATSTGA ATTAGAAAG TCAAATGCTT
 GATGGTTCTC GATACAGTGT GCCAGTAAAA TATTGATGC CTTATTAAAG TCAAGGGGGC
 GTTGTCACAC AAATCGGGAT TCATGACTCC GACCATAAAT TCGATAASTA TGGCGATAAA
 GAAGCCTTTA AAACCGATGC TGGTAGTAAT GCTGTATCA ATACGGCAGG AACAGAAGTT
 TCAAAAATCT TTGATGTATC CTATGACGGA ATGCTGCTAA TTATTATGG ACATATCTAT
 GATGATGCAC CAGGTGAATT TGATAAACCT GTAGATTAGC GCGAAGAAG AT

EF090-4 (SEQ ID NO:344)

TKVNG VSVGWLVNVA AEEKLAQVNG TEEVVVQTGT FHEKIQLEKE YQLDQKFLKD
 HLHSSKVKLP LNEAFKKELE AKLATLSFPE GKPSHNASIR FNGGTFEIVP EEQGTIVVDQ
 RLNQIIADV EAGKGNVQYN AKDFYKAPEI TKEIQTLKAT LTTLNKLNK TITVDINGEK
 VAFDKTQIQN VLNDDGTINK EKLTTWVTQL ETTYGSANQP VLFTDVHGT FRFKNNGSYG
 WSIDGAKTQE LLVNALNSQE QTNAITAPLV GDTKENSRIA NNYIELDLKD QKMYCFIDGK
 KIVTTDVITG RYNKGTATVP GFHTILYRTT DVNLEGGQLD GSKYSVPVKY WMPLLSQGGV
 VTQIGIHDSH HKLDKYGDKE AFKTDAGSNG CINTPSTENS KIFDVSILGM PVIIYGHYID

TABLE 1. Nucleotide and Amino Acid Sequences of *E. gossypii* Genes.

DAPSEFDKPV DYGEEV

EF091-1 (SEQ ID NO:345)

TAATIGGNGG AGATTTTAT GGCTAAAAAA GGTGATTTAT TTTTAAAGG AGTAATTGGT
 GGAACAGCAG CAGCCGTGCG CGCATTATTA GTTGTATTA AATTAGTTAA AGAATTACGT
 GATGATTTAT CAAATCAAAC AGATGATTTA AAAACAAAC CGCAGATTA CACAGATTAT
 GCTGTTCAAA AAGGAACAGA ATTAACAGAA ATCGGAAAC AAAAGGCGG CGTTTATCA
 GATCAAGCCT CTGATTGCGC AGGTTCTGTC AAAGAAAAA CAAAGATTC ATTGGATAAA
 GCACAAGGTG TTTCTGGCGA CATGCTTGTAT AATTGTAAA AAGAAAGAG TGAATTATCT
 GATCAATTTA AAAAAGCAGC TGACGATGCT CAAGATTAAG CAGAGATTT AGGTGAAATT
 GCCGAAGATG CAGCAGAAGA TATCTATATT GAGGTTAAG ATTCTGCGC AGCGGCCAAA
 GAAACTGTTT CTGCTGGTGT CGATGAAGCA AAGAAATTA CCAAGATGT TCCTGAAAAA
 GCTGCAGAAG CAAAAGAAGA TGTAAAGAT GCAGGAAAG AGTTAAAAA AGAATTAAAA
 GGGTAA

EF091-2 (SEQ ID NO:346)

MAKKG GFPLGAVIGG TAAVAALLL APKSGHELRI ELNQTDDLK NKAQDYTDYA
 VQKGTETLTI AKQKAGVLSD QASDLAGSVK ETKKSLDKA QGVSGMLDN FKKQTGLSD
 QFKKAADDAQ DHAEDLGEIA EDAAEDIYID VKDSAAAAKE TVSAGVDEAX ETTKDVPEKA
 AEAKEDVKDA AKDVKKEFKG

EF091-3 (SEQ ID NO:347)

AT CAAATCAAAC AGATGATTTA AAAACAAAC CGCAGATTA CACAGATTAT
 GCTGTTCAAA AAGGAACAGA ATTAACAGAA ATCGGAAAC AAAAGGCGG CGTTTATCA
 GATCAAGCCT CTGATTGCGC AGGTTCTGTC AAAGAAAAA CAAAGATTC ATTGGATAAA
 GCACAAGGTG TTTCTGGCGA CATGCTTGTAT AATTGTAAA AAGAAAGAG TGAATTATCT
 GATCAATTTA AAAAAGCAGC TGACGATGCT CAAGATTAAG CAGAGATTT AGGTGAAATT
 GCCGAAGATG CAGCAGAAGA TATCTATATT GAGGTTAAG ATTCTGCGC AGCGGCCAAA
 GAAACTGTTT CTGCTGGTGT CGATGAAGCA AAGAAATTA CCAAGATGT TCCTGAAAAA
 GCTGCAGAAG CAAAAGAAGA TGTAAAGAT GCAGGAAAG AGTTAAAAA AGAATTAAAA
 GGGTAA

EF091-4 (SEQ ID NO:348)

SNQTDDLK NKAQDYTDYA
 VQKGTETLTI AKQKAGVLSD QASDLAGSVK ETKKSLDKA QGVSGMLDN FKKQTGLSD
 QFKKAADDAQ DHAEDLGEIA EDAAEDIYID VKDSAAAAKE TVSAGVDEAX ETTKDVPEKA
 AEAKEDVKDA AKDVKKEFKG

EF092-1 (SEQ ID NO:349)

TAAGGGGATG AAGAAAAAAT GGCAAAAAA ACAATTATTT TATTTTCTTC CGCAGGAATG
 AGCACGAGTT TATTAGTAAC AAAAATGCAA AAGGAGGAG AAGATGTTGG CATGGAAGCA
 GACATCTTTG CAGTATCGGC TTCTGAAGCA GATACAACTT TGGAAATTA AGAGGTGAAT
 GTTTTACTTT TAGGTCCACA AGTTCGTTTC ATGAAAGGCG AATTGTAACA AAAATTACAA
 CCAAAAGGGA TTCCTTTAGA TGTAAATTAAC ATGGCAGATT ATGGCATGAT GAATGGCGAA
 AAAGTTTATG ATCAAGCAAT CTCATTAATG GGATAA

EF092-2 (SEQ ID NO:350)

MAKKT IMLVCSAGMS TSLLVTKMQK AAEGRGMEAD IFAVSASEAT TNLENKEVNV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LLLGPQVRFM KGQFEQKLQP KGIPLDVINM ADYGMENGEK VLDQATSLMG

EF092-3 (SEQ ID NO:351)

AG AAGATCGTGG CATGGAAGCA
GACATCTTTG CAGTATCGGC TTCTGAAGCA GATACAAACT TGGAAAATAA AGAGGTGAAT
GTTTTACTTT TAGGTCCACA AGTTCTTTTC ATBAAAGGUC AATTGGAACA AAAATTACAA
CCAAAAGGGA TTCCTTTAGA TGTAAATTAAC ATBGEAGATT ATGGCATBAT GAATGGCGAA
AAAGTTTATG ATCAAGCAAT CTCATTAATG GGA

EF092-4 (SEQ ID NO:352)

EDRGMEAD IFAVSASEAD TNLENKEVNV
LLLGPQVRFM KGQFEQKLQP KGIPLDVINM ADYGMENGEK VLDQATSLMG

EF093-1 (SEQ ID NO:353)

TAGTTTTTTT CCGATAAAGG GAGAATTTTA ATGAGGCAAA AATATTCAGG AAACCTTATTG
TTCACGGCCA TGGCCATTGT TTATTTGATG AGTTTCTG CCCTTCAGTT ACTAGAAGAA
CGTCAGTTAA CACAAAAATT TACGCAAGCT ACCCAGCAAT ACTATGCAAG GAAAAGTATC
TTTCATTTAT TTCTTGCAGA TGTAAACAA AATAGACGAA AGTTAAAAAC AGAAGAAAGG
CTCGTATACG CGCAAGTGAC CCTCGATTAT ACATGCAAAA ATGACCAATT AAGAATAACT
GTTTTATTAA ACAAATCTGG TCGAAAATAC CAATATCAAG AGAGACTTTC TCATCAAAAA
AAAGCGGAAA CAATACTGGA ATAG

EF093-2 (SEQ ID NO:354)

M RQKYSNLLF TAMAIVYLS FLALQLLEER QLTQKFTQAT QEYYAGKSIF
HLFLADVQKN RRKLKTEERL VYAQVTLDT YHNEQLRIW LLNKSGRKYQ YQERVSHQKK
AETILE

EF093-3 (SEQ ID NO:355)

CCTTCAGTT ACTAGAAGAA
CGTCAGTTAA CACAAAAATT TACGCAAGCT ACCCAGCAAT ACTATGCAAG GAAAAGTATC
TTTCATTTAT TTCTTGCAGA TGTAAACAA AATAGACGAA AGTTAAAAAC AGAAGAAAGG
CTCGTATACG CGCAAGTGAC CCTCGATTAT ACATGCAAAA ATGACCAATT AAGAATAACT
GTTTTATTAA ACAAATCTGG TCGAAAATAC CAATATCAAG AGAGACTTTC TCATCAAAAA
AAAGCGGAAA CAATACTGG

EF093-4 (SEQ ID NO:356)

LQLLEER QLTQKFTQAT QEYYAGKSIF
HLFLADVQKN RRKLKTEERL VYAQVTLDT YHNEQLRIW LLNKSGRKYQ YQERVSHQKK
AETI

EF094-1 (SEQ ID NO:357)

TAAACATTTG AGACATTCAG AGGTGAATGT CTCTTTTTTA TTAATCAAAA ACGAAAGGGG
ATTAATTATA TGAAAAAAC AACATTTAAA AATTGTCGT TATTTGCGAC TTTGGCTCTA
TTAAGTCAAA CAATGGCGG AACGATTGCT CCTAAGTTG CTTTTCCGA TGAAATTACT
CACCTCAAG AGGTAACAAT TCATTATGAC GTAAGTAAAC TGTATGAGT TGACGGAAC
TTTAGCGATG GCAGCAGCT CTCAGAACGT ACTAGTCTAT TATATGAGA ATACAATGCT
GCAAAACAAA CAGTATTTTG TATTGAACCA GGTCTAGTA TTCCAAACGA AGTGACGCAC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. coli* Genes.

```

GGTTATCAGA AAAACCCCTTT GCCATCAATG TCTTAAATAG CAAATTAAT ATCCGTTCTT
TGGGAAAAAG CTGCAACAGA TATTGATAGG AATATCTTGG CAGCAAAAGT GATTTGGGAA
GAAGTGAACG GTTATAAACT CCATGCCATA AAAAGATTAG CTGCTTCTTC AGTTGATATA
AAATCTATTG AAGGAAAAAT TAATAGGGCA ATTGAGGAGT ATCAATTTAA ACCAAGTTTT
CATAATACCA CTGTAAAAAC AATTTTAAST CAATTAATAA GTTAAATAGA TAAAAATGAA
TTAAATTTAT TTGAGTTTGA TAAAGTCTTC CAAATATGCG CCAATATAGA TTACCGTGTA
ATTGGGAATC AATGAGTGCT TACTTCAAAAC TCTAATTTGA AATCAAGAAC ATTAACATTG
AAAAAATCAG CTGCTACTTC AACTTCACTC CCTTATAGAA AAGCAAGACT TCAAACTGTG
ATGGCTGGTG CGCTTGATAA GCGCAATGCG TACGCTATTA AAATTAATGT GCAAACTAAG
GTTTCTTTAA AGATCAAAAA AATCGATGAA CAATCAAGTG ATATTCTACC AGAAACGGTT
TTCCATTTAG ATTTTGGGAA AGCTTACCTT TCAAAAGATG TGATTAAGA TAAAGATGGG
ATTTCTATTT TCGATGGAAT TCCCAGTGGT ACAAATTA CTATTACTGA AAAATCGGTG
CCAGATCCTT ATATGATTGA TACCAATGCG ATGCTCTGCA CCAATTAAGC GCGCGAGACC
ATTTCCATGA CTTCGAAAAA TATCGGAA AAAGGCTGAA TCTCTTGA GAAGACTGGG
GTABAAACAG GTACTGATCT TTGCAAGGAG AATTAATCTC TACTTGAAG TACATTTGCC
ATTCGTAAAG ACAGCCCACT TGCTCAATTT CTTCAAGAAA TACCTTGGCA TAAAAAGGT
CGTCTGGAAA CACCAAAAGA GCTTCTAAT GCTTCAAGC TGGCAAGCTA TTACGTGACA
GAAACAATCT CTAGTAATGG TTTCTGGAAT AGCTTGAAG CAGCAAGAT CAGGTTAAAA
TATGCAACT AAACCGTGGG TCTTCTTACC AGTAACTAA AAGGCTAAAA CAAAGAAATT
ACTGCGGAAA CCACTTTGAC AAAAAGAGAC AAAGATACCG GTAACTAGAG TAAAGGGAAA
GCTGAGTTTA AAGGAGCTGA ATATACCTTC TTTACTGCAA AAGATGCTCA AACTGTTAAA
TGGAGTGAAG CTTTTAAAC AGAATTATG AAAGGAGGCA AAGCTTCTGA TGAACAGTG
ACTTTGGCTT TAGATGAAAA GAACCAATTT GCGCTTGAAC AGCTACCAAT TAACGACTAT
TTCTGGCAAG AAACCAAAAG ACCTGAAGGA TATCTTTGG ATGAAGGAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACCAAAAA AATCTCTAA TTAATGAGA TTTACGGCA
AAAGAACAAG TTATTGCTT TGGCTTTGAT TTTCTTAAAT TTTCTGATC GCTGATGGC
ACTGCCAAG CTGGATTAA CCACTTATCT TTTAAAGTCT GCGCTTGGCA AAGGACCAAN
GAAATCACAG GTGCTGAAGA TAAAGTGACC ACAGCTTAA ACAGCAATT AGGTTTTCAT
GGCTATGGTA AGTTTGAAAA TCTTCTTAT GCGGATTAAT TATTGAGA AATAGAGGCT
CCAGAAGGAT TTCAAAAGAT TACACCAATA GAAATCTTCT CTACATTTAA GCAAAACAAA
GACGACTATG CGAAGAGTGA GTATGTCTTT ACCATTAAGS AAGAGGACA AAAACAACCA
ATTAAGATGG TGACCGTTCC TTACGAGAAA CTAACTAACA ACAGCTTTTC TGTAGTCTG
AACCGTTTGA TGCTTTATGA TTTGCTGAG AAAGAGATA GTTTGATTT TTTTGGGACT
TGGAAAGACG GAAATAAAAA ATTGAATACC CTTBATTTCA CCGAGGTAGT TGATAAATTG
AGATATAACT TGCATGAAAT CAAAGAAGAC TGCTATGCTG TAGCTCAAGC CATTGATGTG
GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAAAAGCTA AAGGCTGCT GATTGCCGAA
ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGGAATTT GGAATTTCT GCATAAATTA
ACCGCTGAAC AAGTTTTGGA TAAAAAGATC GTCTTCTTCA ATTATCTTA TGAACAACAG
GTAGCTTTTG AAGCAGGCAA TGAGCAATTA GCGAAGGATG CTAGCTTGA CAATCAAGCA
CAAACCGTCA ATTGTACGAT TGAACCCCAT GTTTCATCTC AAGCAAAAGC CCACCTAGAA
GATGGTTTCG AAACCTTTAC TCATGTGAC CTGATGATA TTTTCTATGA TGTGTGCGTT
ACCCATGATG TACTGGATGG CTCAAAAGAA CTTTCTGAAA CAATTTCTGA TGCTTTACTA
CCAGATGGTA CGAACAAAGA AATTTGAAA TCTGGCAAAA TTGAGCTGA AGTGAATGAT
AAAGAATTTA CCAAAACCGT ACTTGGGAAA AAGCTAGATA CCGGAAGTA TCCAGAAGGA
ACTAAGTTTA CTTTTACGGA AATCAATTAC GAAAAAGCTG GAAAGCTGAA TGAAGAACAC
AATGAAGATT TGAAAGAAAA ATCTCAAAAC TTAACAGGAA AAGAACTGCC AACCATACCG
AGTACGCCAA AACAACCGGA AACACAGCT GTTCAAGTA ATTCTAAGA ATCTAGTCCC
ACAGTGAAGA CATTCGCCGA AACTGGGAG AAAAATTCTA ACCTTCTACT GTTAGTTGGC
TTTATCTTGA TTTTTCGAC TGCTGGGTAT TACTTCTAGA ATGCGGCA TTA

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EF094-2 (SEQ ID NO:358)

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MKKTTFKN WSLFATLALL SQTIGGTIGP TIAFADRIH
PQEVTHYDV SKLYEVDGTF SDGSTLSEPT TSLNATYHGA KSTTHNIEPG VSIPTVTHG

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YQKNPLPSMS DKAKLVSVLW EKAGTI IDTN MVAQKMIWEE VNSYFLHSIK FLGGASVDIK
 SIEGKINKAI EEYQKKPSFH NTTVKTLGQ STTLIDNNEL NLSEFNVVQ NTANIDYRVI
 GNQLVLTPTS NSKSGTLTLK KSAGTSTPVA YKAGLITTM AGALENPNTY AIKINVETKG
 SLKIKKIDKE SGDIVPETVF HLDGCHALPS KLVTEDEGI SILENPHST FVTITEKSV
 DPYIMDTTPM AATIKAGETI SMTSPHMQH GQILBERTOV ETGTELVNDN YSLAGNTFAI
 RKDSPAGEIV QEITTTDEKGR AETPHFLANA LELGTYVTE TKSSNGFVNT PKPTKVELKY
 ANQTVLVTNS NVKQGNQEIT GETTITKEDF DTGIESQCHA EFKAETTLF TAKDQAVKW
 SEAFKTELVK GTKASDETVT LALDEFHQVA VHRLAINEYF WQETRAPEGY TLDETKYPVS
 IKFVDNNEKN AVITRDVTAK EQVIRFGDF PEFASSAGST AETGFNDLSF KVSPLGTXE
 ITGAEDKATT ACNEQLGFDG YGKFENLPG DYLLBIEAP EGDHITPLE IRSTFKENKD
 DYAKSEYVPT ITEEGQKQPI FMVTVFYEH TTHETSVSLD RLIDNBLPEK EDSLTSLATW
 KDCGNKKLNTL DFTELVDKLR YNLHEIKEDW YVVAQIEVE ATFAAQEKDE KAKPVVIAET
 TATLANKEKT GTWKILHKLK AEQVLDHSEV LINDTYENFV AFEAGNEPVA KDASLNNQAQ
 TVNCTIERHV SIQTKAHLED GSQTFTHGIA MDHEDFVST HDVILSSKEA PETILYALLP
 DGTNKEIWKs GKIEHEVNDK EFTKTVLAKF VDTGKYEEST KFCUTEINYE HDGIVNGKHN
 EDLKEKSQTL TPKEVPTIPS TPKQPETPAM PCHSDPERMT VKCTTCTGSEK NSNVLLLVGF
 ILIFSTAGYY FWNRRN

EF094-3 (SEQ ID NO:359)

CGA TGAAATTACT

CACCCCTCAAG AGGTAACAAT TCATTATBAC BTAAATAAAC TGTATGAGCT TGACGGAACCT
 TTTTACGATG GCAGCACGCT CTCAGAACTT ACTAGSTGAT TATATGAGAG ATACATGGGT
 GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGTTAGTA TTCGACAGAG AGTGACGCAC
 GGTTATCAGA AAAACCCCTTT GCCATCAATG TGTGATAAAG CGAAATTAGT ATCGGTTCTT
 TGGGAAAAGG CTGGAACAGA TATTGATACA AATATGCTTG CAGAAAAGAT GATTTGGGAA
 GAAGTGAACG GTTATAAACT CCATTGCGTA AAAATATTAG GTGATGCTTG AGTTGATATA
 AAATCTATTG AAGGAAAAAT TAATAAGCA AATTGAGGAT ATCAAAAAAA ACCAAGTTTT
 CATAATACCA CTGTAAAAAC AATTTTTAGCT CAATTGACAA CTTLAATAGA TAAAAATGAA
 TTAAATTTAT CTGAGTTTGA TAAAGTCTG CAAAATAGCG CGAATATAGA TTACCGTGTA
 ATTGGGAATC AATTAGTGCT TACTCCAAAC TTTAATTGCA AATGAGGAAC ATTAACATTG
 AAAAAATCAG CTGGTACTGG AACTCCAGTC GTTATATAAA AAGCAGGACT TCAAACGTG
 ATGGCTGGTG CGCTTGATAA GCCCAATAAC TACGCTATTA AAATTAATGT GGAAACTAAG
 GGTCTTTTAA AGATCAAAAA AATCGATAAA GAATGAGGTG ATATGCTACC AGAAACGGTT
 TTCCATTTAG ATTTTGGGAA AGCTTTAGCT TCAAAAGATG TGACACAGAG TAAAGATGGG
 ATTTCTATTT TGGATGGAAT TCCCCATGCT ACAAAGGTAA CTATTACTGA AAAATCGGTG
 CCAGATCCTT ATATGATTGA TACCACACCC ATGCTTCCCA CCATTAAAGT GGGCGAGACC
 ATTTCCATGA CTTGCAAAAA TATGCGACAA AAABSTCAAA TTTTCTTAGA GAAGACTGGG
 GTAGAAACAG GTACTGATCT TTGGAATGAT AATTATCTTC TATTTGAGAA TACATTTGCC
 ATTCGTAAAG ACAGCCCAGC TGGTGAAATT STCCAAGAAA TATCAAGCGA TGA AAAAAGGT
 CGTGCGGAAA CACCAAAAAGA GCTTGCTAAT GTTTTGGAAC TGTGAGCTTA TTACGTGACA
 GAAACTAAAT CTAGTAATGG TTTGCTGAT ATTTTCAAAC CAACTAAAGT CGAGTTAAAA
 TATGCCAATC AAACCGTGCC TCTTGTTATC AATAAGCTAA AATGAGAAAA CCAAGAAATT
 ACTGGGGAAA CCACCTTGAC AAAAGAAGAC AAAGATCTTC CTANTGAGAG TCAAGGGAAA
 GCTGAGTTTA AAGGAGCTGA ATATACTCCT TTTACTGCAA AAGATGCTCA AGCTGTTAAA
 TGGAGTGAAG CTTTAAAAAC AGAATTACTG AAGGGAACCA AAGCTTCTGA TGAAACAG

EF094-4 (SEQ ID NO:360)

DEITH

PQEVTHYDV SKLYEVDGTF SDGSTLSEFT TSLYAEVHRA KQTVFSTEPS VSIPTEVTHG
 YQKNPLPSMS DKAKLVSVLW EKAGTI IDTN MVAQKMIWEE VNSYFLHSIK FLGGASVDIK
 SIEGKINKAI EEYQKKPSFH NTTVKTLGQ STTLIDNNEL NLSEFNVVQ NTANIDYRVI
 GNQLVLTPTS NSKSGTLTLK KSAGTSTPVA YKAGLITTM AGALENPNTY AIKINVETKG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

SLKIKKIDKE SGDIVPETVF HLDGFKALPS KENITDAI I SLLDTHST KUTITEKSVP
 DPFYMIETPM AATIKAGETI SMTSKNMRQH E. faecalis ETSTEDNDN YSLAGNTFAI
 RKDSPAIEIV QEITTEKGR AETPKELANA LKSTTYNTE TRSSNIPNT FYPTKVELKY
 ANQTVALVTS NVKGCNQEIT GETTLKEDF E. faecalis EHFSAITLF TAND3QAVKW
 SEAFKTELVK GTKASDET

EF095-1 (SEQ ID NO:361)

TAAGAATTGT TGGATTGTTT TTTAGAAAGA AGGATGATA TSLAGTGAAG TAAATGGAAA
 GAATTGATAG TAACGGGCAT CTGCCATATA TTAGTATTTC CCGATAAAT ACAGACAATT
 GTTTTGTGAG AAACATTACC AAGTACAAA CAACTAALAG AAGGATGAA TCAATTCATT
 ACAGCAGAAA AAGCCGAAAG TGAACAACCA CAGATTAAG ATAAATACA TGAATGAAGAA
 ACACTGGCAT TGTCAAAAAG TGAGTTAATC CATAATGAG CTAATTTAC AAGTCAAAACG
 ATTAGAGAAA GAATTGAGAC GCTAACCTA ACTTAATTT ATGSAITTTT TAAATGAAGAG
 GGGCAGCCAG TAAACGCCAA TGAGATCCTT CTACATATC ATAGTTGGCA AGCAATTCC
 CCAGATGGCA TAAATGTGTG GBAAGGTGAA ACTTAATGAG TGACATCATC TACAGTGGCT
 AATTTAAAAG AAGTGGTAAT TCCAATGAG AAATATAGG TCTATGCGA CATGTCAACG
 GTGCTTGCG CGAGTAATCA AACATTTTTT CTATCAATAT ATTATCTTC TTTAAGCTTA
 TACAATAAGA AAGGGGAAAT TGATCCCAAT TATCTCTAC CAATATTTT CAGCGCATCA
 GGAAACCAAT ATCCAACAAC AATTTGCAA TTGSAATGAG AAAAATGTC TGCACAACAA
 TATAGTCAGA AAACAGGAGT AACGTTTAA ATTAGGAGA GTCAAAAAC TATCTGTCCT
 TTGTACAACC AAGTGAAGGT TGATTCATCG AATCAATGT GSCATATGAA TTACTTTAAA
 TTTTCAGGCG CGGTTTATTA TCATGTTACC AATCTGAGG TGACAGAAAC TTTTGTGGAT
 ACTCAAGGGA AACCAATCCC TCCACCACCG GGGTTIAGAC AAGGAAAGCA AAGACTTATT
 GAGCGTGACC CTTACACCTT TAAACAGAAA GATCTTTTC CAAATATCTA TGAATTTGAC
 TCAAAAACGT ATCAATTTCA AGGATGGTAT AAGGAGAAA CCAATCTCA AATTTTAGAA
 AAAAGCGTAA CGCCAGTTA TGATATTACC TATCAATAA ATGATATTT AACIGTTGTC
 TATAAGGAGA TACCTCAAAA AAATTATACA TTGAGGAGG TCAATGCTGT TGAATTTGCA
 CCACCATCTG ATTTTATTTA GGATCACCAA CAATCAATA CAAAGATGAG CTTTCGCTAT
 TTAGCTGGAA AAAAACTGCC ACAACAATAC AGCTTAAAG GTAAAACTTA TTTATATCAA
 GGTGGGTATC AAGATAAAAC NAAACAAGAG AGCTTAAAG AAAGGAGCG AACCATAAAC
 TCCCCTGTTT TTAATGAAAT GAACGCTATT AGAGCAATAT ATAAGGAAAT AACTGCAAAA
 GCTGAAATGC AAATAGAAGG ACTAGTCAA GTCTATCTAA GTGCTTATAT ACAAATTTGG
 CAGATTATGC TTACAAATGT GGGAGAAGTA CGCTTAAAAA AATATAACTT AAAGCCAGCA
 AGTGGTTGGT CACCAGGTCT AGCTCGGCCA ATCCAGTCA CGATTGCTGT TGGATCTGAA
 CCAAAACAAA TTGTTCTTAT TACTGATGAA AATGCGGAG TTGGCATTAC TTTAAATACG
 GAAGTGCCTA TTGGTCAGAC AGCAACTATT ATGATGAGAA CAATTGCTAC AGGTGAACCA
 GATCAAGTGT TACAAGCGGC TGTGAAATG AATGSAATTT TTTCTGCTGT TCACGCAGCT
 GATACTGTCA GAATCCAACC TAAAAATCAA SAAATTTGAG CACCAGATGA GGAAGGTTTT
 ATCAGCACAC CAACTTTTGA TTTTGGCAAA GTGGGATTT CTAGCAACAC GCAGCAACAT
 GGTTTAAAGC AGGCAGCAGA TTATTATGAA AATGCTGAG AAATTCATA TTTACGTTTG
 AAAAAATCAC AACCAATTG GGCACAACT TGAGAACTAT CGCTTTTGA AGGAAGAGTG
 GATCAACTAT CATCAATGAC AAAGTTATTG TTAGGAGCAA CCAATGTTTC AGTTTTTATT
 CAGTACAATC AACCAACGGA AACTAAAGTT TCTTTTCTTA AAACAACGCG TATTCAATTA
 GTTGGCAACG GTGTAGCTAG CCATATTGTT TCCATCTCT ACTTTACGA AAGTGAATGT
 TATCAATTTG ATTTTCTTT TGATCAAATC AATTTAGAAA TCCAGCAAAA TCAAGGTAGA
 AAAGATCAAA CTTATCAAGC AATGGTGACT TGAATTTAG TGACAGGCC ATAA

EF095-2 (SEQ ID NO:362)

MKRSKWKE LIVTGICHIL VFPILQTTV PAETIPSTK VREGNHOLT
 AEKAESQPP TKDKLHDEET LALSKSELID NEANTSTTI RERITPNLT YRYGFINEEG
 QPVNANEILL QYHSWQGNP DGINWEGES QPVTASTVAN LHEITPSEK VAVYSDMSTV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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LAASNQTFFL PRYYTSLSLY NKKGEIDPNY PLPTISDASG NQYPTTISQF ELEKMSAQQY
SQKTGVTFNI SESQKLIVPL YNQVKVDSSN QSGLLNFFNF SGPVYVHVTN RFVTEHFVDT
QGKPIPPPPG FRQ GKQTLIE RDPYTFKQKD LLRSHVINDS KTVDFGWYK GFTKPENLEK
SVTPSYDITY DDNDLLTVVY KEIPQKNYTF EDVNGVEIAP PSDFIQDHQQ PTTDGFYRL
AGFKLPQQYS VNGKTYLYQG WYQDKTKQES LEXHFFPHS PVFNEHIAIT AVYKEITAKA
EMQIEGLVKV MP SGYIQIWQ IMLTNVGEVP LKKINLHFLS GWSPGLAPPI QVTIRVGSEP
NKIVPITDEN WRVGITLNT E VPIGQTATIM MTTIACGKPD QVLSQAAVEMN GHFSAVHAAD
TVRIQPKNQ E IVAPDEEGFI STPTFDGKV AISSNTQCHG LKQADBYEN QQENPYRLRK
KSQPNWALTA ELSPFEGRVD QLSSMTKLLL GTTINSGFIQ YNQPTETHYA LGKTTAQLV
ANGVASHIVA NGQFDES DVY QDFDFSDQIK LEIPANQGER DQTYQAMVTW NIVTGP

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EF095-3 (SEQ ID NO:363)

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ACACTGGCAT TGTCAAAAAG TGAGTTAATC GATACAGAGS CTATTTTAC AAGTCAAAACG
ATTAGAGAAA GAATTGAGAC GCCTAACCTA ACTTATCGTT ATGSAATTTAT TAATGAAGAG
GGGCAGCCAG TAAACGCCAA TGAGATCCTT CTACAGTATC ATASTTGCCA AGGCAATTCC
CCAGATGGCA TAAATGTGTG GGAAGGTGAA AGTCAACGAS TGAACGATC TACAGTGGCT
AATTTAAAAAG AAGTGGAAT TCCAAGTGAG AAAGTAGGDS TCTATTCCGA CATGTCAACG
GTGCTTGCGAG CGAGTAATCA AACATTTTIT TTACCAAGAT ATTATACITC TTTAAGCTTA
TACAATAAGA AAGGGGAAAT TGATCCCAAT TATNACGAT CAACTATTTT CGACGCATCA
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TATAGTCAGA AAACAGGAGT AACGTTTAAC ATTACGCA SA GTCAAAAAGT AATCGTTCCT
TTGTACAACC AAGTGAAGGT TGATTTCATCG AATTAATCTB GBTATTTGAA TTACTTTAAA
TTTTTCAGGGC CGGTTTATTA TCATGTTACC AATTCGAAAS TBAAGAAACA TTTTGTGGAT
ACTCAAGGGA AACCAATCCC TCCACCACCG GGGTTTAAE AABBAAGGCA AACACTTATT
GAGCGTGACC CTTACACCTT TAAACAGAAA GATTTTTTBT CAASTAGCTA TGAAATTGAC
TCAAAAACGT ATCAATTTCA AGGATGGTAT AAAAGGAAA CGAAAGCTGA AAATTTAGAA
AAAAGCGTAA CGCCAGTTA TGATATTACC TATACGCA DA ATBAIGATTT AACTGTTGTC
TATAAGGAGA TACCTCAAAA AAATTATACA TTTAGGATB TCAATGTTST TGAAATGCA
CCACCATCTG ATTTTATTCA GGATCACCAG DAACCAATTA CTACGGATBG CTTTCGCTAT
TTAGCTGGAA AAAAAGTACC ACAACAATAC AGCCTTAATB GTAAAACCTA TTTATATCAA
GGTTGGTATC AAGATAAAAC NAAACAAGAG AGCTTAGAAA AAAAGGAGCG ACCCATAAAC
TCCCTGTTT TTAATGAAAT GAACGCTATT ACAGGACTST ATAAGGAAAT AACTGCAAAA
GCTGAAATGC AAATAGAAGG ACTAGTCAAA STCATGAGAA GTSTTATAT ACAAAATTGG
CAGATTATGC TTACAAATGT GGGAGAAGTA CCGTTAAAAA AATATACCTT AAAGCCAGCA
AGTGGTTGGT CACCAGGTCT AGCTCGGCCA ATCCAGCTTA CGATTCTST TGGATCTGAA
CCAAACAAAA TTGTTCTAT TACTGATGAA AATTCGAGS TTGCGATTAC TTTAAATACG
GAAGTGCCTA TTGGTCAGAC AGCAACTATT ATGATGAGAA CAATTSTTAC AGGTGAACCA
GATCAAGTGT TACAAGCGGC TGTGAAATG AATGSAATTT TTTCTCTGT TCACGCAGCT
GATACTGTCA GAATCCAACC TAAAAATCAA GAAATCTSTG CACAGATSA GSAAGGTTTT
ATCAGCACAC CAACTTTTGA TTTTGGCAAA STGCTCTTIT CTAGCAACAC GCAGCAACAT
GGTTTAAAGC AGGCAGCAGA TTATTATGAA AATGSTACG AAAATCATA TTTACGTTTG
AAAAAATCAC AACCCAATTG GGCACCTAAT GCAGAACTAT CCGCTTTTSA ASGAAGAGTG
GATCAACTAT CATCAATGAC AAAGTTATTG TTABBAACAA CCAATGTTTC AGGTTTTATT
CAGTACAATC AACCAACGGA AACTAAAGTT GCTCTTGCCA AAACAACGSC TATTCAATTA
GTTGCCAACG GTGTAGCTAG CCATATTGTT GCCAATGCTC AGTTTGAGSA AAGTGATGTT
TATCAATTG ATTTTCTTT TGATCAAATC AAATTAGAAA TTCCAGCAAA TCAAGGTAGA
AAAGATCAA CTTATCAAGC AATGCTGACT TGAATTTAG TCACAGGCC A

```

EF095-4 (SEQ ID NO:364)

STKQ VREGTNHSLT

TABLE 1. Nucleotide and Amino Acid Sequences of *Escherichia coli* Genes

AEPAESEBQFI TKUHLDEET LALSSELEI HAHVHJHI HPHITVLT YHGFINEEG
 QFVWANEILL QVHSWJGNSP DGINTWEGES HPHVHJH HPHITVLEH YHVSXDMSTV
 LAASNQTFFL PRYYTSLSLY NKKGEIDPNY HPHVHJH HPHITVLEH ELEKMSAQQY
 SQKTGVTFNI SESQKLIPL YNQKVDSSA HPHVHJH HPHITVLEH RHTTEHFVDT
 QKHPIPPBPB FRQKQTLIE RDPYTFKQK LPHVHJH HPHITVLEH GHTPHENLEK
 SUTPSYDITY DNDDELTVY KEEPCNYTF HPHVHJH HPHITVLEH PHTDGFRLY
 ASHKLPQQYS YNGKTYLYQB WYQDKTKQES HPHVHJH HPHITVLEH AHKEITAKA
 EMQIEGLVKV MFSGYIQINQ IMLTNAGEVF HPHVHJH HPHITVLEH QHTIRVGSEP
 NKIVPITDEN WRAGITLNTN VPIBQATIM HPHVHJH HPHITVLEH GHSFSAVHAAD
 TVRIQPKNQE IVAPDEEGFI STPTFDPGKV AHSKTHHHS HPHVHJH HPHITVLEH SCENPYLRLEK
 KQCPNALWTA ELSFFEGRVD PLSSMTKLL HPHVHJH HPHITVLEH LGKHTAIQLV
 ANGVASHIVA NGCFDESDVY DEFSFDJIE HPHVHJH HPHITVLEH HPHVHJH HPHITVLEH

EF096-1 (SEC II NO:365)

TGAGGTTGGCC	AAGTTAAAAAT	GAAAAAATTA	CAATTAATTT	TATTCGCAT	TATGCGTATT
ATTGTCATCT	TGTTTTTTGG	DGTGCGCCAA	TGAAGAAAG	CAATTCGCAT	GCGAGGAGCA
GATACCTTGA	CGATTACAA	TGSGGGGGAT	TATATATTC	CGCGTTGAT	TAAGAAATTT
GAAAAAGAAA	CAGGCTATAA	AGTCAATTAC	GAAGATTTG	AATTCATGA	AGCTATGTAT
ACAAAAATTC	AGCAAAGTGG	CACAGCGTAT	GAATTAAGA	TTGCTCTGA	ATATATGATT
CAAAAAATGA	TGAAAACGAA	GATGCTTTTA	CAATTAATTC	ATTAAGAAAT	AAAGGGCTTA
GAAAAACATT	ATGCAAGGTT	TTTAGATCAA	TATTTTGA	CAATTAATA	GTTTTCCGTT
CGGTACTTCT	GSGGACCGTT	GGGATTTAT	TATTAAGA	AATTAATGA	DGGGCGTCAG
ATCAACATT	AGGATGATTT	ATGCGCGCC	GAATTAAGA	ATTAATTCAT	GCTATGTGAT
GGCGCTCGC	AGATGTTAG	ATTATCTTT	AATTAATTC	GCTATTCCT	AAACAGTAAA
AACGACCAAC	AATTACGTC	GGCTACCGAT	AATTAATTC	GCTTACGAA	CAATGTCAAA
GCAATTGTT	CGGATGAAAT	CAAAATGTAC	ATGCTTTTG	AAGGAAGTGC	AATTGCTGTA
ATTTTCTCT	GTGAAGCTGC	TGAAATGCTA	GAAAGATTC	AACATCTACA	TTATGTGATT
CCAGTGAA	GCTCAATCT	CTGTTTTCAT	AAGATTAAGA	TGCTTAAGAC	AGGCAAAAAT
AAAGAGGGTG	CGTATGCATT	TATGAACCTT	ATGCTTAC	CAGAAATGC	GGCACAAAAT
GCAGAATATA	TTCGTTATTC	CACACCAAAAT	AAGGAATTA	AGCAATATT	ATCAAAAAGAA
GTTGCCGAAG	ATAAACAATT	TTATCCAGAT	GAATTAATTA	TCAACATTT	AGAAGTTTAC
CAAGACTTAG	GTCAAGAATA	CTTAGGAATT	TATTAATTC	TGCTTTTGA	GTTTAAGATG
TATCGGAAAT	AA				

EF096-2 (SEC ID NO:366)

MKKLQ SLFIGIIAI VILFFGVRQL EKASGMAGAE LTIYINWSEY IDPALIKKFE
 KETGYKVNYE TFDSNEAMYT KIQQGGTAYD IATFENWIDQ KIKWAFMLLP LSHSKLKGLE
 NIDARFLDQS FDPYKFSVP YFWGTLGIY NENFIDWPI QNDTMRPE LYNWMLIDG
 AREVLGLSLN SLGYSLSKN DQQLRQATDK LNKLTWMA IWADLIKMYM ANEESAVAVT
 FSGEAAEMLE NNEHLHYVIP SEGSLNWFND IIMPHTAHNK EGAYAFIKFM LRPENAAQNA
 EYIGYSTPNK EAKLLPKFV AEDKQFYPDG STINHLWVD DLSQEVLSIY NOLFLEPKMY
 RK

EF096-3 (SEQ ID NO:367)

AAGTGGCAT GGCAGGAGCA
GATACCTTGA CCATTACAA TTGGGGGGAC TATATAGATC GGGATTGAT TAAGAAATTT
GAAAAAGAAA CAGGCTATAA AGTCAATTAC GAAGCGTTG ATTCTAATGA AGTATGTAT
ACAAAAATTC AGCAAGGTGG CACAGCCTAT GATATTTTGA TTGGTCTGTA ATATATGATT
CAAAAAATGA TGAAGCGGA GATGCTTTTA CGACTTATC AGAGCAATT AAAAGGCTTA
GAAAAATG ATGACGCTT TTTAGATCAA TGGTATGTC CCAAAATAA GTTTCCGTT
CCGTACTTCT GGGGCACGTT GGGGATTATT TGTATGTA AAGTATGTA CTTTGCTCAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATCCAACATT GGGATGATTT ATGGCGCCCC GANTTAAGAA ATAATSTCAT GCTGATTGAT
 GGCCTCGCG AAGTGTAGG ATTATCTTTG AACSTTTAG GCTATCGTT AAACAGTAAA
 AACGACCAAC AATTACGTCA GGCTACCGAT AACTTAAGG GATTAAAGAA CAATGTCAAA
 GCAATTGTTG CCGATGAAAT CAAAATGTAC ATGGCTAAG AAGAAAGTSC AGTTGCTGTA
 ACTTCTCTG GTGAAGCTGC TGAAATGCTA GAAAACAAAT AACATCTAAT TTATGTGATT
 CCCACTGAAG GCTCTAATCT CTGGTTTGAT AACATTCTTA TGGCTAAGAC AGCCAAAAAT
 AAAGAGGGTG CCTATGCATT TATGAACCTT ATGTTACCA CAGAAAAATG GGCACAAAAAT
 GCAGAAATATA TTGTTTATTC CACACCAAAT AAGAAAGCTA AAAAACTATT ACCAAAAGAA
 GTTGCCGAAG ATAAACAATT TTATCCAGAT GATGAAGCTA TTAACATTT AGAAGTTTAC
 CAAGACTTAG GTCAAGAATA CTTAGGAATT TATTAAGCTA TGTTCCTTCA GTTTAAGATG
 TATCGGAAA

EF096-4 (SEQ ID NO:368)

SGMAGAD TLTIYNWGDY IDPALIKKFE

KETGYKVNYE TFDSNEAMYT KIQQGGTAYD IAIPTKMTT KMKRHHILP LSHSKLKGLE
 NIDARFLDQS FDPKNKFSVP YFWGTGLIY NDAFIDDTL QWDELWRPE LFNVMMLIDG
 AREVLGLSLN SLGYSLNSKN DQQLRQATDK LNELTNWML JVADEIKMYM ANEESAVAVT
 FSGEAAEMLE NNEHLHYVIP SEGSNLWFDN IVDNETHNKK EDAVAEINFM LEPENAAQNA
 EYIGYSTPNK EAKKLLPKEV AEDKQFYPDD ETRHLLTTP DLGQBYKGIY NDLFLEFKMY
 RK

EF097-1 (SEQ ID NO:369)

TAGAAGTATT CTAATTATCT ACATAGAGAG CGATGSAAG GANTATGAA GAAAAAGAA
 ATGCATTCGC TCTTTTAA ACATAAGTTT GTGAAGCTA CTCCCTATT AGTCGTTTT
 GGTCATCGTT TGAGTGGGAT GATTATGCCA AATTGSAAT TTTTMTTSC CTGGAGCTTA
 TTGCTTTTGG TGGCTGGCTA TACGACTGGG AATTATGAT TAGCTCTTC TBAAGTCGAA
 ACGATAATGA TTCGAGTTGT TTTACCGATT CTATTGCTT TTACAGGCGG AAAAAATGTTT
 GAGGAACAAC GTGGCGCGCT TGTGCTGCT ATTGSAAG TGGGCTGAT TGTTCACACA
 GATGTTCCAC AGTTGTTTGG TGCTATGTTT ATTGCTCTT TAGAGGATA TACTTTCGCC
 AAAATTGAAC AAATTCTCTT ACCGAAAGTT AAGSAAGCT AGSABATGT GACTAAAAAC
 TTTTATAGCAG GAATTGTGGG AGGACTGCTG TGGCTCTT GATTCTTST TGTAGCTCCG
 GCTGTTGAAA GCGCTAGTTT TTGGCTGTAT CAATTCTCTT CTGCTTAAT TBAAGCCAAT
 CTTTACCAT TGGTTCACGT TTTCTTAGAG CCCTTAAGG TGTATTTTT TAATAATGCC
 ATTAACCAT GCTTATTAAC GCCTCTAGGT TTAAAGCTT CTACTCAAC AGGTCAGTCC
 ATTTTATTTT TATTGGAAC AAACCTGGA CCAGGCTGA GGTTHIGST TGTCTTTCTG
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 GTAATTGCTG GAGGAATGAG TGGTACGCTT GTTCTTAA TATTAAATGT GGGTCTAAGT
 GCTCCAGCTT CGCCAGGTTC ATTGGTTGCG ATTTTAAAT ATCCCTCAC TATGCGAGG
 CTGGCGGTTT TTAGCGGAAT TTTTGTAGC TTTCTGTCT CTCTTCAAT ASCAAGCTTG
 TTATTAACAAC GTCAACGAGG AATTGAACCA GTTCAATTA TAAAGATGAA GGAGGAAGAC
 CAAGTGGAAA CAGTCACACC TAACTATCAG CAATTTTAT TTGTTTGTGA TGCAGGAATG
 GGCTCAAGTG CCATGGGGC TAGTTTGCTA AGCGCAAT TAAAAGCTGT GAACCTGGAG
 ATGCCCTGTGA CTTACCATC CGTTCATCAG ATSAAGTCT AGCCTAGAC ATTAGTGGTC
 ATTCAAGCAG AATTGAAACA GTTAGCACAA AASTACCTC CAGAAAAGGA TATGGTGAAGT
 GTTCAAAATT TTTTAGAAAT TAAATCTAT TATCGGAGT TTTTATCAA ACTGACTGCT
 TCTTCTCAAG AGCAATCTTC ACTTGGTTCA GATCTACTT AAGCGAATC GACAAAACAA
 ATACAGAAGC TTGTTTTTTT ATATGCCGAG AATGTTTCT GATGGAAC AATGGGAATG
 GAATTATTGC GGCAACAAGC GGCGAAACAA GGACTCTTA TCGAATATC TAAAGAGCCA
 CTGGAAACAG TCTTTTTTAC CAAGGAGACA ACCTACCTAG TGAATCTGA ACTGGCGCAA
 GCCTATCATT TAGATCTAAC GCAACAAAAT TTATCTTAG TTACTATTT TTTGAATAAG
 AAAGAGTATC AAGAATGGCT GGAAGGAGGA GCTGATATAT TTTTCTTA

TABLE 1. Nucleotide and Amino Acid Sequences of Putative Genes.

EF097-2 (SEQ ID NO:370)

MLTHNF LAGIVGGLIC CPGILVWAPA
 VESASFPLYQ FSSWLIBANL LPLVHNFIEP IFVCHNFI LLSGLHSL LKASQTGQSI
 LFLLETNPSP GNGVLVAFLL FGPVSGRATA GAAHIIHSL GHHIHTIFV LKDPRLFLAV
 IAGGMSGTLV FQIFNVGLSA PASPGSLVAI LAHSHHALL AVEFHINSEF LQSPAIASLL
 LKRQGIIEPV SMIKMKEEDQ VETVTPNYQQ ILFVCIAMR HAMGASLLR EQLKAWNLEM
 PVTYQSVHQM KWQPKTLVVI QAEKQLAQK YVPHHIFVY QTFLEINCYV PQVLAKLTAS
 SQEQSSLGSE STETNSTKQI QKLVFLYAEN VEGHTYHME LLRQIAHQG VAIEVSKEPL
 ETVFFTKETT YVVTRELAQA YHLDLTQQNL YVHTSFINKK EYDEWLESGA DRGF

EF097-3 (SEQ ID NO:371)

ACGAGG AATTGAACCA GTTTCATGA TAAAGTAA CAGGAAAA
 CAAGTGCAAA CAGTCACACC TAACTATCAG CAAGTTTAT TIGTTTGTGA TCGAGGAATG
 GGTTCAAGTG CCATGGGGG TAGTTTGCTA AATGAAAT TAAAGTTST GAACTTGGAG
 ATGCGTGTGA CTTACCACTC CGTTTATCAG ATGAAATAG AGCTTAAAG ATTAGTGGTC
 ATTCAAGCAG AATTGAAACA GTTATACAA AASTAGTTC CAGAAAAGA TATGGTGAAT
 GTTCAAAAT TTTTAGAAAT TAAATCTAT TAGTAAAG TTTTAGGAA ACTGACTGCT
 TCTTCTCAAG AGCAATCTTC ACTTGTGCA GASTTATG AAGGAACTC GACAAAACAA
 ATACAGAAGC TTGTTTTTTT ATATGCGGAG AATGTTAG GATGAAAD AATGGGAATG
 GAATTATTGC GCAACAAGC GGCGAAACAA GCAATGGA TTGAATATC TAAAGAGCCA
 CTGAAACAG TCTTTTTTAC CAAGSAGACA ACCATGAG TGAATGTGA ACTGCGCAA
 GCGTATCATT TAGATCTAAC GCAACAAAAT TTTTAAATG TTACTATTT TTTGAATAAG
 AAAGAATATC AAGAATGGCT GGAAGGAGGA GCTTATAT GTTTT

EF097-4 (SEQ ID NO:372)

RGIEPV SMIKMKEEDQ VETVTPNYQQ ILFVCIAMR HAMGASLLR EQLKAWNLEM
 PVTYQSVHQM KWQPKTLVVI QAEKQLAQK YVPHHIFVY QTFLEINCYV PQVLAKLTAS
 SQEQSSLGSE STETNSTKQI QKLVFLYAEN VEGHTYHME LLRQIAHQG VAIEVSKEPL
 ETVFFTKETT YVVTRELAQA YHLDLTQQNL YVHTSFINKK EYDEWLESGA DRGF

EF098-1 (SEQ ID NO:373)

TAAATGAAAA AGACAAAAGT AATGACATTC ATGGGAAATA GAAGTTTAGG CGCACTGGCA
 CTTGTACCAA TGAGTGCATT AGCACTCGAC GGTGCTGAT ACCAAAGCAA CGSAGCGATT
 CAATTTGCAC CAAATACGAA CCCAACGAAT GASTTATG CGACGAATGC AGACCCAGAT
 AAACCAATTA CACCAGTTGA TCCAACTGAT CTGACAGGTC CTAAGCCAGG GACAGCAGGT
 CCGTATATCCA TTGACTATGC ATCTAGCTTA TTTTTCTTC AACAAAGAT TACCTCAAAA
 AATATGACCT ACTATGCAGA AACACAAAA TAGAAAGATA AGGCTGCTTC GACCAAGAA
 GGCCCAAAC TGTTCAGT CTCAGATAAT GGTGCTGAT AGACAGGTTG GATGCTAAAA
 GTAAAACAAA ATGGTCAATT CAAAACGTAA GCAATCTAG AACTACAGC GGCCAAAGTA
 ACTTTAAGCA ACGGACGCGT GTTTTCAGCT TCACATCTG CAAAGGCAAC GACAGCGCCA
 GCTACGATTG AATTAAACCC AACTGGGCT GATGCTGCT TATGCTGCT TGGCGATAAA
 GAAGGTGCGG GTACGTACTT AATGAGCTGG GCGATGCTG TAGATAGGCT TAAACAAGT
 ATTTTCATTAG AAGTACCTGG TTCAACCACA AATATCTGA AAAAATACAC GACAACTTTT
 ACTTGGACTT TGACAGATAC ACCTGCTAAC ACAGCAAT AA

EF098-2 (SEQ ID NO:374)

MKKTVMITLM ATTLGALAL VPMSALAVDG GHTTTCAGG PARUTGTPNP VDPNPDNDK
 PITVPDPTDP TGPKPGTAGP LSIDYASSLS FGFHTFTH MTHHMTYKY EDNAGADQEG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PNFVQVSDNR GTETGWLKLV KQNGQFKTEA NQETTAQKVT LSNGRVVSAS QSAKPTTAPA
 TIELNPTGAE SVVMAAGDKE GAGTYLMSWG DEWETATPTSI SLEVPSTSTK YAKKYTTTTFT
 WTLTDTPANT GN

EF098-3 (SEQ ID NO:375)

AGTCGAC GGTGGTGAAT ACCAAACAAA CGGAGCGATT
 CAATTTGCAC CAAATACGAA CCCAACGAAT CCAGTTCATC CGACGATATCC AGACCCAGAT
 AAACCAATTA CACCAGTTGA TCCAACGTAT CCGATAGGAC CTAAGCCAGG GACAGCAGGT
 CCGTTATCCA TTGACTATGC ATCTAGCTTA TTTTCTGCTG AACAAACGAT TACCTCAAAA
 AATATGACCT ACTATGCAGA AACACAAAAA TACAAAGATA ATGCTTBTGC CGACCAAGAA
 GGCCCAAACT TTGTTCAAGT CTCAGATAAT CTTTACGCTG AGACAGSTTG GACGCTAAAA
 GTAAAACAAA ATGGTCAATT CAAAACGAA CCGAACGAG AACTAACAGC GGCCAAAGTA
 ACTTTAAGCA ACGGACGCGT GGTTCAGCT TTAATATCTG CAAAGCCAAAC GACAGCGCCA
 GCTACGATTG AATTAAACCC AACTGGGGCT GAATCACTG TATGCTTGC TGGCGATAAA
 GAAGGTGCGG GTACGTACTT AATGAGCTGG GAGTATAGTG TAGATATGCG TAAAACAAGT
 ATTTTCATTAG AAGTACCTGG TTCAACCACA AATATGCGA AAAAATACAC GACAACTTTT
 ACTTGACTT TGACAGATAC ACCTGCTAAC AATGAAACT

EF098-4 (SEQ ID NO:376)

VDG GEYQTNGAIQ FAPNTNPTNP VDPNTNPDPE
 PITPVDPTDP TGPKEGTAGP LSIDYASSLS FQETITSEN MITYAETQKY KDNAGADQEG
 PNFVQVSDNR GTETGWLKLV KQNGQFKTEA NQETTAQKVT LSNGRVVSAS QSAKPTTAPA
 TIELNPTGAE SVVMAAGDKE GAGTYLMSWG DEWETATPTSI SLEVPSTSTK YAKKYTTTTFT
 WTLTDTPANT GN

EF099-1 (SEQ ID NO:377)

TGATGTTGTA GAGGGCTGAT GAAATGTTTA TCACTCTCTT TTTTACTGAA AGGAGAGATC
 ATGAAGAAAT TAGGCAAGGT TTTAATTGTT ATCTGCTTTA TTTTATCTCT TCTTTTTTTA
 TTATTTTTAG GTGATTTTTT TTCTAGTGAA ACGGCGATT CTTCGAGTT TCAGCCCGCT
 ACACCACAGG AAAAAGTAGC ATTAGAAGTT TTTAAGTAGG TGACGTCACA TCGCGGAACG
 TTGCAAGTTG CTTCGCTTG GATTGGCAAT ATGCAACATG AAAGTGCATT AAATCCTGCT
 AGAATTCAAA GTGATTTATC GTTTAATTCA GGTATAGCTT TTAATCTCTG GTTAGGCGGT
 TATGGAATTG GGTAGGACA ATGGGATTCA GGACGAGAG TTAATTATT AAATTITGCA
 AAAAGTCAAA AAAAGGAATG GAAATCAGTA GCTTTACAAA TGSATTTTGC GTGGAATAAG
 GATGTTCTG ATAGTGACTT ACTTAAAAGA ATGCTTAAT CAAAAGATGT GAATACACTT
 GCGGTAGATA TTTTGAAGCT GTGGGAACGA GCTGGAACAA AAGATGATCC CGCAGAACAA
 GTAAAAAGAA AGGCTAGTGC TAATAATTGG TATTAATGAC TTTCTACAGG TTCCATGGGC
 GGAGGTTGAG CCAATGTTGG TGGAGGAAAA ATTGATGCTT TGSAAAGAT GATGGGGCAA
 ACTATTAATG GTGGTCAATG TTATGGCTTA TCTGCTTTT TTTTCAAAA ACAAGGAGGT
 CTACAAATGA TGGGTACGGG GCATATGTTT GCGAGTAAAA TTGTAATGA TTATCCTTGG
 AGTTCAATTG GTTGGACAGT CATAAAGAAT CCAATTATT CAGATATTAA AGCAGGAGAT
 GTCATTAATT TTGGTCAAGG TGGTGTGGCT ACTAGTATT ATGCGCATAC TGGTGTAGTG
 GCAAGTGTG AAGGTAAAAA CAAGTTTACT ACTATGAGC AAAACGGTGA ACAAGGTCAA
 ATTGTTGCTA AGTATTTTCG GACTTGGGGA TTAGTTTTTC CACATGTGAC CAGCATAGTA
 AGGAAATAG

EF099-2 (SEQ ID NO:378)

MKCLS VFLLKGEIM KKLGVLIIV CFIFILFFIL ELGVFSSFEQ GDSQFQPAT
 PQEKVALEVS NYVTSHGGTL QFASAWIGNM EHESULNPAR IQDLSPNSA IAFNPSLGGY
 GIGLGQWDSG RRVNLLNFAK SQKKEWKSVA LQMTFANNED GDSSELNRM SKSKDVNTLA

TABLE 1. Nucleotide and Amino Acid Sequences of the Invention Genes.

VDILKLWFERA GTKDDPAEQV KKKASANTWY FKKKKKKKKKK GKKKKKKKKKK KKKKKKKKKKK
 INGGQCYGLS AFFVEKQGL QMMGTGHHFA SEIKKKKKKKK SEIKKKKKKKK KKKKKKKKKKK
 INFGQGGVAT SIYGHTGVVA SVESKKNKFTT YKKKKKKKKK YKKKKKKKKK KKKKKKKKKKK
 K

EF099-3 (SEQ ID NO:379)

TAGTGAA AGCGAGAAIT GTTCCCACTT TCAGTAA
 ACACCCACAGS AAAAAGTATC ATTAGAACTT TTTTAAAGG TTAATGTACA TGGCGGAACG
 TTGAGTTTTS GTTCCGCTTG GATTGGCAAT ATTAAATG AGACTGCAAT AAATCCTGCT
 AGAATTCAAA GTGATTTATC GTTTAATCCA GTTAAATG TTAATGTTC GTTACGCGGT
 TATGGAATTG GTTTAGGACA ATGGGATTCG GAGGAGAGAG TTAATTTATT AAATTTTGCA
 AAAAGTCAAA AAAAGGAATG GAAATGACTA GTTAAAGG TGGATTTTGC GTGGAATAAG
 GATGCTTCTG ATAGTGACTT ACTTAAAGAG ATTTTAAAT GAAAGATGT TAATACACTT
 GGGGTAGATA TTTTGAAGTT GTGGGAAAGA GTTAAAGG AAGATTTTGC TGCAGAACAA
 GTAAAAAGAA AGTTTAGTGC TAATAATTGG TATAAGAG TTTTAAAGG GTTCATGGGC
 GAGGTTTCAG CCAATGTTTG TGGAGGAAAA ATTAAAGG TGGAAAAAGT GATGCGGCAA
 ACTATTAAAG GTGCTCAATG TTAATGCTTA TTTTAAAG TTTTAAAGG AGAAGGAGGT
 CTACAAATGA TGGGTACGGG GCATATGTTT GAGGAGAA TGGGAAAGG TTATCCTTGG
 AGTTCAATTG GTTGGACAST CATAAAGAT GTTAAATG CAGATATTAA AGCAGGAGAT
 GTCATTAAAT TTGCTCAAGS TGGTGTGCT ATTAAATTT ATGCGGATAC TGGTGTAGTG
 GCAAGTGTG AAGGTAAAAA CAAGTTTACT ACTTAAAGG AAGAGCTTGA AGAAGGTCAA
 ATTGTGCTA AGTATTTTGG GACTTGGGGA TTAATTTT CAGATGTGAC CAGCATAGTA
 AGGAAAT

EF099-4 (SEQ ID NO:380)

SES GDSSQFQPAT
 PQEKVALEVS NYVTSHSGTL QFASAWIGIZ EREKKKKKKK KKKKKKKKKK KKKKKKKKKK
 GIGLGQWDSG RRVNLLNFAK SQKKKKKKVA LKKKKKKKKK KKKKKKKKKK KKKKKKKKKK
 VDILKLWFERA GTKDDPAEQV KKKASANTWY FKKKKKKKKK GKKKKKKKKK KKKKKKKKKK
 INGGQCYGLS AFFVEKQGL QMMGTGHHFA SEIKKKKKKKK SEIKKKKKKKK KKKKKKKKKK
 INFGQGGVAT SIYGHTGVVA SVESKKNKFTT YKKKKKKKKK YKKKKKKKKK KKKKKKKKKK
 K

EF100-1 (SEQ ID NO:381)

TANTTATGGC AATATGGAAG GAGTTTTATA ATGAAAGAAA AACAAAAATA GGCAGGGTTT
 ACATTATTAG AAATGTTGAT TGTCTTATG ATTATTTTGG TATGATTTT ACTTTTGTG
 CCTAAGTTAG CGAAACATAA AGAAACAGTT GATTAAGAAA GCAATGGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAA ATAAAGAGGC TTCTTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGTAAATAG ATAAATATAC AGCAGAAAAAG
 CAATGA

EF100-2 (SEQ ID NO:382)

MKKKQKYAGF TLEMLIVLL IISVLILLFV PHLAKKHEV DKKGHEATVK
 IVESQIELYT LEKNKTPSLN ELVNEGYICK EQLIKTAEK

EF100-3 (SEQ ID NO:383)

TAA AGAAACAGTT GATAAAAAAG GCAATGAATG ATTCCTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAA ATAAAGAGGC TTCTTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGTAAATAG ATAAATATAC AGCAGAAAAAG

10

TABLE 1. Nucleotide and Amino Acid Sequences of *S. faecalis* Genes.

CAAT

EF100-4 (SEQ ID NO:384)

KETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLEHYTAER Q

EF100-1 (SEQ ID NO:385)

TANTTATGGC AATATGGAAG GAGTTTTATA ATGAAACGAA AACAAAAATA CGCAGGGTTT
 ACATTATTAG AAATGTTGAT TGTCTTATTC ATTATTTCG TATTGATTTT ACTTTTTGTC
 CCTAACTTAG CGAAACATAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCACTAG ATAATATAC AGCAGAAAAAG
 CAATGA

EF100-2 (SEQ ID NO:386)

MKKKQKYAGF TLLEMLIVLL IISVLILLFV PNLANNHETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLEHYTAER Q

EF100-3 (SEQ ID NO:387)

TAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCACTAG ATAATATAC AGCAGAAAAAG
 CAAT

EF100-4 (SEQ ID NO:388)

KETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLEHYTAER Q

EF101-1 (SEQ ID NO:389)

TGAGGAGATG AAACGAAGAA AATGAAGAA AAAACGATTA TTATATTGGG GGCAGTTGCG
 GTAATTGCGG TTGGGGGCAT CGTAACTGTG AATGCTTAA ATAAAAATGC ACAACAAGTA
 GCTGTCAAGC AAGCGCCTAA AGATGACTGG GGAATTACT ATTTTGACBT TCCCGACTTG
 CAACAAATTT ATATTAACGG TGTCAATCAA CCGGAAATAA TGGAAAGCCTT TCGCGGTGAT
 CAAAAAATAA CAAAGGATCC AGAGATTAA GTCAAAAAG GCGATGTCTT AGATGCAGGC
 ACAGAATTAT TTAATTATGA AGATGAGGCG GTCAAAAAAG AAATTGAGGC ACAACAAAAT
 AGCTTAGCCA AATTAGAAAC GAAGCGGGCG AATATTGATA ATAAGTGGAA TCGGGCCATT
 GATAAATTTA ATAAAACTAA AGAAGAAGAT CCGACCTTCT CTGGTGATGA TTTAAATGAA
 CAATATCAAA CAGAAGTCGA TGCAGTAGAT GAAGAAATA CCTTCACCAA TGAAACCTTA
 GCGGATTTAG GAGCGAAGCA ATATATTTCT AAAAACTA ATTTGAAAGG TCGTGATATCA
 ATTCCAGAAG TAAAAGATGC CAATTCACCG ATTTTAAAGT TAATTTGABA AGATCTTTAT
 TTAGCTGGAA AAGTGAATGA AAAGGACTTG ACTAAATTA GTGTGGGCA AAAAGCTAAA
 CTAATTCTGT TTTCCAACAA TGTGGTTGTG GATGCTTAA TTTCTTACAT CGATGATAAT
 CCTCTGAAG GCAACAGCGA TGCCGCGAGT GGCATTTGAG AGGCGGGCAC AACGATGTCT
 AGTTATAGCG TCAAAATTGC GTTGGCCAAT TTAGAAAAAG TCAAAAATGG CTACCATATG
 CAAGCAACCA TTGATTTAGG CGATTTAGGG GCGATTTAGT TACCGAAAAA AGCGATTCAA
 AAAGAGGGTG AACAGGCCTA CGTTTTAGTG AATGATTTTG GAACCATCAT TCGTCGTGAT
 GTCCAAGTCG GGCAAGAAAA TGGCGACAAA ATGCGGATTT AATCTGGCTT AGAATCAGCC
 GACCGAGTGG TTATTTCTTC AAAAAACCA GTAAATTTCT GTGATATTGT TSAATCAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of the Invented Genes.

GCAGCGATTG CTTCTGATGA ATCAGCAACG AATGATGAA TGAATGATGC GTGAAATAG

EF101-2 (SEQ ID NO:390)

MEKK TIIILGAVAV IANGSINTTN ALINKNAQ, QK LAKHNS IYEDUHL,
 QIYINGVIQP EQMEAFARD; KITHDPEIKV KNSDNEHAST ELFTYEDEAV TREIEAQONS
 LAKLETKRAN IYNKWNRAID KFNKTKEDR TMSGGLNEJ YQTEVDANBE EITFTNETLA
 DLGAKQYIST KANFKGRVSI PEVKDANSPI LELTGLNLVL AGHVNKELT KISVQKAKL
 TSVSNNVVVD GSISYIDNP PEGNSDAASG NPEGGTMSG YSVKIALANL DKVKNGYHMQ
 ATIDLGLGA IELPKKAIQK EGEQAYVLVN DFHTTGLNVL QVSGENGKHM AIESBLESAD
 RVVSSKKPV KVGDIVESDA AIASDESATN ESHTLAKV

EF101-3 (SEQ ID NO:391)

TAAAAATGC ACAACAAGTA
 GCTGTCAAAGC AAGCGCCTAA ABATGACTGG GGAAGGAGG ATTTGAGGT TCGGACTTG
 CAACAAATTT ATATTAACGG TGTGATCCAA GGTGAGGAG TGGAAAGGTT TCGCGGTGAT
 CAAAAAATAA CAAAGGATGC ABAGATTAGG GTGAGGAGG GGAATGTTGT AGATGCAGGC
 ACAGAATTAT TACTTATGA ABATGAGGAG GTGAGGAGG AATGAGGAG ACACAAAAAT
 AGCTTAGCCA AATTAGAAAC GAAAGCGGAG AATGAGGAG AATGAGGAG TCGGCGCATT
 GATAAATTTA ATAAAACTAA ABAAGAAGAG TCGAGGAGG CTGGGAGTGA TTAAATGAA
 CAATATCAAA CAAAGTGA TCGAGTGA TCGAGTGA GGTGAGGAG TGAACCTTA
 GCGGATTTAG GAGCGAAGCA ATATATTTTC ACAAAGGAG ATTTGAGG TCGGTATCA
 ATTCGAGAAG TAAAGATGC CAATTCAGG ATTTGAGG TAACTGAG ABATCTTTAT
 TTAGCTGGA AATGAGTGA AAGGAGTGA ACTGAGGAG GTGTGAGG AAAAGCTAAA
 CTAAGTTCTG TTTCCAAACA TGTGAGTGA GATGAGGAG TTTGAGGAG CAGTGAAT
 CCTCCTGAAG GCAACAGCGA TCGGCGAGT GGTGAGGAG AGGCGGAG AAGGATGTCT
 AGTTATAGCG TCAAAATTGC GTTGGGCAAT TTGAGGAGG TCAAAAGG CTAGCATATG
 CAAGCAACCA TGTATTTAGG CAGTTTGGG GGTGAGGAG TCGGAGGAG AAGGATCAA
 AAGAGGGGTG AACAGGCGTA GGTGAGTGA AATGAGGAG GAGGAGGAG TGTGAGGAT
 GTCCAAGTCG GCAAGAAAA TCGGAGGAG AATGAGGAG AATGAGGAG AGAATCAGCC
 GACCGAGTGG TTATTTCTTC AAAAAAGCA GTGAGGAG GTGAGGAG TGAATCAGAT
 GCAGCGATTG CTTCTGATGA ATCAGCAACG AATGAGGAG TCGAGGAGG GTGAAAT

EF101-4 (SEQ ID NO:392)

KNAQQVA VKQAPKDDWG IDYFVDPDLQ
 QIYINGVIQP EQMEAFARDQ KITHDPEIKV KNSDNEHAST ELFTYEDEAV TREIEAQONS
 LAKLETKRAN IYNKWNRAID KFNKTKEDR TMSGGLNEJ YQTEVDANBE EITFTNETLA
 DLGAKQYIST KANFKGRVSI PEVKDANSPI LELTGLNLVL AGHVNKELT KISVQKAKL
 TSVSNNVVVD GSISYIDNP PEGNSDAASG NPEGGTMSG YSVKIALANL DKVKNGYHMQ
 ATIDLGLGA IELPKKAIQK EGEQAYVLVN DFHTTGLNVL QVSGENGKHM AIESBLESAD
 RVVSSKKPV KVGDIVESDA AIASDESATN ESHTLAKV

EF102-1 (SEQ ID NO:393)

TAAACATTTG AGACATTCAG AGGTGAATGT CTTTCTTTA TTAATCAAAA ACCGAAAGGGG
 ATTAATTATA TGAAAAAAC AACATTTAAA AATGAGGAG TATTTGCGAC TTTGCTCTA
 TTAAGTCAAA CAATTGGCGG AACGATTGCT CCTACGAGT CTTTGGCGA TGAATTACT
 CACCTCAAG AGGTAACAAT TCATTATGAC GTAGGAGAG TGTATGAGT TGACGGAAT
 TTTAGCGATG GCAGCAGCT CTCAGAACGT ACTAGGAGT TATATGAGT ATACAATGGT
 GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGAGGAG TTGCAACAG AGTGACGCAC
 GGTATCAGA AAAACCTTT GCCATCAATG TGTGAGGAG GAAAGTAT ATCGTTCCTT
 TGGGAAAAGG CTGGAACAGA TATTGATACA AATATGAGT CAGAAAGAT GATTGGGAA
 GAAGTGAACG GTTATAAACT CCATTCCATA AATGAGGAG GTGAGGAGT AGTTGATATA

TABLE 1. Nucleotide and Amino Acid Sequences of *Trichoplax* Genes.

AAATCTATTG AAGGAAAAAT TAATAAGGCA ATTGA - GAT ATGAAAAAAA ACCAAGTTT
 CATAATACCA CTGTAAAAAC AATTTTAGGT CATTCTACAA CTTTAATAGA TAAAAATGAA
 TTAAATTTAT CTGAGTTTGA TAAAGTCGTC CAATAATAGG CGAATATAGA TTACCGTGTA
 ATTGGGAATC AATTAGTGCT TACTCCAAAC TCTAAATCCA AATCAGGAAC ATTAACATTG
 AAAAAATCAG CTGGTACTGG AACTCCAGTC GCTTATACAA AAGCAGGACT TCAAACGTG
 ATGGCTGGTG CGCTTGATAA GCCCAATACC TACGCTTTTA AATTAATAT TGAAGCTAAG
 GGTTCTTTAA AGATCAAAAA AATCGATAAA GAATCAGCTG ATATTCTATC AGAAACGGTT
 TTCCATTTAG ATTTTGGGAA AGCTTTACCT TCATAATATG TGAACACAGA TAAAGATGGG
 ATTTCTATTT TGGATGGAAT TCCCCATGGT ADATAATATA CTATTACTTA AAAATCGGTG
 CCAGATCCTT ATATGATTGA TACCACACCC ATGCTTTTCA CATTAAAGC GGGCGAGACC
 ATTTCCATGA CTTCGAAAAA TATGCGACAA AAGGCTTAAA TTCTTTTAGA GAAGACTGGG
 GTAGAAACAG GTACTGATCT TTGGAATGAC AATTAATCTG TACCTGGAAA TACATTTGCC
 ATTCGTAAG ACAGCCAGC TGGTGAAATT GTCTAAATA TAAACAGTGA TAAAAAGGT
 CGTGCGGAAA CACCAAAAGA GCTTGCTAAT GTCTTAAA TGGTAAGCTA TTACGTGACA
 GAAACTAAAT CTAGTAATGG TTTCTGTAAT ATCTTAAAT CAAATAAAT CAGTTTAAAA
 TATGCCAATC AAACCGTGGC TCTTGTTACC AGTAATCTAA AAGGCAAAAA CCAAGAAATT
 ACTGGGAAA CCACTTTGAC AAAAGAAGAC AAAGATACCG TAAATGACAG TCAAGGAAA
 GCTGAGTTTA AAGGAGCTGA ATATACTCTC TTTATTTCAA AAGATGCTCA AGCTGTTAAA
 TGGAGTGAAG CTTTAAAAAC AGAATTAGTG AAGGCAAGCA AAGCTTTCTA TGAACAGTG
 ACTTTGGCTT TAGATGAAAA GAACCAAGTT GCGCTTAAAT AATAAGCAAT TAACGAGTAT
 TTCTGGCAAG AAACCAAGC ACCTGAAGGA TATAATTTG ATGAAACGAA GTATCCTGTA
 TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGCTTAA TTAATGAGA TTTACGGCA
 AAAGAACAAG TTATTCGCTT TGGCTTTGAT TTCTTAAA TAACTGATC GGTGATGGC
 ACTGCCGAAA CTGGATTAA CGACTTATCT TTTAAATCT TGGATTTCA AGGGACCAAN
 GAAATCAGAG GTGCTGAAGA TAAAGCGACC AAGCTTTCTA AAGAGAAAT AGGTTTTGAT
 GGCTATGGTA AGTTTGAAAA TCTTCCTTAT GGGATTTAT TATTGAGA AATAGAGGCT
 CCAGAAGGAT TTCAAAAGAT TACACCACTA GAATTTCTT CTACATTTAA GAAAAACAA
 GACGACTATG CGAAGAGTGA GTATGCTTTT AAGATTTCTA AAGAAATCA AAAACAACCA
 ATTAAGATGG TGACCTTCC TTACGAGAAA CTAACTTACA AAGATTTTTC TGTAGTCTG
 AACCGTTTGA TGCTTTATGA TTTGCCCGAG AAAGAAATTA GTTTGACTTC TCTTGCGACT
 TGGAAGACG GAAATAAAAA ATTGAATACC CTTGATTTTA CCGAATCTAT TGATAAATTG
 AGATATAACT TGCATGAAAT CAAAGAAGAC TGGATTTCTA TAACTTATC CATTGATGTG
 GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAATAATCA AAGGCTTCT GATTGCCGAA
 ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGTAATCT GAAAAATCT GCATAAATTA
 ACCGCTGAAC AAGTTTTGGA TAAAGCATC GTCTTTTCA ATTATTTCTA TGAACAACAG
 GTAGCCCTTG AAGCAGGCA TGAGCCAGTA GCGAATCTA TAACTTTCA CAATCAAGCA
 CAAACCGTCA ATTGTACGAT TGAACGCCAT GTTTTCTCTA AATCAAAAGC CCACCTAGAA
 GATGGTTCCG AAACCTTTAC TCATGGTGAC GTGATTTCTA TCTTTATGA TGTGCTGGTT
 ACCCATGATG TACTGGATGG CTCAAAAGAA GCTTTTAAA CATTCTCTA TGGCTTACTA
 CCAGATGGTA CGAACAAGAA AATTTGAAA TCTGCTTAA TGAAGATGA AGTGAATGAT
 AAAGAATTTA CAAAACCGT ACTTGCGGAA AAATTAATA CCGAATCTA TCCAGAAGGA
 ACTAAGTTTA CTTTACGGA AATCAATTAC GAAATTTAT GAAATCTGA TGGAAAACAC
 AATGAAGATT TGAAAGAAA ATCTCAAACC TTAACATCA AAGAAATCT AACCATACCG
 AGTACGCCAA AACAACCGGA AACACCAGCT GTTCAATTA ATTCTCAAGA ATCTAGTCCC
 ACAGTGAAGA CATTCCCGCA AACTGGGGAG AAAAAATCTA AGCTTTTACT GTTAGTTGGC
 TTATCTTGA TTTTTCGAC TGCTGGGTAT TATTCTTGA ATCGCTGCAA TTAA

EF102-2 (SEQ ID NO:394)

MKKTTFKN WSLFATLALL SQTIGGTIGP TIAFADEIIE
 PQEVTHYDV SKLYEVDGTF SDGSTLSERT TSLYALINGA KQTVFOIEPG VSIPTFVTHG
 YQKNPLPMS DKAKLVSVLW EKAGTDIDTN MVAQKMLWEE VNGYKLHSIK RLGGASVDIK
 SIEGKINKAI EEYQKKPSFH NTTVKILGQ STTLINPHEL NLSEFDEWVQ NTANIDYRVI
 GNQLVLTPNS NSKSGTLTLK KSAGTGTPVA YKEAGLFWK AGALDKPNTY AIKINVETKG

TABLE 1. Nucleotide and Amino Acid Sequences of the Genes.

SLKIKKIDKE SGDINPETVF HLDPSKALPS KKKK...
 DPMIETTPM AATIKAGETI SMTSKNMAIF...
 RHDSPAGEIV QBITTDEKGR AETPKELANA...
 ANQTVALNTS NYFGQNQEIT GETTLTYEDK...
 SEAFKTELVK GTHASDETVT LALDEANQVA...
 IKKVDINNEKN AVITRDVTAK EQVIRFGPDF...
 ITGAELKATT ACNEQLGFDS YGKFENLPYG...
 DYAKSEYVFT ITEEGQKQPI KMTVVPYEKL...
 KDGNNKLNLT DFTLVKDLR YNLHEIKEDW...
 TATLANKEKT GTWKILHKLT AEQVLLKSIV...
 TVNCTIERHV SIQTKAHLED GSQTFTHGDV...
 DGTNKEIWKs GKIEHEVNDK EFTKTVLAEK...
 EDLKEKSQTL TPKEVPTIPS TPKQPETPAV...
 ILIFSTAGYY FWNRRN

EF102-3 (SEQ ID NO:395)

TT TAGATGAAAA GAACCAAGTT GCGGTTAAAG AC...
 TTCTGGCAAG AAACCAAAGC ACCTGAAGGA TAAAG...
 TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGC...
 AAAGAACAAG TPATTGCGTT TGGGTTTGAT TTTT...
 ACTGCCGAAA CTGGGATTTAA CGATTTATCT TTTA...
 GAAATCACAG GTGCTGAAGA TAAAGCGACC AAGCT...
 GGCTATGGTA AGTTTGAAAA TCTTCTTAT GAGGT...
 CCASAAGGAT TTCAAAAGAT TACACCACTA GAAAT...
 GACGACTATG CGAAGAGTGA GTATGTCCTT ATCAI...
 ATTAAGATGG TGACCGTTTC TTACGAGAAA CTAAT...
 AACCTTTTGA TGCTTTATGA TTTGCCCGAG AAAGA...
 TGSAAAGACG GAAATAAAAA ATTGAATACC CTTT...
 AGATATAACT TGCAATGAAAT CAAASAAGAC TGTAT...
 GAAGCTACAA AAGCTGCCCA AGAAAAAGAC GAAAA...
 ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ATTGA...
 ACCGCTGAAC AAGTTTGGGA TAAAGCATC TCTTT...
 GTAGCTTTTG AAGCAGGCAA TGAGCCAGTA GAAAA...
 CAAACCGTCA ATTGTACGAT TGAACCGCAT GTTCT...
 GATGGTTTCG AACCTTTTAC TCATGGTGAC TGAT...
 ACCCATGATG TACTGSATGG CTCAAAAGAA GTTT...
 CCAGATGGTA CGAACAAAGA AATTGGAAGA TTTGG...
 AAAGAATTTA CCAAAACCGT ACTTGCGGAA AAGTA...
 ACTAAGTTTA CTTTACCGA AATCAATTAC GAAAA...
 AATGAAGATT TGAAAGAAAA ATCTCAAACC TTAAG...
 AGTACGCCAA AACAACCGGA AACACCAGCT GTTCC...
 ACAGTGAAGA

EF102-4 (SEQ ID NO:396)

LDEKNQVA VKHLAINEYF WQETKAPEGY TLIETK...
 IKKVDINNEKN AVITRDVTAK EQVIRFGPDF FHFAG...
 ITGAEDKATT ACNEQLGFDS YGKFENLPYG LYLLE...
 DYAKSEYVFT ITEEGQKQPI KMTVVPYEKL TIENE...
 KDGNNKLNLT DFTLVKDLR YNLHEIKEDW YVVAQ...
 TATLANKEKT GTWKILHKLT AEQVLLKSIV LFNTV...
 TVNCTIERHV SIQTKAHLED GSQTFTHGDV MDNFD...
 DGTNKEIWKs GKIEHEVNDK EFTKTVLAEK VETBY...
 KFTTTEINYE KDNVNGKHN

TABLE 1. Nucleotide and Amino Acid Sequence of *E. faecalis* Genes.

EDLKEKSQTL TPKEVPTIPS TPKQPETPAV PSNSQVPSST VK

EF103-1 (SEQ ID NO:397)

TAAGATAGGT TTATCAAAGA AAAGGAGCGA TGGTTLATGA AAAAGAAAGT ATTAAGTTCTG
 ATTACTTTAG TAACATTAAG TACGTTACTT ATAGCAATT ATGCAAGTCC AGCATTGCA
 GATCATGCAG CCAATCCAAA TAGTGCTACA GCAAAATTAG GCAAACATCA AAACAATGGC
 CAAACAAGAG GCGACAAGGC GACTAAGATT TTATTTTSCA CGGACTGGCA AGGAACCCGT
 GTTTATGATG CTGCTGGTAA TGATTTAACG GAGAAATATG CTAATTTTAT TGGTTTAGCA
 AAATATGATG GTGAAACCGG TTTTACGAG TTTTTCAGCA AAAATACTGG GGAACCCGT
 GGTGACGAAG GAACATTTTT TGTGACAGGT GATGTCACAA AACGAATTTT AATTTCGCGG
 ACACAAAATT ATCAAGCCGT AGTGGATTTA ACGGATTTGA GTAAAGACNA ATTTACTTAC
 AAGCGTTTAG GGAAAGATAA ACTGGGGAAT GATGTTTAA TTTACGTGCA ACACATCCCT
 TATCATGGGA AAAAATTAGC TTTTACAAAT GAGCTTAAAG CATTAACTAA TCAAACTGGC
 AAAATTGTGA CAAATAAATC AGGGGATAAA ATTTTACAAA CAACCTTTTG GAATGGCACA
 AAAGTCGTAG ATAAAAACGG TAATGATGTG ACAGCTTCCA ATCAAAATTT CATTAGTTTA
 GCGAAATTTG ATCCAAACAC AAGTAAATAT GAATTTTCTA ATTTACAAAC AGGTGAAACC
 CGCGGCGACT TTGGGTACTT CCAAGTGGTG GACAAATACA AGATTGGGCG CCATGTATCT
 ATTGGTACGA ATCGTTACGG CGCGGCGCTA GAATTTTAAAG AACTAAACAA TGATCGATTT
 ACGTATACTC GAATGGGTAA AGATAATGCT GGTAAATATA TTCAAGTETT CGTGGAACAT
 GAACCTTACC AAGGCACATA TCATCCAGCC TTTATCTTCT AA

EF103-2 (SEQ ID NO:398)

MKKKVLSSI TLVTLSTLLI AGYASPAFAD HAANPNESATA NLGKHQNNQ
 TRGDKATKIL SGTDWQGTRV YDAAGNDLTA ENANF LAK YDGETGFYEF FDKNTGETRG
 DEGTFFVTGD GTRKILISRT QNYQAVVDLT EVKKNITVK RLKDKKLEND VEYVVEHIPY
 HGKKLAFTNG REALTNQTGK IVTNKSGDKI LSTT LCTK YVDKNSNEVT AANQNIFSLA
 KFDPNNTSKYE FPNLQTGETR GDFGYFQVVD NKKIRATYI STNRYGAALD LTELNNDRFT
 YTRMGKDNAG NDIQVFVEHE PYQGYTHPAF TF

EF103-3 (SEQ ID NO:399)

TCATGCAG CCAATCCAAA TAGTGCTACA GCAAAATTAG GCAAACATCA AAACAATGGC
 CAAACAAGAG GCGACAAGGC GACTAAGATT TTATTTTSCA CGGACTGGCA AGGAACCCGT
 GTTTATGATG CTGCTGGTAA TGATTTAACG GAGAAATATG CTAATTTTAT TGGTTTAGCA
 AAATATGATG GTGAAACCGG TTTTACGAG TTTTTCAGCA AAAATACTGG GGAACCCGT
 GGTGACGAAG GAACATTTTT TGTGACAGGT GATGTCACAA AACGAATTTT AATTTCGCGG
 ACACAAAATT ATCAAGCCGT AGTGGATTTA ACGGATTTGA GTAAAGACNA ATTTACTTAC
 AAGCGTTTAG GGAAAGATAA ACTGGGGAAT GATGTTTAA TTTACGTGCA ACACATCCCT
 TATCATGGGA AAAAATTAGC TTTTACAAAT GAGCTTAAAG CATTAACTAA TCAAACTGGC
 AAAATTGTGA CAAATAAATC AGGGGATAAA ATTTTACAAA CAACCTTTTG GAATGGCACA
 AAAGTCGTAG ATAAAAACGG TAATGATGTG ACAGCTTCCA ATCAAAATTT CATTAGTTTA
 GCGAAATTTG ATCCAAACAC AAGTAAATAT GAATTTTCTA ATTTACAAAC AGGTGAAACC
 CGCGGCGACT TTGGGTACTT CCAAGTGGTG GACAAATACA AGATTGGGCG CCATGTATCT
 ATTGGTACGA ATCGTTACGG CGCGGCGCTA GAATTTTAAAG AACTAAACAA TGATCGATTT
 ACGTATACTC GAATGGGTAA AGATAATGCT GGTAAATATA TTCAAGTETT CGTGGAACAT
 GAACCTTACC AAGGCACATA TCATCCAGCC T

EF103-4 (SEQ ID NO:400)

HAANPNESATA NLGKHQNNQ
 TRGDKATKIL SGTDWQGTRV YDAAGNDLTA ENANF LAK YDGETGFYEF FDKNTGETRG
 DEGTFFVTGD GTRKILISRT QNYQAVVDLT EVKKNITVK RLKDKKLEND VEYVVEHIPY

TABLE 1. Nucleotide and Amino Acid Sequences of *E. coli* Genes.

HGHKLAFTNG REALTNQTHK IUTNHSSEFI IUTNHSSEFI IUTNHSSEFI IUTNHSSEFI IUTNHSSEFI IUTNHSSEFI
 KFDPNSTKYE FPNLQGTETR GDFGFFYFWD KDFGFFYFWD KDFGFFYFWD KDFGFFYFWD KDFGFFYFWD KDFGFFYFWD
 YTRMGKDNAG NDIQVFWEHE PYQSTYHIA

EF104-1 (SEQ ID NO:401)

TGAAAGSSGA TTAGTATGAA GAAAAAAAT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GCACAAAATT TCGGGTTTBT TGTAAATGAC TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GAGACCACTG ATACAGCAAA AAAAGAGGGA GATTATGGA ACTCAACACC ATCTTTTACCT
 TTAGCAACAA CGACTACTT AGAAATGANT GAAATGACTG CAACCAATGA ATCGCAAAACC
 ACAGAGGCGA GCACAAACAT TTCCAGTAT CTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GAGGACAAGG ACACCTCACT TAATGAAAAA GATT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 BATGAACATG TTGACAGTAT GATGTTTGG GATGTTTGGT GATGTTTGGT GATGTTTGGT GATGTTTGGT
 GAGGTTTACC GCGAATTAAA TACAACAGTG GATGTTTGGT GATGTTTGGT GATGTTTGGT GATGTTTGGT
 AACACAGGTT ATGCAACCTG ATGCAACCTG ATGCAACCTG ATGCAACCTG ATGCAACCTG ATGCAACCTG
 TCAACTTCTA GCGGAGAAAT GATGTTTGGT GATGTTTGGT GATGTTTGGT GATGTTTGGT GATGTTTGGT
 AAAACATTAA GTATTACGTT TAATGAAATG GATGTTTGGT GATGTTTGGT GATGTTTGGT GATGTTTGGT
 AAAAGTTATC TAACAACABA GCGGGAAGTA TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AAAAAAACCT ACTGTTTGA TTTATATGAA GATGTTTGGT GATGTTTGGT GATGTTTGGT GATGTTTGGT
 ACCAGAACGA CCGGTTTGA TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AATCAACAT TAGAATTAT TACAACAGAG ACTGTTTGGT GATGTTTGGT GATGTTTGGT GATGTTTGGT
 AACTTGAAC CTCAAGTTTT CATTATGAT GATGTTTGGT GATGTTTGGT GATGTTTGGT GATGTTTGGT
 ACGCAAAACCT TGTAAACACC TGGCAAAAT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ATTGCTGTAA CTGTTCCAAA CATGAATGAA CAACCAACCT ATGTTTATC GATTAATCGG
 ACAATTTATT TAGAGAGTG TCGGAGTAT AATTATTTAT ATTTGAGCA TTTTCAACA
 AAAAAAATTG GGTCAATTT TTTGAAAAT AGCAACGAA CTAAACAAAC AATCGATTTT
 ACTGCTAAGA CGAGTCAAA AATGAAATTA ATTTTATC GTTAAATGCG TATATGTCC
 TATATCAGTT TTCAAAGCAA AGGGAATAT TATGTAACA TTTATGTC GTTAACAGAA
 AAAAAAGTGG GTCAACAAAT CGTATTAAG ATTTTAAAG GTCAACAAAT TAAGAATCCT
 AAAATTACGG CGTATGTTT TTTATATGAA AATTGAAAT TTTTCAACA TTTTCAACA
 AAACTGAAAG GTGGCAAGCT CACTTTAAAG GATGTTTGGT ATAGTTATTT AAGAATAAAT
 ATTTCTGATT TAACAATGGA TTTTGACAA GATGTTTGGT ATTTATCCTT AATACACCT
 GTAATTGGTC CTAATAAAGC CATTCAATTA GTATGATC AATATATGAA AATTAATAGT
 GTTGTAAATC CTTGAATGC TGAAACTGCT TTTTCAATTT ATGATTAATA TTTTCAATTT
 TCATCAAGAA CACTGTCTC AGTTATGGA AGCAACGAA AATCGATTTA AATTTTAGAA
 ATTAAGGTAA AGCATCCTAA TTATCTTTCA TTACGAGCTA CAAAGAAAT TTTATTTTAT
 TACAAGTTAG GAACGGATTA TACAGTAAG CCAACCTCAG ATGGTTTCACT TATTAAGTTC
 ACTACGCCAA TAACCAACGA AATCCAAAT CCAATTTGTT TTAATTATGT GCGAGATAGT
 TTGCCAAAAG ATAAAAGTAT CCCAGTCTAT AGGATCCGA TAACAATGAG TTTTGAAGGT
 TTAACCTCAG TTGATACGAC AGTAACAT AATAGTAAGC GTGGTTCTGA ACGAACACTT
 CAAAGTAGTA AAAATCAATT CTTTCTCAAT GATGTTTGGT ATTTCTTTGA CTCACTAAGC
 GTCCGTACAA AATTTCCAGC TGGCGGCTAT GTTCTTTTTC ACATTTATGA TTTTCAAAAC
 GATCAGGTAG ATTCAATTTA TCCACAATAC TTTTCAAGCG GTCAATACCT TATATAACCA
 ATGACGCCAA ACAGCCCTGG ATATCAAGG ATTTATTTTG ACGAAATAT CAAATAGTTAC
 ACGTTTGATT TTGGAAAAAC CAACAAACCT TATATTTATG AGTATAAATA CCGCAATGGC
 TGGATCGACG TGCCAACCTT TTATATAACA GATGTTTGGT AAGAAACACA ATCGAATAAT
 AATGAAGGCT CTGCTTCGGT TTCTGTTTAA AATGATCGCT TAGACATTTT GATGCAACA
 CAAGCGGCGA ATCCAACATT AAAAAATTTA AATGATCGCT CAGTACACAC AAAAAATATT
 GATAATAAAA CACATCGTGT GAAAAATTTA AATGATCGCT TAACATCGAA ACGCAACACC
 AATGCTCAAA TCGATTTGAA TTCTATTACC GTTAAAGCGG TGCCABAAGA TTTTATTCA
 TTAGAGAAGA CTACAAACGG TGGGAAAGTC ATTTTAAAG ACTATACATT GACAGAAAAC
 ATTACGATTG AATACAATAC GGTCTCTTAA AATGATCGCT AAATCTATAC AAAAAACAAC
 ATCGACTCTG AAACATTGAA CCAGATGTCT GATGTTTGGT AAAAACTAC CACTGCGCCA
 ATCACATTGA AATCTCAGA AGGTGATCGG GATGTTTGGT TTTATTTATC AACTGCCACA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTCTACACGC ATAACGTAGA GGATGAAAAC CAGGCGATTG CGAAGGTTTC TTTTGAAC TA
 ATTGATAATG TCACGCATAC AGCAACCGAA TTAAACACAG ATGAAAAGG TCAATACTCC
 TTTGATGCCA TCATGACAGG TGATTATACT TTGGGAGTAA CGAATGTACC GCAGGAATAT
 TCCGTGGATG AAGAGTATTT GACAGGAAAA GGCATTAAAGC TGGTCAAAAG AGACAACCAA
 CTAAAAATTC CATTAACGAA AACAATTGAT CACAGTCGTT TACAAGTCAA AGATTCAACG
 ATTTATGTCG GCGATTTCATG GAAACCAAGAA GAGAGCTTTG TTTCAGCAAC AGATAAAACA
 GGTCAGACG TTCCCTTCGA AAAAATCACT GTTTAGGCTC AAGTTGATAA CANCAAAGCA
 GGCGTTTATC CAATTATTTA CAGTGACGAA GGTAAAGAAG AAACAGCCTA TGTGACCGTC
 AAACCCGACC AATCTAAGTT AGAGGTCAAA GATATAACGA TTTATGTTGG TGATTTCGTGG
 AAACCAGAAG ATAATTTTCGT TTCAGCGACA GATATAACAG GTCAAGAGCT NCCGTTTGAA
 AAAATTGATG TTCAGGGAAC AGTGAATGTT GATTAATATAG GCGATTATGA AATTGCTCTAT
 AAAAATGGCA NAAAAGAAGC GAAAGCAATC GTTCTGCTCC GTGATGACAG TCAGTTAGAG
 GTTAAAGATA CAACGATTTA TGTGGTGTAT TGGTCAAAAC CAGAAGATAA TTTCGTTTCA
 GCAACAGACA AAACAGGCCA AGACGTTCCG TTGAAAAA TCACTGTCTC AGGTCAAGTT
 GATACTAGCA AAGCAGGCGT TTATCCAATC GTTACAGTT ACGAAGGTAA AGAAGAAACA
 GCTAATGTGA CTGTCAAACC CGACCAATCT AAGTTAGAGG TTAAAGATAC AACGATTTAT
 GTGGGCGATA AATGGGAACC AGAAGATAAT TTCTTTTCAG CAACAGACAA AACAGGTCAA
 GATGTCCCGT TTGAAAAAAT TGACGTTTCAG GGAAGAGTGA ATGTTGATAA AATAGGCGAT
 TATGAAATTG TCTATAAAAA TGGCACAAAA GAGGCAAAAG CAATCGTTCA TGTCCGTGAT
 GACAGTCACT TAGAGGTCAA AGATACAACA ATTATGCTGG GTGATAAATG GSAAGCAGAA
 GATAACTTCG TTTCCGCGAC AGACAAAACA GGTAAAGACG TTCCGTTTGA AAAAATTGAT
 GTTCAGGGAA CAGTGAATGT TGATAAAATA GGGGATATG AAATTGCTTA TAAAAATGGC
 ACAAAGAAG CGAAAGCAAT CGTTTCATGTG GGTGATGATA GTCGTTTACA AGTCAAGGAT
 ACAACGATTT ATGTCGGCGA TTCNTGSANA CCAAAENGA ACTTGTTTIC AGCNACAGAT
 AAAACAGGTC AAGATGTCCC ATTCGAAAAA ATCACTGTT

EF104-2 (SEQ ID NO:402)

MKKKTF SFVMSILLA QNFGFAVNAY AVTTTEAQT TDTAKKEAE LSNSTPSLPL
 ATTTTSEMNQ PTATTESQTT EASTTASSDA ATPSEQTTE DKDTSLNEKA LPDVQAPITD
 ELLDSMSLAP IGGTEYSQTE VHRELNTTPV TATEQFAVGN TGYAPGSVYT VQLPEHLGYS
 TVSGEVTGIG ATWAVDAATK TLSITFNQRV SETSEFVELK SYLTTEAEPL IKIETPGKNK
 KTYSFDLIEQ VEPIQYNERT RTTGLDGEIF YRLDEI LTGN QTLELLTTET PGAVFGKQDN
 LEPQVFSYDV DINGQILPET QTLTTPGKDY TISDNLGRI AVTVPNMNMQ KAYSLSINRT
 IYLESASDYN YLYSQQYPTT KIGSISLKST TCTHQTDFD AKTSYTSKVI ADREMRMSY
 ISFQSKGKYY VTLYGTLTET KVGQQIVLES TGGQENKNPK FTAYGPLYEN VFLEDYFDIK
 TEGGKLTLTA TKDSYLRINI SDLTMDFDKK TINKST STPV IGPNEAIQLV SDQYIEPISV
 VNPLNAETAW GNYDQNGAYS SRTTVSVMGS KEFPIANLEI KVKHPNYL SL FATKEIYFYY
 KLGTDYTVTP TSDGSVIKFT TPITNEIQIP IGFNYVPDSL PKDKSIPVDT IPITMSAEGE
 TPVDITVTTN SKRGSERTLQ SSKNQFLVNA ENLSFISLSV RTKIPAGAEV LFDIYDVSND
 QVDSIYPQYW DRGQYFDKPM TPNSPGYPTI TPDENTINSYT FDFGKTNFRY IIEYKNANGW
 IDVPTLYITG TAKEPQSNNN EGSASVSVQN EALDILSATQ AANFTLKINT KTTVTTKNID
 NKTHRVKNPT IELTPKGTIN AQIDLNSITV KGVPELAYSL EKTINGAFVI FHDYTLTENI
 TIEYNTVSAN AGQIYTETTI DSETLNQMSA SKKKVTTAPI TLKFSEGIKAE GIVYLATATF
 YTHNVEDENQ AIAKVSFELI DNVHTTATEF TDEKQQYSF DAINTGDTL FVTNVPQEYS
 VDEEYLTGKA IKLVKGDNL KIPLTKTIDH SKLQVHDSTI YVGDGSKHEE IFVVSATDKTG
 QDVPFEKITV SGQVDNXXKAG VYPIIYSDG KBBTAYVTVK PDQSKLETKD TTIYVGDSWK
 PEDNFVSATD KTGQDVPFEK IDVQGTVNVD KICDYNHIVYK NGXKEAKAIV HVRDSSQLEV
 KDTTIYVGDS WKPEDNFVSA TDKTGQDVPF ENLTVGQVD TSKAGVYIV YSYEGKEETA
 NVTVPKPDQSK LEVKDTTIYV GDKWEPEDNF VBATDKTGQD VPFEKIDVQG TVNVDKIGDY
 EIVYKNGTKE AKAIVHVRDD SQLEVKDTTI YGDAWEAED NFVSATDTG QDVPFEKIDV
 QGTNVNDKIG DYEIVYKNGT KEAKAIVHVR DLSRQVVKDT TIYVGDSWXP EXNFVSATDK
 TGQDVPFEKI TV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF104-3 (SEQ ID NO:403)

TGTAA CAACGACAGA AGCACAACA
 GAGATCACTG ATACAGCAAA AAAAGAGGCA GATTATCGA ACTCAACAGC ATTTTACCT
 TTAGCAACAA CGACTACTTC AGAATGATC GATTAACTG CAACACTGA ATCGCAAAAC
 ACAGAGGCGA GACAAATAGC TTCTAGTATC GATATACAC CATCTGATTA ACAAACAACG
 GAGSACAAGG AACCTTCACT TAATCAAAAA GCTTTGACAG ATGTTCAAGC GCGAATTACA
 GATCAACTAC TTGACAGTAT GAGTTTTCAG GGTATGCTG GAACAGATTA TAGCCAAACA
 GAGTTTCACG GCGAATTAAA TACAACATCG GTAAACGATA CGTTCCAACT TGTTGTTGGA
 AACACAGGTT ATGCACTGCG ATCACTTTAT ACAGTTCAT TACCAGACA TTGAGGTTAT
 TCAACTGTCA GCGSAGAACT GACAGGCACT GGTTCAACT GGGCAGTCA TGCTGCGACC
 AAAACATTAA GTATTACGTT TAATCAAGCA GTTTGAGATA CTTCCTTTAA AGTAGAATA
 AAAAGTTATC TAAACAACAG GCGSAAATCA TTAACAAAA TTGAAGCTCC AGGAAAAAAT
 AAAAAAACCT ACTCTTTTGA TTTATATGAA GAAGTGGAC CAATTCACTA TAACGAACGA
 ACCAGAACGA GCGSSTIAGA TGSCTAACT TTTTATACT TAGACGGAAT GTTAACCTGCC
 AATCAACAT TABAATTATT AACAACAGAG AAGTAAAGCG CTGTCTTTG AAAACAAGAT
 AATTGGAAC TCAAASTTTT GATTACGAT TTGACATTA ATGCTCAAT TTTACAGAA
 ACCTAACCT TTTTAAACAG TGSCTAAAGT TATAATTTAA GCGATAACT ACCTGGGCGG
 ATTCTGTAA CTGTTCCAAA CATCAATCAA CAAAAAGCT ATTCTTATC GATTAACTCG
 ACAATTTATT TAGAGASTGC TTGCACTAT AACTACTTAT ATTCCAGCA CTATCCAACA
 ACAAAAAATG GGTCAATTTT TTTGAAAACT AGCAGAGGAA CTAAACAAAC AATCGATTTT
 ACTGCTAAGA CGAGTCAAG AATAAAGTA ATGCTGATC CTGAATGCG TATATGTCC
 TATATCAGTT TTCAAAACAA AGGGAATAT TATTTAACA TTTATGGAC TTAAACAGAA
 ACAAAAGTGG GTCAACAAAT CGTATTAGAG ACTACAAACG GTCAAGAAAT TAAGAACTCT
 AAATTTACGG CGTATGCTC TTTATATGAA AATTTAAAA TTGAAGACTA TTTTATATTT
 AAAACTGAAG GTGGCAAGCT CACTTTAAG GCAAAAAAG ATAGCTATTT AAGAAATAAT
 ATTTCTGATT TAACAATGGA TTGTGACAA AGCAGACTTA ATCTATCATT AATACACCT
 GTAATTGGTC CTAATAAAGC CATTCAAATTA ATATCGATC AATATATGA ACCAATTAGT
 GTTGTAAATC CTTTGAATGC TGAAACTGCT TGGCTAATT ATGATCAAAA TGCTGCTAT
 TCATCAAGAA CAACTGTCTC AGTTATGGA AGCAAGAGA AACCGATTCA AATTTAGAA
 ATTAAGTAA AGCATCTAA TTATCTTTCA TTAGAGCTA CAAAAGAAAT TTTATTTTAT
 TACAAGTTAG GAACGATTA TACAGTAAAG CCAAGTCAAG ATGGTTCACT TATTAAGTTC
 ACTACGCCAA TAACCAACGA AATCCAAAT CCAATTGCTT TTAATTATGT GCGAGATAGT
 TTGCCAAAAG ATAAAGTAT CCCAGTGGAT AGGATACCGA TAACAATGAG TGCTGAAGGT
 TTAATCCAG TTGATACGAC AGTAACACT AATAATAAGC GTGGTTCTGA ACBAACACTT
 CAAAGTAGTA AAAATCAATT CCTGTCAAT GCAGSAAATG ATTCTTTTGA CTCACTAAGC
 GTCCTACAA AAATCCAGC TGGCGCGGAT GTTCTTTTTC ACATTTATGA TGTTCAAAC
 GATCAGGTAG ATTCAATTTA TCCACAATA TGGGACCGCG GTCAATACCT TCAATAACCA
 ATGACGCCAA ACAGCCCTGG ATATCCAAG ATTAATTTTG ACGAAATAC CAATAGTTAC
 ACGTTTGATT TTGGAAAAAC CAACAAAGCT TACATATTG AGTATAAAA CBTCAATGGC
 TGGATCGACG TGCCAACTCT TTATATAACA GCGATAGCGA AAGAACCAAA ATCGAATAAT
 AATGAAGGCT CTGCTTCGGT TTCTGTTCAA AATCAAGCGT TAGACATTTT GASTGCAACA
 CAAGCGGCGA ATCCAACATT AAAAAATGTA AAGAAACGA CAGTACAAAT AAAAAATATT
 GATAATAAAA CACATCGGT GAAAAATGCA AGGATTGAAT TAACACCAAA AAGCAACACC
 AATGCTCAAA TCGATTTGAA TTCTATTAC GTGAAGGCG TGCCAGAGA TGTATTTC
 TTAGAGAAGA CTACAACGG TGGGAAAGTC ATTTTAAAG ACTATACAT GACAGAAAAC
 ATTACGATTG AATACAATAC GGTCTCTGCA AACCTTGGCC AAATCTATAC AGAAACAACA
 ATCGACTCTG AAACATTGAA CCAGATGCTT GGTATCAAGA AAAAGTCACT CACTGCGCCA
 ATCAGATTGA AATTCTCAGA AGGTGATGCG GAAGCTATTG TTTATTTAGT AACTGCCACA
 TTCTACACGC ATAACGTAGA GGATGAAAA CAGCTAATTG CGAAGSTTT TTTTGAACATA
 ATTGATAATG TCACGCATAC AGCAACCGAA TTTAACAAG ATGAAAAAG TCAATACTCC
 TTTGATGCCA TCATGACAGG TGATTATACT TTGCTAGTAA CGAATGTACT GCAGGAATAT
 TCCGTGGATG AAGAGTATT GACAGGAAAA GCAATTAAGC TGGTGAAGG AGACAACCAA
 CTAAAAATTC CATTAACGAA AACAATTGAT CACTCTGCTT TACAACTCAA AGATTCAACG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATTTATGTCG GCGATTCATG GAAACCAGAA GABAA TTTG TTTCAACAAO AGATAAAACA
 GGTAAGACG TTCCCTTCGA AAAAATCACT GTTTGAGTC AAGTTGATAA CAACAAAGCA
 GGCGTTTATC CAATTATTTA CAGTGACGAA GGTAA GAAG AAACAACCTA TGTGACCGTC
 AAACCCGACC AATCTAAGTT AGAGGTCAAA GATAACABBA TTTATATTG TATTCTGTGG
 AAACCCAGAAG ATAATTTTCGT TTCAGCGACA GACAA ACAG GTCAAGACAT NCCGTTTGAA
 AAAATTGATG TTCAGGGAAC AGTGAATGTT GATAAAATAG GCGATTATTA AATTGTCTAT
 AAAAATGGCA NAAAAGAAGC GAAAGCAATC GTTCAAGTCC GTGATGACAG TCAGTTAGAG
 GTTAAAGATA CAACGATTTA TGTTCGTGAT TGTGAAAAC CAGAAATATA TTTCGTTTCA
 GCAACAGACA AAACAGGCCA AGACGTTCCG TTTCA AAAA TCACTATTTC AGGTCAAGTT
 GATACTAGCA AAGCAGGCGT TTATCCAAATC GTTAAAGTT ACGAAGGTAA AGAAGAAACA
 GCTAATGTGA CTGTCAAACC CGACCAATCT AATTGAGAG TTAAGATATC AAGGATTTAT
 GTGGGCGATA AATGGGAACC AGAAGATAAT TTGTGTTGAG CAACACACAA AACAGGTCAA
 GATGTCCCGT TTGAAAAAAT TGACGTTTCA GAAACAGTGA ATGTTGATTA AATAGGCGAT
 TATGAAATTG TCTATAAAAA TGGCACAAAA GAAACGAAAG CAATCCTTA TGTCCGTGAT
 GACAGTCAGT TAGAGGTCAA AGATACAACA ATTTATGTGG GTGATAAAG GGAAGCAGAA
 GATAACTTCG TTTCGCGAC AGACAAAACA GGTCAAGACG TTCCGTTTAA AAAAATTGAT
 GTTCAGGGAA CAGTGAATGT TGATAAAATA GGTGATTATG AAATTGTCFA TAAAAATGGC
 ACAAAGAAG CGAAGCAAT CGTTCATGTC GGTGATGATA GTCGTATTAA AGTCAAGGAT
 ACAACGATTT ATGTCGGCGA TTCNTGGANA CCAGAAGNGA ACTTTGTTTC AGACACAGAT
 AAAACAGGTC AAGATGTCCC ATTC

EF104-4 (SEQ ID NO:404)

VTTTEAQTE TTDATKEAE LSNSTPSLPL
 ATTTTSEMNO PTATTESQTT EASTASSDA ATPSEQCTTE DKDTSLNEHA IPEVQAPITD
 ELLDSMSLAP IGGTEYSQTE VHRELNTTPV TATFQFAVGN TGYAFGSVIT VQLPEHLGYS
 TVSGEVTGIG ATWAVDAATK TLSITFNQFV SITSFKVELK SYLTTEAEHL IKIETPGKNK
 KTYSFDLYEQ VEPIQYNERT RTTGLDGEIF YNLEETLTGN QTLELLTET PGAVFGQDN
 LEPQVFSYDV DINGQILPET QTLTTFGKPY TLENSLGR I AVTVPIIMNQ KAYSLSINRT
 IYLESASDYN YLYSQQYPTT KIGSISLKST TGTQCTTDFI AKTSQTSKNI ADEMRMSY
 ISFQSKGKYY VTIIYGLTET KVGCCIVLES TNGQBIKNPK FTAYGPLYEN VKLEDYFDIK
 TEGGKLTLLTA TKDSYLRINI SDLTMDFEKK ENLSLSTPV IGPNEAIQLV SDQYIEPISV
 VNPLNAETAW GNYDQNGAYS SRTTVSVMGS KENFIQNL EI KVKHPIYLL FATKEIYFY
 KLGTDTYVTP TSDGSGIKFT TPITNEIQIP IGFNYVFDL PKDKSIPVET IFITMSAEG
 TPVDTTVTN SKRGSERTLO SSKNCLANA ENESFDLSLV RTKIPAGADV LFDIYDVSND
 QVDSIYPQYW DRGQYFDKPM TPNSPGYPTI TFEINTSYT PDFGKTNFRY IIEYKNANGW
 IDVPTLYITG TAKEPQSNNN EGSASVSVQN EALEILSATQ AANPTLKNRT HTTVTTKNID
 NKTHRVKNPT IELTPKGTN AQIDLNSITV KGVFEDAYSL EKTNGAPVI FKDYTLTENI
 TIEYNTVSAN AGQIYTETI DSETLNQMSA SHKVTTAPI TLKFEQDAE GIVYLATATF
 YTHNVEDENQ AIAKVSFELI DNVHTATFP TTDEFGQYSF DAIMTSDYTL FVTNVPQEYS
 VDEEYLTKGA IKLVKGDNL KIPLTKTIDH SLLQVKDSTI YVGDSWKPEE NFVSATDKTG
 QDVPFEKITV SGQVDNXXAG VYPIIYSDG KEETAYVTVK PDQSKLEVHD TTIYVGDSWK
 PEDNFVSATD KTGQDVPEK IDVQGTNVND KIGDYEIVYK NGXKEAKAV HVRDDSQLEV
 KDTTIYVGDS WKPEDNFVSA TDKTGQDVPE EKITVSGQVD TSKACVYPTV YSVEGKEETA
 NVTVKPDQSK LEVKDTTIYV GDKWEPEDNF VBATDKTGQD VPFEKIDVGB TVINVDKIGDY
 EIVYKNGTKE AKAIHVHRRD SQLEVKDTTI YVSDPWEAED NFVSATDKTB QVVPFEKIDV
 QGTNVNDKIG DYEIVYKNGT KEAKAIHVHR DSRLOVHDT TIYVGBSWEP EXNFVSATDK
 TGQDVPE

EF105-1 (SEQ ID NO:405)

TAAATGAAAA AAACAGTCGT CTACTCCTTS TTATTCGSA CAATGTTGNT TGGCGCCACT
 GTTCCTGCTG AAGCGGCGAC GGTCGTTTTT GATAGCGAAC AGTCGATTNT TTTTACCCCA
 AGCACAGATG GGACGGATCC AGTAAATCA GAAAATCCCG ATCCAGAAAA ACCAGTTTCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGTCGATC CAACGAATCC TGATGGAAT AATCGAGTA CCCCTGATTC ACTTTCCATC
 GATTATGCCT CAAGTTTGGA TTTTGGGAGT AATGAGATAT CGAATAAGSA TCAAAACGTAT
 TTTGCCAGAG CGCAAACCTA TAGAAATCCA GATGGTTCAG CAAGTGAAAT GGCACCTGCT
 AATTATGTAC AAGTAAGTGA TTTAAGSASA ACCAATGCTG GCTGGGTTT AAAAAGTAAA
 CAAAATGCTC AATTTCGTAA TGACAGAAAC TTACACAAA3 AATTAAAG33 GGCACCGTC
 GCCTTTACTG AGCCCAGTGT TGGTCAAAAT GCGACGAGC TATTGCGG33 AATTGCTACC
 GCAAACATTC AATTAGATGC TGGGGGGGCA GAAAGTGT3 TCATGCAAG3 CCGAGAAAAG
 ACCGGCGGCC GAACGTGGAT CAGGTGTG33 GCGCAAGCAG AAAAAGT3AC CCAAAAAAAT
 CAACAAGGAC AGCAAGTAAA TGACACAATC ACACGGGCAA TCTCACTAAC TGTTCCTGGG
 AAAACCCCTA AGGATGCAGT ACAATTTAAA ACAACATTC CTTGGGCTAT TTAATGTGA
 CCAGTAAATA ATGGAGGGAA ATAA

EF105-2 (SEQ ID NO:406)

MKKTVVYSL FGTMLLGATV PAAATVYFD SEQSIIVFTS TDGTDVNPPE NPDPEKPVVP
 VDPTNPDPNP PSTPGPLSID YASLDFGSN EISNKDQTYF ARAQTYRNPD GSASELATAN
 YVQVSDLRGT NAGWVLKVQK NGQFRNAETL HKELTGATVA FTEPSVRSNA TDVLPPTATA
 NIQLDAAGAE TVVMQAPEKT GAGTWITLWG QAEKVTEKNQ QGQVNAITIT RAISLTVPGK
 TPKDAVQYKT TLTWLLSDVP VNXGGH

EF105-3 (SEQ ID NO:407)

GGCGAC GGTCGTTTTT GATAGGGAAC AGTCGATTGT TTTTACCCCA
 AGCACAGATG GGACGGATCC AGTAAATCCA GAAATCCCG ATCCAGAAAA ACCASTTCGA
 CCAGTCGATC CAACGAATCC TGATGGAATC AATCGAGTA CCCCTGATTC ACTTTCCATC
 GATTATGCCT CAAGTTTGGA TTTTGGGAGT AATGAGATAT CGAATAAGSA TCAAAACGTAT
 TTTGCCAGAG CGCAAACCTA TAGAAATCCA GATGGTTCAG CAAGTGAAAT GGCACCTGCT
 AATTATGTAC AAGTAAGTGA TTTAAGGGGA ACCAATGCTG GCTGGGTTT AAAAAGTAAA
 CAAAATGCTC AATTTCGTAA TGACAGAAAC TTACACAAA3 AATTAAAG33 GGCACCGTC
 GCCTTTACTG AGCCCAGTGT TGGTCAAAAT GCGACGAGC TATTGCGG33 AATTGCTACC
 GCAAACATTC AATTAGATGC TGGGGGGGCA GAAAGTGT3 TCATGCAAG3 CCGAGAAAAG
 ACCGGCGGCC GAACGTGGAT CAGGTGTG33 GCGCAAGCAG AAAAAGT3AC CCAAAAAAAT
 CAACAAGGAC AGCAAGTAAA TGACACAATC ACACGGGCAA TCTCACTAAC TGTTCCTGGG
 AAAACCCCTA AGGATGCAGT AC

EF105-4 (SEQ ID NO:408)

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 VDPTNPDPNP PSTPGPLSID YASLDFGSN EISNKDQTYF ARAQTYRNPD GSASELATAN
 YVQVSDLRGT NAGWVLKVQK NGQFRNAETL HKELTGATVA FTEPSVRSNA TDVLPPTATA
 NIQLDAAGAE TVVMQAPEKT GAGTWITLWG QAEKVTEKNQ QGQVNAITIT RAISLTVPGK
 TPKDAV

EF106-1 (SEQ ID NO:409)

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 AATCCCAATA ATTTAGGGGA TTTACCTGAG TATTTACGTT CAGTTGCTAT TAGACAAGAT
 GAAGGATTAT CAGAAAAAGA TTGGGCTGGA ACACGCGTTT ATGATCGAAA TGGGAATGAC
 TTAACAGATG AAAATCAAAA CCTATTACAT GCAATCAAAAT TTGATGTAAC CACTAGTTTC
 TATGAATTTT TTGATAAAGA GACT3GAGAA TCAACAGGAG ATGAAGSAAC CTTCTTTATG
 ACCGCTGGTA TTACAGATGT TTCCGCTGTT GTAATTTATTT CTGAAA33AA AAATTATCAA
 GGTGTATACC CACTTAGAAC TTTATACCAA GATACTTTTA CGTATAGACA GATGGGGAAA
 GATAAAAACG GAAATGATAT TGAAGTTTTC GTAGAAAACA AAGCAACCTC AGGACAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TATGGTCGTC CGCAGCCATA CCCCATAAT CGTCCCAGAA CACTAGAATT CACGAATGGA
 CGCCGTGCCA TGACAGAACA AACAGGCCAG ATTGATGTAA ATCGACAAGG GGATGAAATT
 ATTGGTAAAA CTTCCTTTGA TGGGACACCG CAACTTCTTT GGAATGGGAC AAAAGTAGTG
 GATAAAGATG GCAATGACGT AACTTCGBCG AACCAAACT TTATCAGCTT AGCGAAATTT
 GACCAAGATA GCAGCAAATA TGAATTTTTC AATTTACAAA CTGGTGAAC TCCTGGCGAC
 TATGGCTACT TTAAAGTAGG AAATCAAAAT AAATTCCGTG CCCATGTTTC CATTGGAACC
 AATCGCTATG GCGCTGTCTT AGAGTTAACA GAATTGAATG ATAATCGTTT TACGTACACA
 CGAATGGGTA AAGATAACGA AGGAAACGAT ATCCAAGTCT ATGTGGAACA TGAACCATAC
 CAAGGAACCT TTAATCTGA ATTTACCTTT TAA

EF106-2 (SEQ ID NO:410)

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 GLSEKDWAGT RVYDRNGNDL TDENQNLHA IKFDATTSFY EFPDKETGES TGDEGTFMT
 AGITDVSRV IISSETKNYQG VYPLRTLYQD TFTYRQMGKD KNGNDIEFV ENKATSGPVY
 GRPQYPNNR PRTLEFTNGR RAMTEQTGQI DVNRQGDIEI GKTSFDGTPQ LLWNGTKVVD
 KDGNDVTSAN QNFISLAKFD QDSSKYEFPN LQTGETRGDY GYFKVGNQNK FRAHVSIGTN
 RYGAVLELTE LNDNRFTYTR MGKDNENNDI QVYVEHEPYQ GTFNPEFTF

EF106-3 (SEQ ID NO:411)

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 TTAACAGATG AAAATCAAAA CCTATTACAT GCAATCAAAT TTGATGAAAC CACTAGTTTC
 TATGAATTTT TTGATAAAGA GACTGAGAAA TCAACAGGAG ATGAAGGAAC CTTCTTTATG
 ACCGCTGGTA TTACAGATGT TTCCCGTCTT GTAATTATTT CTGAAACCAA AAATTATCAA
 GGTGTATACC CACTTAGAAC TTTATACCAA GATACTTTTA CGTATAGACA GATGGGGAAA
 GATAAAAACG GAAATGATAT TGAAGTTTTC GTAGAAAACA AAGCAACCTC AGGACCAGTT
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 ATTGGTAAAA CTTCCTTTGA TGGGACACCG CAACTTCTTT GGAATGGGAC AAAAGTAGTG
 GATAAAGATG GCAATGACGT AACTTCGBCG AACCAAACT TTATCAGCTT AGCGAAATTT
 GACCAAGATA GCAGCAAATA TGAATTTTTC AATTTACAAA CTGGTGAAC TCCTGGCGAC
 TATGGCTACT TTAAAGTAGG AAATCAAAAT AAATTCCGTG CCCATGTTTC CATTGGAACC
 AATCGCTATG GCGCTGTCTT AGAGTTAACA GAATTGAATG ATAATCGTTT TACGTACACA
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EF106-4 (SEQ ID NO:412)

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 GLSEKDWAGT RVYDRNGNDL TDENQNLHA IKFDATTSFY EFPDKETGES TGDEGTFMT
 AGITDVSRV IISSETKNYQG VYPLRTLYQD TFTYRQMGKD KNGNDIEFV ENKATSGPVY
 GRPQYPNNR PRTLEFTNGR RAMTEQTGQI DVNRQGDIEI GKTSFDGTPQ LLWNGTKVVD
 KDGNDVTSAN QNFISLAKFD QDSSKYEFPN LQTGETRGDY GYFKVGNQNK FRAHVSIGTN
 RYGAVLELTE LNDNRFTYTR MGKDNENNDI QVYVEHEPYQ GT

EF107-1 (SEQ ID NO:413)

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 CTTTATAGAG ACTATAGATT GAATTTTAC ATAGAAAGAA GGAGCAAGAT GAAGCGAGTA
 AATTGAAAA GATGGCTAGT TGTGGGTTA AGTTGTTCTT TGTTCATGTA TTCAGTGGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GGTGTGACTG TGTTAGGDBA AACGATTACT GGGGGGACCG AGCAAGGANN ASCAACATCT
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BAAAAAATGC CCAATAAGCTT GAGTTTTGCT CCAAAAAABA CGTTTAAATA TACBGTAGCT
ACGGCACACG GAGGCGTTAT CTATGGBCTG ACCTATTTTT ATGGAGATCT CGGCBCTCCA
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ACGCAGGATA AGAAAACCAT TGTAAACABGB GAGGATTTTA CTTTTATGTA ABAABBCACC
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ACTCGCAACC CTTATTTACG CCTGAATACT AGCCAAGCBA ATTGGAGTTT AACG3CCCAG
CTATCGCAAC CAAAATCAGC CACAGACAGC TTGCCAACA CGACCCGCTT GTTGGTAGGA
ACGGCCGCTG CTGCCAGCTT TACCGATTAC AACCAACCAA CAGAAACGAG GACACCACTT
GGCAAGACCA GCACCGTGAC TTTAACCGCC GACAATACCB CAACAGGCBT GGTGCAAAAC
CAACAGTTCA CAGGCAGTGA CGTCTATCAG TTGGACTTCA CGTTTGCTAA CATCAAACTA
GAAGTGCCAG CCAACCAAGG TATGGCTGGC CAACAATAAC AAGCCGCGCT CACGTGGAAT
TTAGTGACTG GCCCCTAA

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EF107-2 (SEQ ID NO:414)

MKRVN

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SEAKTVPPQE TARIASRAIG YSSVEGREIP FFFVEEDGTL FDPDRITMAN NLSTFSFYEE

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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QDKKTIIVTGE	DFTFTQEGTL	PERYTGSDGK	TYLFKGWYFG	NAKPSTLETP	KTPSYAVTYD
DNDDLHVVE	EAVMKTYTLP	AREALFGYVD	EQCNLINPAK	FKLSATMGES	DGATGEMTTF
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DKTKYPVPNE	VRRGIENPDN	IVSSLVGXXA	YNLTQKSATR	YTARRSYWXW	GPTKTLYSMS
IYSGTAGGNY	NLSTPDGTIY	YYLENRRVTE	HFVDESGAHI	TPPTGFTQSH	QLVVDSENVV
YTVAKALPKI	YQAGEKTYIF	CGWFKGKTKP	ATLKTTTTTFS	FTPTFNEDEDD	MTAVYQEAIP
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GQNTKAFPVT	KEQWTTGAGV	SITLDQPLPA	GGQLKMNLLG	TAVTGNPSQV	LTADVEVTGN
FGSLTAKDTV	RIKDLDQEIT	SPDGDGFIST	PTDFGKLAI	SGSKQQTSLK	KAADYYGNGT
RNPYLRLNTS	QANWSLTAQL	SQPKSATDSL	PTTTRLLLCT	AAAASFSDYN	QPTETRTPLG
KTSTVTLTAD	NTATAVVANQ	QFTGSDVYQL	DFTFANIKIE	VPANQGHAGQ	QYQAAVTWNL
VTGP					

EF107-3 (SEQ ID NO:415)

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GGTTATTCTT	CTGTGGAAGG	GCGCGAGATT	CCCTTTTTCT	TTGTGDSASA	AGACGGGACG
TTGTTTGATC	CCGACCGAAT	TACGATGGCG	GTCAATCTTT	CCACGTTTTC	GTTTTATGAA
GAGAAATTAC	AACGAACCCC	CCTTGAGCCC	ACCACTGTGA	ATGGCGGAAA	GTTACTGTCT
ATTCCAACGT	CACCAGCTTT	TAAATATGAT	ACAAATAACC	AGAATCCGAG	TAATATTAT
GGCGTTTCTG	AAGTGTCGTT	TACTATTCCCT	AAGGAGTATC	AAAGCCTGSA	CATTTCGACCA
AGTACGTTTT	ATACAGGAGA	CACTACGCAA	TATCCAGTGC	CAACGGTTTT	TGCGAACGTT
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GAAAAAATGC	CCAATAAGCT	GACGTTTGGT	CCTAAAAAGA	CGTTTAAATA	TACGGTAGCT
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CGTGTACCGG	AAAAATTTGA	GAATCCCGCA	GGCGGGGCGA	TTCTTGCGGC	AGAAGGTTAT
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GATGACAATG	ACGATTTGCA	TGTGGTCTAT	GAAGAAGCAG	TGATGAAAAC	CTATACGTTG
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TTTCCCACAA	TTGATGGAAT	CGATATGCCA	GCAAGTCAAT	TAAAGAAATT	AGCCATCCCG
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GGGGATAAAA	CCAAGTATCC	AGTACCAAAT	GAAGTGCGCC	GTGGCATGSA	AAACCCCGAC
AACATTGTTA	GTAGTTTAGT	GGGAANCNCT	GCGTATAAAT	TGACCCGAAA	AAGTGCCACA
CGCTATACTG	CCCGCCGTTT	TTACTGGANG	TGGGGCCCCA	CGAAGAACTT	TTACTCAATG
AGTATCTATT	CAGGAACTGC	TGGGGGCAAC	TATAATTTAT	CGACCGCTSA	TGGCACCATT
TATTATTACT	TAGAAAATCG	GCGGGTCACT	GAACATTTTG	TAGACGAAAG	TGGCGCAAAA
ATCACGCCAC	CAACTGGCTT	TACACAAGGA	AATCAGCTAG	TGGTGGACAG	TGAAAACATAT
GTCTACACTG	TCGCAAAAGC	TTTGCCGAAG	ATCTACCAAG	CTGGTGAAAA	AACCTATATC
TTCCAAGGCT	GGTTTAAAGG	CAAAACCAAG	CCAGCAACAT	TAAAGAGGAC	AACGACCCCA
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CCCACCGCGG	AACCTAACGTT	AACAGGTGCC	GTTGACATAA	TCGAAAATGG	CGCCACAATG
GATTACTGGG	AGGCGCTACT	GAAGAACACA	GGCGAAGGBC	CGTTAAACAC	CATTAAAAATC
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ACGGGTCAAA	ACACCAAAGC	TTTTCTGTCT	ACCAAAGAAC	AATGGACGAC	CGGTGCAGGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGTCTATCA CBTGGATCA GCCTTTACCA GCTGGGGGTC AATTAAATAT GAATTATTA
 GGAACGGCCG TTACAGGAAA TCCTGGTCAA GTTWTAAACC CTGATCTTGA AGTAACGGGC
 AACTTTGGCA GTTTAACTBC CAAAGATAGC GTTCTATTA AAGACTTTGA TCAAGAAATT
 ACGASTCCTG ACGGCGACCG CTTTATTATG ACCGCGACAT TTGATTTTGG TAAGCTAGCA
 ATTTGAGGAA GTAAGCAACA ATATGCTTGG AAGAAGCGCG CAGATTCTA CGGCAATGGC
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 CTATGCAAC CAAAATCAGC CACAGACAGC TTGCAACAAA CGACCCCTTT CTTGCTAGGA
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 GGCAAGAGCA GCACCGTAGT TTTAAGCGCG GACAATAGCG CAACAGCGGT CGTGGCAAAAC
 CAACAGTTCA CAGGCGAGTA CGTCTATCAG TTGCACTTCA CGTTTCTTAA CATCAAACTA
 GAAGTCCAG CCAACCAAGG TATGCTGCGT CAACAATAGT AAGCGCGGT CACGTGGAAT
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EF107-4 (SEQ ID NO:416)

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 TFYTGDTTQY PVFTVFANVG GKVTNIVGAN AETELTLNE KMPNKLTEGP FKTFPKYTVAT
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 VTGP

EF108-1 (SEQ ID NO:417)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 ATCACTGCAC CAACAGGCTT CACCCAGGT AACCAAGTAC CAATGAAGAG TAACACCTTC
 AAGTACACAG CCGCAAAAGC TTTACCAGCG ACGTATACTA CAGGTGGCAA ACTCTATACG
 TTCCAAGGGT GGTATAAAGG GAAAACCAAG CCAAGTACGT TGAACAAAAC AACAACTCCA
 ACGTTCAATG CGACCTTTGA TGGCAATGAC GATATGACCG CCATGTATAA GGAAGAAATA
 CCAACAGCTA GTGTACATT AACTCCACCA AAAGAAGTGA TTGATAGTAA TACCAATGTA
 ATCTGGACAA CAACGATCAC GAATACTAGC AAAGCACCTT TACAAAATCT CACCTTGAAA
 AAAGGGCCCC ATTGCTCAGC TGGTCTGACG ATCCCGACCT TTATGGAGCT GATACCAGAA
 GGAGAAACGA CAAAATCAAT CCCAGTAAAT AGTACACTTT GGACAGAGGG GGTTCCTTTA
 CCAAATGCCG TTCCTATCGG CAAAAAGTT TCAGTTGCTT TCACAACTCC CGCAACAGGG
 AAACCAACA CTGTTTGAAG AGCAGAAGTT GTAGTATTTG GTGGTATTAAG AGATAGTACA
 GTGGATAACT TCGTGAGAAT TCGTCCAAAT GATCAAGAA TAGTCACACC AACGACCGAA
 GGCTTCATCA GTGTGCCAAC CTTGCACTTC GGCCAAGTGG GCGTTGCAGG AACTAAGCAA
 CAACACAGCT TGAACAAGC CGCGGATTAC TACGGTAACG GCACACGAAA TCCGTATCTG
 CGGATTAAGA AAACGCAACC CAATTGGAGC TTAACAGCCC AACTGTCACA ACCAAAATCA
 GCGACAGACA GCTTGCCTAC AGCGACCCGC TTATTATTAG GGGCGGCGCC TGTCTCTAGC
 TTTACCAATT ACAATCAACC AACCGAGTTG AAAAATACCG TCGGTACCAAG GAGTGCCATT
 AGCTTAACAG CCAACAACAC AGCAACAGAG ATTATTGCCA ACAAGCAAT CACAGGTAGT
 AATGTTTATC AGTTGGACTT CACCTTCAAT AATGTCAAAC TTGAAGTCC AGCCAATCAA
 GGTGTTAAAG GGCAACAATA CAAGGTCGCA GTTACATGGA ACCTAGTAC AGGTCTTAA

EF108-2 (SEQ ID NO:418)

MKQTKWQ RLATIGLCSS LVINAFSGVT AVAETVTIES SPTAESSAKF
 ETQASSVKEE TTKASTENSQ VTTDTSQEEA TKEAEKEEPQ AEVEQAETPI IKPKKINMK
 ATYSFSAETY QFGFVNESGQ LINPIIPIT YSYAKGSWFT DGYNRKNTSM VQGSASTVGN
 LKNVIMPATS VVMPPGPSYE GTQEVYTNFS IRIPKYYASA SLYNREGHID STYPLPAIAL
 AGTRPLSLTQ SSVISALALT SKGENVYTPR ETFFGGDPAG VKFTNFLERI NDFDVKGNNI
 GYKTVSSPIY YHLTNRRVTE NFVDTSGAKI TPPSNFTQSK QTVINSIDYT FQSGFLPET

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YKVGTKSYRF KGWYKSKTKT EPLATYKTPS YKNTYDLNND LTAAYEY ES VELPASTNQF
 GFVDEATNKL IAPDQVQMKY NLTLNENRKK TMSSNLNNT STATLKN SV FNNYFEQYRV
 NTFYGAQDIT FTLPKRYKSI NITFPLSKTE PAFPLPYIT IDQNEK SMP NTTYNKLKQL
 SGQTFGFNAL ADQPEFYTKT LFGTESGIDD PNYNYTMSPP WYYYLEN HW TENFVDTNGA
 KITPPTGFTQ GKKTIVITSDA YTFHJASTLP DTYTTGGHLY KFKGWTY KX IDNTLTTTKA
 PSYQVITYDDN TDLNAYEIEE TTTTTFPSND MNFVNEKUSA FTPALTFNKK NYAQSTSAYL
 RTDLYDVTSK NNGNGQYTVS INNGSMPLSQ ELLKKYVINEQ PISATNKLQF HWOKLAIDQQ
 LKYVDSIQLD TAQSSNLKSY RYTYTNNSL VFDPNVAFAB NDLSSSEKXL LNFDSDGTYF
 SMANNRLFYT HLGYSSTPGV NYLLNMFLEN AKPADKSKLV YKVTRKITE NFMDVNGAKI
 TAPTGTFTQN QVPMNSNTFK YTAAKALPAT YTTGGKNTTF QGWYKSKTKP STLNKTTTPT
 FNATFD3NDD MTAMYKEEIP TASVTLTRPK EVIDTNTNFI WTTTITNTSK APLQNLTLKK
 GPNWSAGLTI PTFMEVTPFG ETTHSIPVNS TLWTEGVPIF NAVPIGHTYS VAFTRATRGK
 PNTVLKAEVU VFGGIKDSV DNFVRIKPNQ QEVVTPPTES FISVPTDFEG QVGVAGTKQQ
 HSLKQAAHY GNGTRNPYLK IKHTQPNWSL TAQLSQPKFA TDSLPTATFL LLGAAPVSSF
 TNYNQPTCLK NTVGTTSAIS LTAINTATSI IANKQETGSH WYQLDFEEN EKLEVPANQG
 VKGQQYKAAV TWNLVGTG

EF108-3 (SEQ ID NO:419)

CGT GACGATTGAA AGTAGTCCGA CCGCGGAAAG TAGTSCCAAG
 GAAGAGACGC AAGCAAGTAG CGTCAAGGAA GAAACAACCA AAGCCATAC GGAAAAATAGT
 CAAGTAACAA CTGACACGAG TCAUGAAGAA GCAACGAAAG AAGCGGAAA AGAAGAACCG
 CAAGCAGAAG TGAACAAGC AGAAACAACA ATCATTCCTA AACCAAAATA AATCAATATG
 AAGGCAACTT ATTCATTTTC TGCAGAAAT TATCAGTTG GATTTGTA TGAATCAGGT
 CAATTAATAA ATCCAGATAT TATACCAATT ACGTATAGCT ATGCCAAGG ATCATGGAAG
 ACAGATGGTT ATAATCGAAA GTGGACTAGT ATGGTTCAAG CGAGTGTTC AACCGTAGGA
 AACTTAAAGA ATGTAATAAT GCAAGCAACT TCTGTAGTCA TGCCACGAGG AAGGTTCATAT
 GAAGGAACCT AAGAGGTGTA CAGAAACTTT TCAATTGCA TACCAAAATA TTATGCATCA
 GCGAGTCTCT ACAATAGAGA AGATAAAAT GATTCTATCT ATCCGTGAGG TGTATATGCA
 CTAGCAGGTA CTAGACCGCT ATTTTTGAAT CAAAGTATG TAATTAGGAT ATTGCGCGCTG
 ACCAGTAAAG GAGACAATGT TTATACACCA CGGGAACAT TTTTTCGAGG AGATCCTGCA
 GGTGTAAAGT TACTAATTT TTTTATCTGT ATAAATGACT TTGATGTAAA AGTAATAAC
 ATAGGTTATA AGACTGTGAG TATCCCAATC TATTACCATC TGACCAAGCG GGTGTGTCAC
 GAAAACTTCG TAGATACAAG TGCGGCCAAA ATCACGCAAC CAAGTAAATT CACCCAGGG
 AAACAAACGG TCATTAACAG TGATCCTTAC ACGTTCDAAC AAAGTGCTTT TTTACCCGAG
 ACCTACAAAG TTGGCACGAA ATCTTACCGA TTCAAAGGCT GGTACAAAGG GAAAACCAAA
 ACCGAGCCTT TGGCCACCAC TAAAACACCT AGCTATAAAG TCACGTATBA TACAAATGAT
 GATTTGACGG TGTCTATGA GGAATTTTCA GGGTACGAGC TGCCTGTCTC GACCAATCAA
 TTTGGCTTTG TGGATGAAGC GACGAACAAA TTAATTGCTC CCGACCAATG GCAGATGAAG
 TATAATCTTA CTTTAAATGA AAATAATAAA AAAACAGTAA TGAGCACTAA CTTAACGGGG
 ACAGATACAG CGACACTGAA AAATTTCTCC CTGCCTGTCA ACTATTCTBA ACAATATCGC
 GTCAATACGT TTTATGGCGC GAGTBAATTT ACGTTTADAT TGCCCAAGCG GTACAAATCA
 ATCAATATTA CCAAAATCAGA TGGCAAAACG GACCCAGGTT TTCTCTCTCC TAAAATCTAT
 AATATAGATC AAGTAGAAAT GTCADATATG CCTGTGACTA CTTATAAGAA GTTGAAACAG
 CTGTGCGGCC AAACGTTTGG CTTTAATGCT TTAGCCGATC AACCTGAATT TTATACGAAA
 ACGTTATTTG GGACAGAGTC TGGATATGAT GACCCAGTCA ATTATTATAC AATAGTGGC
 CCTGTTTACT ATTATTTAGA AAATCGCAAA GTCACCGAGA ACTTCGTAGA CACCAACGGC
 GCTAAATCA CACCGCCAAC AGSTTTCAAC CAAGGTAAAA AAACGGTAT TACAAGCGAC
 GCCTACACTT TCAACAAGC AGGCACCTTA CCAGACACTT ACACAAGAGG CGTAAGACC
 TACAAGTTCA AAGGTTGGTA CAAAAGCAAG TCCATAGTCA ACACATTCAC AACTACCAAA
 GCGCCAAGTT ATCAAGTGAC CTACATGAC AATGATGATT TGAATGTGCT GTATGAAGAA
 GAAACAGTTA CGACAGTGTA TCCATCAGTC GATATGAAT TTGTGAATBA AAAAGCGGG
 GCTTTACAC CCGCGTTAAC TTTTAGTGCT AAGTACTATG CGCAAAGTAC GAGTGGGTAC
 TTAAGAACCG ATTTATATGA CGTBACTCA AAAAATAATG GTAATGACCA ATATACGGTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AGTATTAATA ATGGTAGTAT GGCATTGTCC CAAGAATTAT TGAAAAATA TAATAATGGA
CAACCAATCA GTGCTACCAA CAGATTACAG TTTAATGTTG ATAAATAGC CATCGACCAA
CAACTAAAT ATGTTGACAG CATTGAATTA GACACAGCTC AAAGTAGCAA TGTGAAATCC
TATAGATATG TGTACACGAA CAATAGATCA CTGTTTTCG ACCCAATGT AGSACCAGCA
GAGGTTGACC TTAGTTCAGA ATCTTTTAACT TTGCTTAATT TTGATTGAA TGSCACCTAT
TTTTCTAATG CAAATAATAG ACTTTTCTAC ACGCATTTAG GATATAATG CACACCAGGA
GTTAACTATC TTCTCGTAAT GTTTCTTTT AACGCCAAAC CTGCCGATAA GTCAAAACCTT
GTCTACAAAG TCACTCGCAA ACAAGTCACC GAAAACCTG TGGATGTCAA CGSTGCCAAA
ATCACTGCAC CAACAGGCTT CACCTAAGGT AACCAAGTAC CAATGACAA TAACACCTTC
AAGTACACAG CGGCAAAAGC TTTACGACG ACGTATACTA CAGGTGTCAA AGTCTATACG
TTCCAAGGGT GGTATAAAGG GAAAACCAAG CCAAGTACCT TGAACAAAC AACAACTCCA
ACGTTCAATG CGACCTTTGA TGSCAAATGAC GATATGACCG CCATGTATTA GSAAGAAATA
CCAACAGCTA GTGTCACATT AACTGACCA AAAGAAGTCA TTGATAGCA TACCAATGTA
ATCTGGACAA CAACGATCAC GAATACATAG AAAGCACCTT TACAAATGT CACCTTGAAA
AAAGGGCCCA TTTGGTCAGC TGCTCTGACG ATCCCGACCT TTATGCAAT GACACCAGAA
GGAGAAACGA CAAAATCAAT CCCAGTAAAT AGTACACTT GGACAGAGG GTTCTCTTTA
CCAAATGCCG TTCCTATCGG CAAAAAAGTT TCAGTTGCTT TCACAAATG CGCAACAGGG
AAACCAACA CTGTTTTGAA AGCAGAGTT GTAGTATTT GTGGTATTA AGATAGTACA
GTGGATAACT TCGTGAGAAT TGCTCTAAT GATCAAGAAG TAGTCAACG AACGACCGAA
GGCTTCATCA GTGTGCCAAC CTTCGACTTC GGCCAAGTGG GCGTTCCAGG AACTAAGCAA
CAACACAGCT TGAAACAAGC CGCTGATTAC TACGGTAAAG GCACACGAA TCCGTATCTG
CGGATTAAGA AAACGCAACC CAATTGAGC TTAACAGCAG AACTGTACA ACCAAATCA
CGCAGACACA GCTTGCCCTAC AGCTGACCG TTATTATTAG GGGCGGCGCT TGTCTATAGC
TTTACCAATT ACAATCAACC AACCGAGTTG AAAAATACGG TCGGTATCAC GAGTGCCATT
AGCTTAACAG CCAACAACAC AGTAAGAGT ATTATTGCA ACAAGCAAT CACAGGTAGT
AATGTTTATC AGTTGGACTT CAGCTTAAAT AATGTCAAAC TTGAAGTGG AGCCAATCAA
GGTGTTAAAG GGCAACAATA CAAGCTCGCA GTTACATGCA ACCTAGTAC AG

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EF108-4 (SEQ ID NO:420)

VTIES SPTAESSAKE

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ETQASSVKEE TTKASTENSQ VTTEISPEEA TKEAEKEEFQ AEVEQAETFI IPKPKKINMK
ATYSFSAETY QPGFVNESGQ LINFDIIPIT YSYAKGSWKT DGYNRFWTSM VQGSASTVGN
LKNVIMPATS VMPPPGPSYE GTQEVYTNFS IRIPKYYASA SLYNREKID STYPLPAIAL
AGTRPLSLTQ SSVISALALT SPQDNVYTPR ETFFGGDFAG VKFTNELYFI NDFDVKGNNI
GYKTVSSPIY YHLTNRRVTE NEVETSSAKI TTPSNFTGCK QTVINSTPYT FQQSGFLPET
YKVGTKSYRF KGWYKGKTKT EFLATFTTPS YKVTYDDNDD LTVVYENFEG YELPASTNQF
GFVDEATNKL IAPDQVQMKY NTLNENENKK TVMSSNLGCT DTATLNLNLSV PVNYFEQYRV
NTFYGASDIT FTLPKRYKSI NITKSLGKTD PAFPLPKLYN IDQVENHMP VTTYNKLKQL
SGQTFGFNAL ADQPEFYTKT LFGTESGIDD PVNYYTMSGP VYYYLENHFKV TENFVDTNGA
KITPPTGFTQ GKKTIVITSDA YTFPQAGTLP DTYTTGGFTY KFKGWYFGKS ILNTLTITKA
PSYQVYDDN DDLNVVYEEE TWTTVYFVSD MNFVNEKGGG FTPALTFSGK YYAQST SAYL
RTDLYDVTSK NNGNGQYTVS INNGEMFLSQ ELLKKYNIGQ PISATIELQF NVDKLAIDQQ
LK YVDSIQLD TAQSSNLKSY RMVYTHNSSL VFDPNVAFAE VDLSSERLNL LNFDSDGTYF
SNANNRLFYT HLGYSCTPGV NYLLVMFLFN AKPADKSLV YKVTRKQTE NEVDVNGAKI
TAPTGTQGN QVPMNSNTFK YTAALFALPAT YTTGGKVYTF QGWYKGHTFP STLNKTITPT
FNATFDGND MTAMYKEEIP TASVILTRPK EVIDNTNVI WTTTITNTSK APLQNLTLKK
GPNWSAGLTI PTFMEVTPG ETTKSIPVNS TLWTEGVFLP NAVPIGIVS VAFTRATGK
PNTVLAKEVV VFGGIKSTV DIFVEIRPND QEVVTPTEG FISVPTLPG QVGVAGTKQQ
HSLKQAADYY GNGTRNPYLR IFKTPNWSL TAQLSQPFSA TDSLPTATL LLGAAPVSSF
TNYNQPTLTK NTVGTTS AIS LTANNATSI IANKQFTGSN VYQLDPTENN VFLEVPANQG
VKGQQYKAAV TWNLVT

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EF109-1 (SEQ ID NO:421)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

AGGAGTAAAT TAATGAAAAA AACTTTTATA ACTAGTTTAA TGTAG AGT TTTGTTGTCTG
 GGATTTCTCG TTACCCCTAT TTTTCTTAC GCTTTTGAAC CCTCTATGG AACTACTGAA
 GAAACGGTGG CTTGAGAAAC ATCTTTAAGG GAGCGACAAA TGAGTATGG TGTCACTGAA
 GAAATGAACC CAAGCATCAT AAATTCTCAA GAGGAAACAG AAACAA CTC CACTTCTCA
 ACCTCCGATT CCACCACTGA ACTTTTACA TCAGAACTAA CAACTCTTAA TCATACAGAA
 NATAGTAGGG AGTACTGAA ACTATTTTGG NAACATCAAT AAGTAA AG GACACACCTA
 TAG

EF109-2 (SEQ ID NO:422)

MKKSVI TSSMLAVLLS GFLVTPISAY ALERSKOTTE ETVAGETSLT ERQMSGGVTE
 EMNPSIINSQ EETETTSTSS TSDSTTEVST SEVTTTNTTE KSSDVLKLDV KHHXVMRTHL

EF109-3 (SEQ ID NO:423)

GGAAC GCTCTAAGGG AACTACTGAA
 GAAACGGTGG CTTGAGAAAC ATCTTTAAGG GAGCGACAAA TGAGTATGG TGTCACTGAA
 GAAATGAACC CAAGCATCAT AAATTCTCAA GAGGAAACAG AAACAA CTC CACTTCTCA
 ACCTCCGATT CCACCACTGA ACTTTTACA TCAG

EF109-4 (SEQ ID NO:424)

ERSFGTTE ETVAGETSLT ERQMSGGVTE EMNPSIINSQ EETETTSTSS TSDSTTEVST S

EF110-1 (SEQ ID NO:425)

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 AATGCAGAAG AGTATATCGT TCCTTCCGAA AGTCATTAC GACAAAAAAG ATCGTTACTG
 GACCCGTAGG ACAGAAGACA AGAAGTGGCA GATACAACGG AAGCGCTTT TCGGTCAATC
 GGAAGAATCA TTTCCCCTGC CAGTAACCA GGCTATATTT CTTTAGAAC ABCTTTGTT
 GTTGAACCA ATACAATTGT CAGCAATAAT CATGTGGGCG AAAGTTTAA GAATGCCAAA
 GTATTAAATC CGAATGCCAA AGATGATGCT TGGTTTATC CAGGTCCAGA TCGAGTGCG
 ACACCATTTG GCAAATTCAA AGTGATGAT GTAGCTTTT CCCCAGATGC CATATTGCG
 GTAGTGACTG TCGGCAAAACA AAACGATCGT CCAGATGGCC CAGAGTGGG AAAAAATTTA
 ACGCCATTTG TTTTGAAAAA GTTTGAATCT TCAGATACCC ATGTCAAAAT ATCAGGCTAT
 CCAGGTGAGA AAAACACAC ABAATGCTCT CATGAAAATG ATTTGTTTAC ATCTAATTTT
 ACAGACTTAG AAAATCCATT ACTATTTTAT GATATGATA CAACCGGCG TCAATCTGGT
 TCACCAATCT ATAATGATCA GGTGAAAGTA GTTGGTGTTC ATTCCAAAGG CCGCATTAAG
 CAAACAGGAA ATCATGGTCA AAGACTAAAT GAAGTGAATT ATAATTAT TGTTAATCGA
 GTGAATGAAG AAGAAAAATA AGTTTATCC GCTGTGCGAG CAGCGTAA

EF110-2 (SEQ ID NO:426)

MKKFSIRKIS AGFLFLILVT LIAGFSLSAN AEEYIVPAES HSRQKRLLD
 PEDRRQEVAD TTEAPFASIG RIISPASKPG YISLGTGFV GTNTIVTINH VAESPKNKV
 LNPNAKDDAW FYPGRGSAT PFGKFVIDV AFSPNADIAV VTVGKQDRP DGPGLGEILT
 PFVLKFFESS DTHVTISGYP GEKNHTQWSH ENDLFTSNFT DLENPLFYD IDTTGGQSGS
 PIYNDQVEVV GVHSNGGIQ TGNHGRLLNE VINYNFIVNEV NEEENKLSA VPAA

EF110-3 (SEQ ID NO:427)

AG AGTATATCGT TCCTGCCGAA AGTCATTAC GACAAAAAAG ATCTTACTG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GACCCTGAGG ACAGAAGACA AGAAGTGGCA GATACAACCG AAGCGCCTTT TGGCTCAATC
 GGAAGAATCA TTTCCTCTGC CAGTAAACCA GGCTATATTT CTTTAGCAAC AGGCTTTGTT
 GTTGGAACCA ATACAATTGT CACCAATAAT CATGTGGCTG AAAGTTTAA GAATGCCAAA
 GTATTAAATC CGAATGCCAA AGATGATGCT TGGTTTTAT CAGGTGAGAG TGGCAGTGCG
 ACACCATTTG GCAAAATCAA AGTGATGAT GTAGCTTTT CCCCGAATGC GATATTGCG
 GTAGTGACTG TCGGCAAACA AAAGGATGCT CCAGATGGCT CAGAGTTGGG AAAAAATTTTA
 ACGCCATTTG TTTTGAAAAA GTTTGATCT TCAGATACCG ATGTCACAAT ATCAGGCTAT
 CCAGGTGAGA AAAACCACAC ACAATGCTCT CATGAAATG ATTTGTTTAC ATCTAACTTT
 ACAGACTTAG AAAATCCATT ACTATTATAT GATATGATA CAACCGGCGG TCAATCTGGT
 TCACCAATCT ATAATGATCA GGTTGAAGTA GTTGTGCTT ATTCCAATGG CGGCATTAAG
 CAAACAGGAA ATCATGGTCA AAGACTAAAT GAAGTGATTA ATAACCTTTAT TGTAAATCGA
 GTGAATGAAG AAGAAAAATA ACGTTTATCC GCTGTGCGAG CAGCGT

EF110-4 (SEQ ID NO:428)

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PEDRRQEVAD TTEAPFASIG RIISPAKPKG YISLGTGFVV GTNTIVTNNH VAESEKNAKV
 LNPNAKDDAW FYPGRDGSAT PFGKPKVIDV AFSPNADIAV VTGKQND RP DGPGLGEILT
 PFVLKKKFESS DTHVTISGYP GEKNHTQWSH ENDLFTSHFT DLENPLLEFYD IDTTGGQSGS
 PIYNDQVEVV GVHSNGGIKQ TGNHGRQLNE VNYNFIVHEV NEEENKELSA VPAA

EF111-1 (SEQ ID NO:429)

TGATCAATAC ACTTCGATAC GGTGCGCTTT TTTCTAGAGA AAGTTGAATC TTTCAATAAT
 AAAAAGGGAT ACACTCCATT TGGCATAGTC CTTGCTGATA ATAAATCAGT GTATAAAGCG
 CTATCATTTT ATAGGAGGGG TTTTATGAAG GGTTTATCAA AAAAGAAACG GGTGCTACT
 TGGTTAGCGT TAGGAATCAC CGTAGTCAGC TGTTTTGCGT TAAGCAGGGA AGTGCAAGCA
 AGTGTGAA GAACAAAAGT TGATGAATTT GCAATGCTT TAGATGTGAG TGCATCACCA
 ACCGAACGGA CGAATGGCGT ATACGATACC AATTATTTTA ATAATTTTTC TGATTTAGGT
 GCATGGCATG GCTACTATTT ACCTGAAAAA AGCAATAAAG AGCTACTGGG TGGTTTGGCG
 GGGCCATTGA TTATTGCGGA AGAATATCCA GTAACTTGG CGGCAACTTT AAACAAATTA
 ACGGTCAAAA ATAAAAAAC GGGAGAAACC TATGATTAA GCCAAAGCAA CCGCATGGAC
 CTGTCTTATT ATCCTGGGCG CCTAGAGCAA ACCTATGAAT TAGACGATTT AACGATTCAT
 TTAGCTTTAA TTTTGTGAG CAATCGAAGC GCGCTTATCC AAACGACACT TGAAACACT
 GGTGAAGAGC CCTGTGCACT TGGAGCAAGC TGGACAGGTG CGGTCTTTGA CAAAATTCAA
 GAGGGAACGG AAACCTTAGA TATTGGCACT CGTTTAACTG CTAAAGACAA TGACATTCAA
 GTGAATTTTG GTGAAGTCAG AGAAAGCTGG AATTATTTTG CTACGAAGA CACAAAATAT
 ACGATTCATC ATGCGGATAA AGTTTCAACA AAAATTGATA ATCGGAATTA TACAGCAACC
 GCTGAACCAA TTGAATTGAA GCCTAAACAA ACGTACAACA CCTATACGAC AGAAAGCTAT
 ACTTTTACAA AAGAAGAAGA GGCAAAAGAA CAACAACAAB CACCCGATA TACCAAAAAT
 GCGGCGCGCT ATTTCAAAGA GAACAABCAA AGATGGCAAB GATATCTAGA TAAAACGTTT
 GATCAAAAGA AAACAGCAGA ATTTCTGAA TATCAAAAB CGCTAGTCAA ATCGATTGAA
 ACGATTAATA CCAATTGGCG AAGTGCGGCA GGTGCTTTA AGCATGACGG GATTGTCCG
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 GCAACGGCTG ATTTTAATCC TGAGTTAGCT AAAAATAATA TGCGGGCTT GTTTGATTAT
 CAAATTCAAA AAGATGATAC CGTACGTCCA CAAGATGCAG GAGCGATCAT TGATGCTGTC
 TTTTACAATC AAGACAGTGC CGGTGGTGGT GAAGGTGGCA ACTGGAATGA ACGAAATCTT
 AAACCACCAT TGGCTGCATG GGCAGTTTGG CATATTTATC AAGAAACCAA AGATAAGGAA
 TTTTAAAAAG AAATGTATCC CAACTTGTG GCTTATCATA ATTGGTGGTA TACCAACAGA
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 AAAGACGACA AGGATCAAAT CATTAAGAT AAAAATGGCC ACTTAAATG CATGATGATG
 CTGTTATTGA AGCAGCCGCG TGGGAAAGTG GCATGGATTA CACTACCGG TTTGACAAAG
 AAGGTGTGGG CAAAGCGGAC GTTGGAGTTA AAGTTTTTGA AAACAAAAT AAAGGAAAAG
 TAG

TABLE 1. Nucleotide and Amino Acid Sequences of *Arabidopsis* Genes.

EF111-2 (SEQ ID NO:430)

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LALGITVVSQ FALSREVQAS VERTWIERFA NVLDVSAAPT ERTNGVYDTN YFNNFSDLGA
 WHGYLPEKS NKELLGGFAG PLIIAREYVPV NLAASLNHIT VNNKKTSETY DLSQSNRMDL
 SYYPGRLEQT YELDDLTIHL ALIFVSNRTA LIQTTLNLT EEPFLSLGASW TGAVFDFKIQE
 GTETLDIGTR LTAKNDNIQV NFGEVRETWN YFATKDTHTT IHHADKYSTK IDNRNYTATA
 EPIELKPKQT YNTYTTESYT FTKEEEAKEQ CQAPETHTHA ARYFKENKQR NQGYLDKTFD
 QKKTAEFPEY QNALVFSIET INTNWSAAG AFKHGGINTE MSYKWFIMN ANDSWKADVA
 TADFNPELAK NNMRALFDYQ IQKDDTVRPQ DAGALIDANF YNQDSAFSGE GSNWNERNSK
 PPLAAWAVWH IYQETKDFEF LKEMYPHLVA YHNWYTHED HUKNGIAEYG SMVSDAHWQK
 DDKDQIIKDK NGHLKWMMLL LLKQPRGKVA WITLHGLTHK WAKATLELK FLKTHIKEK

EF111-3 (SEQ ID NO:431)

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 ACCGAACGGA CGAATGGCCT ATACGATACG AATTATTTTA ATAATTTTTC TGATTTAGGT
 GCATGGCATG GCTACTATTT ACCTGAAAAA AGCAATATAAG AGCTACTGSS TGGTTTTGCG
 GGGCCATTGA TTATTGGGGA AGAATATGCA GTAAACTTSS CGGCAAGTTT AAACAAATTA
 ACGGTCAAAA ATAAAAAAC GGAGAGAAIC TATGATTTAA GGCAAAACAA GGGCATGGAC
 CTGTCTTATT ATCCTGGGCG CCTAGAGCAA ACGTATGANT TAGACSNITT AAGGATTCAT
 TTAGCTTTAA TTTTGTGTCAG CAATGAAAGG GGGCTTATCG AAAGGAGACT TGAAAAACAT
 GGTGAAGAGC CTTGTGCACT TGGAGGAGG TGGACAGSTG GGTCTTTTGA CAAAAATTCAA
 GAGGGAACGG AAACCTTAGA TATTGGCACT GCTTTAAGTG CTAAAGACAA TGADATTCAA
 GTGAATTTTG GTGAAGTCAG AGAAAGGTGG AATTATTTTC CTAGGAAAGA CACAAAATAT
 ACGATTCATC ATGCGGCATAA AGTTTGAAGA AAAATTGATA ATGGGATTTA TADAGCAACC
 GGTGAACCAA TTGAATTGAA GCCTAAGCAA AGGTACAGCA CCTATACGAC AGAAAGCTAT
 ACTTTTACAA AAGAAGAAGA GGCAAGGAA CAACAGAAAG CACCGGANTA TACCAAAAAT
 GCGGCGCGCT ATTTCAAAGA GAACAAGCAA AGATGGDAAG GATATCTABA TAAAACGTTT
 CATCAAAAAGA AAACAGCAGA ATTTCTGAAA TATCAAAAAG CGCTAGTCAA ATGATTTGAA
 ACGATTAATA CCAATTGGCG AAGTGGGACA GGTGCTTTTA AGCATGACGG GATTGTTCCG
 TCCATGTCTT ATAAATGGTT TATTGSTATG TGGGCTTGGG ATTCGTGGAA AGCGATGTA
 GCAACGGCTG ATTTTAATCC TGAGTTAGCT AAAAATAATA TGGGGGCTT TTTTGATTAT
 CAAATTCAA AAGATGATAC CGTAGGTGCA CAAGATGCAAG GAGCGATCAT TGATGCTGTC
 TTTTACAATC AAGACAGTGC GCGTGTGGT GAAGGTGGCA ACTGGGATGA ACGAAATCTT
 AAACCACCAT TGGCTGCATG GGCAGTTTGG CATATTIATC AAGAAATCAA AGATAAGGAA
 TTTTAAAAAG AAATGTATCC CAAACTTGTG GCTTATCATA ATTGGTGGTA TACCAACAGA
 GACCACAATA AAAATGGGAT AGCAGAAATAT GGAAGCATGG TCAGTGATGC TCACTGGCAA
 AAAGACGACA AGGATCAAAT CATTAAAGAT AAAAATGGGG ACCTAAGTG GATGATGATG
 CTGTATTGA AGCAGCCGCG TGGGAAAGTG GCATGGATTA CGCTACAGG TTTGACAAAG
 AAGGTGTGGG CAAAGCGCAC GTTGAGGTTA AAGTT

EF111-4 (SEQ ID NO:432)

DEFA NVLDVSASPT ERTNGVYDTN YFNNFSDLGA
 WHGYLPEKS NKELLGGFAG PLIIAREYVPV NLAASLNHIT VNNKKTSETY DLSQSNRMDL
 SYYPGRLEQT YELDDLTIHL ALIFVSNRTA LIQTTLNLT EEPFLSLGASW TGAVFDFKIQE
 GTETLDIGTR LTAKNDNIQV NFGEVRETWN YFATKDTHTT IHHADKYSTK IDNRNYTATA
 EPIELKPKQT YNTYTTESYT FTKEEEAKEQ CQAPETHTHA ARYFKENKQR NQGYLDKTFD
 QKKTAEFPEY QNALVFSIET INTNWSAAG AFKHGGINTE MSYKWFIMN ANDSWKADVA
 TADFNPELAK NNMRALFLYQ IQKDDTVRPQ DAGALIDANF YNQDSAFSGE GSNWNERNSK
 PPLAAWAVWH IYQETKDFEF LKEMYPHLVA YHNWYTHED HUKNGIAEYG SMVSDAHWQK
 DDKDQIIKDK NGHLKWMMLL LLKQPRGKVA WITLHGLTHK WAKATLELK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF117-1 (SEQ ID NO:433)

TAATTCGATG GAGAAGGTGG TTTAGTGAAG AGATTTCGAT TTTTCTTACT AATTTTACTT
 GCTTTAACAG GTTGTAATC CGGTGAAAAA GAATTTCGAT AAGAATCTCT TCAAAATCTA
 AAGGAAACGN CACAGTCTTA NTCAGAAACA GAATTACAAA ATGCTGACGT TCGTTTAAAT
 GAATATATTT CTTTGAAAGG GGAGATTGTT GAGAGTGACA GTGCTTCCAG TTTAATAAAA
 AAAGGTGATC GTTTTATTTT GAAAAGTGGT TCTAGTAAAT ATCAAGTTTN TAATGAGCAA
 AAGAAAAAAT TGAAGATTGG TGACGAAGTG ATAGTTTACG GAGAATATTA CGGCTTTTGG
 AAAGGGACAT TAATTGAAAG TGAGGAGAAT CATGATTGAG CCACGAATTA G

EF117-2 (SEQ ID NO:434)

VKR FSFFLLILLA LTGCKSGEKE FDEESLQNLK ETXQXSETE LQNGDVRLNE
 YISLKGEIVE SDSRSSLIKK GDRFILKSGS SKYQVXNEQK KKLKIGDEVT VYGEYYGFLK
 GTLIESEENH DSATN

EF117-3 (SEQ ID NO:435)

TG AAGAATCTCT TCAAAATCTA
 AAGGAAACGN CACAGTCTTA NTCAGAAACA GAATTACAAA ATGCTGACGT TCGTTTAAAT
 GAATATATTT CTTTGAAAGG GGAGATTGTT GAGAGTGACA GTGCTTCCAG TTTAATAAAA
 AAAGGTGATC GTTTTATTTT GAAAAGTGGT TCTAGTAAAT ATCAAGTTTN TAATGAGCAA
 AAGAAAAAAT TGAAGATTGG TGACGAAGTG ATAGTTTACG GAGAATATTA CGGCTTTTGG
 AAAGGGACAT TAATTGAAAG TGAGGAGAAT CATGATTGAG CCACGAA

EF117-4 (SEQ ID NO:436)

EESLQNLK ETXQXSETE LQNGDVRLNE YISLKGEIVE SDSRSSLIKK GDRFILKSGS
 SKYQVXNEQK KKLKIGDEVT VYGEYYGFLK GTLIESEENH DSATN

EF118-1 (SEQ ID NO:437)

TGAGGGGGAA AAAGTGTGTT AAAAAGAAAA GTGGGGATTT TGCAGGCGT TTTCTGTCA
 GCTTTTGTAC TGACAGGTG TGGCAAAAGT GCGAAAGATG AGTTCATTCA AGGAATCGGC
 AATCANAACG CACAAGAATC TGGGGTTTGN GATTTCTCTA TGTCAATTAG TGACATGAAA
 TTTTCACAAG AAGATGGTGC ACAAACGAAT CTTATGATTT GGATGCTCAT CACGCAAATC
 AAAGACGCAT CGCTTTCTGG GGAAGATTCA ATAGATGCG AAAAAAGAAA AAGCATTCAA
 CTTAGAGATG AAATTAAAAG CGATGGGAAT GATGTATGCG ATTTCAATGG TTGGATCGTT
 AGATAA

EF118-2 (SEQ ID NO:438)

VLKRKV GIVAGVFCSA LLLTGCGKSA KDEFIQGIK XHAQESGVXD FSMSISDMKF
 SQEDGAQTNP MIGMLITQIK DASLSCEDSS RQQRKSIQL RDEIKSDGN3 CTDFIGWIVR

EF118-3 (SEQ ID NO:439)

GAAAGATG AGTTCATTCA AGGAATCGGC
 AATCANAACG CACAAGAATC TGGGGTTTGN GATTTCTCTA TGTCAATTAG TGACATGAAA
 TTTTCACAAG AAGATGGTGC ACAAACGAAT CTTATGATTT GGATGCTCAT CACGCAAATC
 AAAGACGCAT CGCTTTCTGG GGAAGATTCA ATAGATGCG AAAAAAGAAA AAGCATTCAA
 CTTAGAGATG AAATTAAAAG CGATGGGAAT GATGTATGCG ATTTCAATGG TTGGATCGTT
 AGAT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. trachalis* Genes

EF118-4 (SEQ ID NO:440)

KDEFIQGIGN XNAQESGVXD FMSISDMKF SVEEDANRP MISMILIQIK DASLSGEDSS
RCQKRKSIQL RDEIKSENG CTDFIGWVR

EF119-1 (SEQ ID NO:441)

TAAAGAATAC CGAGTAAAT TTTGGGAAGC CTTTTTTTAA AAAATTSTAT ATGCAAAAGA
AGTGCAACGG AAGGAGGCTC GGAATGCTG AATAAGCTAC CTTTACTTAT TTTATTGTTA
GGCGGAGTGT TGCTTGTTAG TGGCTGTCAA AGCATAAAG AAGAAACAA STCTAGTAAA
GTATCGACAG AAGAAACGAC AGTGATTGAA ACAGTAGCAA GGAACAATC GAAGGAATCG
TTTACGAGTG AAGCAACTAA AAAACAGACA GAAACAADGA AATTAGAAGA ACCAGATCAT
GTAAACTTTC TAGAAGCTTA TGGAAATGCG TATGGGAAT TTACAAGTAT TAATGATCGC
AATGAAAAGC TAAAGCCCCT CATGAGTGAA AATGCTATCA AAAAAAATGG AATTGATGTT
AAAAGTGGAG TAGCGTTAGT TTCCGTAGGA AAGGTTAGAA CATTATATAA AATGATCAA
CATGAATATG CTTTACTTTT GGATTGTGAA CAAATGGA CACAGACACG AGTGTTACTT
TTGGCTAAGG TGAAGAACAA TAAATTTCT GAAATGAGT ATAATTGAGT TAAGCAAGAG
TATTAG

EF119-2 (SEQ ID NO:442)

VN KLPLLILLG GVLLVSGCQS HKENKSSKV STEETTVIET VAREQSKESF TSEATKKQTE
TTKLEEDPHV KLEAYGNAY ANFTSINDRN EKLKPLMTEK CIKKNIDVK TGVALVSVGK
VTTIYKNDQH EYALLDCEQ NGTQTRVLLL AKVKNNKISE MTYNSVKQEY

EF119-3 (SEQ ID NO:443)

AGAAAACAA GTCTAGTAAA
GTATCGACAG AAGAAACGAC AGTGATTGAA ACAGTAGCAA GGAACAATC GAAGGAATCG
TTTACGAGTG AAGCAACTAA AAAACAGACA GAAACAADGA AATTAGAAGA ACCAGATCAT
GTAAACTTTC TAGAAGCTTA TGGAAATGCG TATGGGAAT TTACAAGTAT TAATGATCGC
AATGAAAAGC TAAAGCCCCT CATGAGTGAA AATGCTATCA AAAAAAATGG AATTGATGTT
AAAAGTGGAG TAGCGTTAGT TTCCGTAGGA AAGGTTAGAA CATTATATAA AATGATCAA
CATGAATATG CTTTACTTTT GGATTGTGAA CAAATGGA CACAGACACG AGTGTTACTT
TTGGCTAAGG TGAAGAACAA TAAATTTCT GAAATGAGT ATAATTGAGT TAAGCAAGAG
TAT

EF119-4 (SEQ ID NO:444)

ENKSSKV STEETTVIET VAREQSKESF TSEATKKQTE TTKLEEDPHV KLEAYGNAY
ANFTSINDRN
EKLKPLMTEK CIKKNIDVK TGVALVSVGK VTTIYKNDQH EYALLDCEQ NGTQTRVLLL
AKVKNNKISE MTYNSVKQEY

EF120-1 (SEQ ID NO:445)

TGAATAGGCG TGAAAAAGGG AATGTTAGCG TTTTTCCTG TCCTAGCGGT TTTATCATTA
ACTGCTTGTC GGAACCAAAA AGNAAAGAAA GTAACCGCTT CAACGAGGC ATCCTCTAAA
GTTGAAGAGA CGAATGAAAA AACGAGTGAA ACAATTGATA AGACAAAGGA ACAAGCGAGC
AGCAGTGTCT AGTCTAACGA ATCAGTGAAA AATGAAGAGC CGACAGCTGA TGGAAACAAT
AGTCAGCTAA CTGTAGCTGA TTTAGATACT ACAGCGATTA ATGCTGCGCA TTTTACTACT
TTAGTTGGAA TATGGAAAAA TGGTAAGGA GAGAGTTTGA TCATTGATCC TSATGGTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACAAATACCG GAGGAATGAT TACGAAGGAT TCACCTACTG ATGAGTGGCG ACCAATTACA
AGCTTAAGTA TTAGGTGGGG GCCTACTGGT GCTGCCCTAT TATTATATAA AATTGGTGTT

EF120-2 (SEQ ID NO:446)

VKKGMLAF FVVLAVLSLT ACREPKKKKV TASTEASSKV EETNEKTSET IDKTNEQASS
SVESNESVKN EEPTADGNNS QLTVADLDTT AINAGDFTTL VGIWKNEKGE SLIIHPDGST
NTGGMITKDS PTDESRPITS LSIRWGPTGA ALLLYKIGV

EF120-3 (SEQ ID NO:447)

AAGAAA GTAACCGCTT CAACGGAGGC ATCCTCTAAA
GTTGAAGAGA CGAATGAAAA AACGAGTGAA ACAATTGATA AGACAAACSA ACAAGCGAGC
AGCAGTGTGC AGTCTAACGA ATCAGTGAAA AATSAAGAGC CGACAGGTSA TGGAAACAAT
AGTCAGCTAA CTGTAGCTGA TTAGATACT ACACGAGTTA ATGCTGSCSA TTTTACTACT
TTAGTTGGAA TATGGAAAAA TGGTAAAGGA GAAATTTTSA TCATTCTATC TGATGGTAGT
ACAAATACCG GAGGAATGAT TACGAAGGAT TCACCTACTG ATGAGTGGCG ACCAATTACA
AGCTTAAGTA TTAGGTGGGG GCCTACTGGT GTGSCCTAT TATTATATAA AATTGGTGTT

EF120-4 (SEQ ID NO:448)

KKV TASTEASSKV EETNEKTSET IDKTNEQASS
SVESNESVKN EEPTADGNNS QLTVADLDTT AINAGDFTTL VGIWKNEKGE SLIIHPDGST
NTGGMITKDS PTDESRPITS LSIRWGPTGA ALLLYKIGV

EF121-1 (SEQ ID NO:449)

TGAAACACAA GGAGGAAATT TGTGAAAAAG TTGAGCTTAA AAAAAAGTGAA GTGGGGCATG
CATT'TTTTAA TGGCTGTTGC GTTGATAGCG CCAAGTGTTA CTAGTACGGC ATATGCAGTA
GAAACAACGA GTCAACAAAG TTCAGAAGCA GTAACAAGTA CCACCGATTC AAGTAGAAAA
AAGAACCAG TCATTACACA GGAAACAACA GATATCAAA AAGAAGCACC AATCAGGCT
ACGAGTGACA GTGTCAAGCA GTCACAAGAA ACCACAGCAG CACAGAGAC GACGAATTTA
GAAACGTCAA TCGCTGAAAA AGAAGAAACG ACCACGGCGG AAAAAATAAC AATTTTAGGT
ACGTCAGATG TTCATGGTCA ATTATGGAAT TGCTTTATG AAGATGATAA AGAACTACCA
GTTGGTTTTGT CCAAGTAAG TACAGTCGTT AACCAACTCC GGGCACAAAA CCCAGCAGGC
ACCGTTTTAA TTGATAATGG CGACAATATT CAAGCACTA TTTTAACAGA TGACTTGTAT
AATAAAGCGC CTTTAGTGAA TGAAAAGACC CATCAATGA TCACCGCCAT GAATGTGATG
AAGTATGATG CAATGGTTTT GGGAAATCAT GASTTTAATT TTGGTTTACC GTTAATCAAA
AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTGCTTCCGA ATACCTACAA TAAGGAAGAT
GGTCTTCGTT TTGTTGAAGG GACTACCAG AAGGAACCTG ATTTTAATCA AGATGGGCAG
CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTCCG ACATTCCCTT GTGGGATGGC
CCTCGTGTTA CTTGCTTAA TTTTTTACCT TTGAAAAG AAGCAGAAAA AGCAGTTACT
GAGTTGAAAG CTAACGATCA GGCTGACATT ATTGTTCCCT CGATTCTATG GGGACAACAA
AATAGTGATC CGGCTGCCAG TGCCGACCAA GTAATTGAAA ATGTCGCGGG GATTGATGCG
TATATTCTGG GTCATGACCA CCTTCTTTT ACCAAGIAG GAGCAGGCCC GAATGGAAAA
ACTGTACCGG TAGGGGGACC GAAAGATACG GGGACAGAG TTGTCAAAAT TGATCTTTCA
GTTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAAAGTA CAGCAACGAT TGTACCAACA
ACGAATGTTT CAGCAGATGA AGCAGTTAAG GTAGCGACAA AAGAATACCA TGAAAAAACG
CGAGCGTTTA TTCAGGAGGA GATCGGCACA GAAACAGCTG ATTTTTTACC AAAACAAGAA
ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAACAGCGA TGATTTCCTT AATTAATAAC
GTTCAAAAAG AAGTAACGGG CGCACAATTA AGTGGGCGG CGCTGTITAA ATACCACAGT
AAATTACCTG CGGGGAAGAT TTCCTATGCC ACGATTTTTG ATATCTACAA ATACCCGAAT
ACCTTAGTGA GTGTTCCCAT TAACGGTGAA AACTTACTGA AGTATTTAGA AAAACAAGGG

TABLE 1. Nucleotide and Amino Acid Sequences of *Maculalis* Genes.

GGGTACTATA ACCAAACACA GGCAGATGAT TGATATATAT GTTTATATCG AAACATTCTGT
GTATATAACT ATGACATGAT TTCTGGAGTG GATTAATAT GTACATATTC AAAACCCAGTG
GGTGAACGAA TTGTAGATGC GAAAAATGAT GGATATAT TTGATCTTCT CAAAGAATAT
AGGATTGCTA TGAATAATTA TGGTTACGGG GGTATATAT GCTAAGGAT TCAAGTAGGG
GAACCTATTA AAAATTCTGA TGCAGAAAGC TTACGATAT TGATTCTTCA TTATATTAAAG
AAAAAAGGAA CTCTTGATCC ABAACAAGAA ATGAAATAT ATTGGTATAT TATTGGGACA
AATTTTGATG AAAAATGCGG TGCAGAAAGC ATGAAATAT TCAATGATGG CACTCTTCAA
ATTCCGACTT CTCTTGATGG ACCTACAGCA AATGATAT TTATTAT AA ACAAGATGTC
CGTAATGCGG GCTTTGATTT AGATAATGCA TATACGATTA TGCACAGAAA TGACGTTTCAT
GGCGGACTAG AAGCAGGAGAA AGGCGAATTA GGTATGCGCT GTCTAAAGAC CTTTAAAGAC
CAAGAAAACC CAACCTTGAT GGTGGATGCA GCGGATCTTT TCGAAGGACT AGGAATCTCC
AATTTCTCCA AAGGCGGCGA TATGGCGAAA GCAATGAAAT AAGTTGGTTA TGATGCCATG
GGGGTGGGAA ATCAGCAGTT TGATTTTGCT TTAGAGATTA CACTAGTTTA TAAAGACCAA
CTGAATTTTC CGATTTTATG TAATTAATAG TATTAGAAAT ATGGGATGCG AGGGTTTTTT
GATCCGTATA CAATCGTACA AAAATCGCGG AAAAAATGCT GAATTTGTTG TGTGACGACC
CCAGAAACAG CAATGAAAAC ACACCGGAAA AAGTATAT AAGTGAATTT TAAAGACCCG
ATTCCAGAAG TAGAAGCAAT GATTAAGGAA ATTAAAGATA ACTAGGCGAA TATNCAAGCT
TTGGTGGTTA CTGGGCATTT AGGCGTAGAT GAAAGCAAT TGCATATTTG GGTGTGTGAT
ACGCTAGCAG AAACCCCTTA TCAACATAT CCTGAGTTAG ATATGATGCT GATTGATGGA
CATTCCGATA CAGCCGTCGA AAGTGGCAAA CGTTATGTTA AAGTGAATTA TGTCTAAACA
GTAATTATT TAAATAATGT TGGGATCGTC ACAGCAGTAA AAGTGAATTT AATTAAGAAA
ACAACAAAAT TGATTTCAAG AGCAGAGCTG CTAGAAATCT TACAAAAGCT GGTAGTTAAA
GCCATCGTTG ATGAAGCAG TACGAATTTT AAGGCTGAAA ATGAAAAGCT AATTTGCGAT
TATATTCCAT TCACATTGGA TGGACAACGA TATGGCGAAA AGGCTGTTAG CCAACCTGCT
GGGAATTTGA TTGGTGATGC GATTATGTCA TATGGCGAAA AGGCTGTTAG CCAACCTGCT
GATTTTGCAG TAACTAATGG TGGCGGCATT CGGCTGATTA TTAACAGGG GGTAAATTAAA
GTGGGGGATG TCATTGCTGT GTTACCTTTT GGTAAATGCA TTGGCGAAT TGAAGTAACC
GGCGCCCAAG TTAAAGAAAT GTTTGAAATG TGTGTTGCTT GATTTCTTCA AAAAGATGAG
AATGGCAGAA TTTTACTAGA TGATGCTGCG CAGCAGAAAT TTGGCGAAA TGGTGGTTTC
CTACATGTTT CAAGCTCCAT TCGTATCCAC TATGATGCTT TAAAGCTGG TACTGCGTTG
GCTAGTGACG AAGGCAATGA AACAGGACAA AGGATTTGCT GTAGTGGCT ATTAGGAATA
GAAATTAAAA ATCGGCAAAAC ACAAAGTTT GAACCAATTA ATGAGAAAGG ACAATACCGG
ATGGCTACCA ATGATTTCTT AGCTGCTGCT TTAATTGAAAT ACTTGAAAG TGTAAACCAGC
CGAGAAGAAG GCATTTCACT AGATTCTGTC GATTTAGCAAT AATATAAGGA ATCATTTCCA
TTGCGGTTGT ATCGTGACGC AACGACGATT GCTTACAAAT AGTTAATGG TGTAGGAGAG
GGCGAACGAA TTGTTCTAT TTGGAAGAA AAACCAACAG CAGAAATAGC ATTAGCAACC
ACGCCAAAAC CAGATCCAAA ACCAGACCCG AGCAATGCTAT CGGTAACAGA GAGAAAAAG
AATAAACAAA ACCAAGCGGG AGCAAGACAG GAAACAGAAA CGCTTGCAAT ATATGGTTTA
TATGGCGGCT TTTTACCTAA AACGGGTACA TATATTATA AACGAGTAA CAAAGCTAGT
TAG

EF121-2 (SEQ ID NO:450)

VKKL SFKKVKWGMH FLMAVALIAP SVTSTAYAVE TTHLSSSEAV TSTTDSSRNQ
EPVITQETTD IKQEPNQAT SLSVKQSQET TATTTETTHL TSIAEKERTS TPQKITILGT
SDVHGQLWNW SYEDDKELPV GLSQVSTVVN QVRAQNPAAV VLDNGENIQ GTILTDLLYN
KAPLVNEKTH PMITAMVMK YDAMVLGNHE FNFGLFLIAT IQEATPHIL SANTYKNEDG
LRFVEGTTTK ELDFNQDQGP DLKVGIIIGLT IPRIPNKEH RVTSLNELPL KEEAEKAVTE
LKANDQADII VASIHAGQQN SDPAASADQV IENVAGIDAV ILGHDHLGPT KQDAAPNGKT
VPVGGPKDTG TEVVKIELSV AKNADKWEVQ EGTATINPTT NTPADEAKA ATKEYHEKTR
AFIQEEIGTA TADFLPFQEI FGIPEAQLQP TAMISLNNV QFEVTGAPLS AALFKYDSK
LPAGKISYAT IFDIYKYPNT LVSVPINGEN LLNYLEKQSA YNNQTQPDOL TISFNPINRV
YNYDMISGVD YKIDISKPVG ERIVDAKIDG QPDEPAKENT IAMNNYRFGG LRSQGIQVGE

TABLE 1. Nucleotide and Amino Acid Sequences of *H. faecalis* Genes.

PIKNSDPETL RGMIVDYIKK KGTLDPEQEI ERNWSLIECH FDEKWRKAI ELVNDGTLQI
 PTSPDGRTPN AAAITKQDVR NAGFDLDNAY TIMHTTTHHG RLEAGKGELG MARLKTFKDQ
 ENPTLMVDAG DVFQGLPISN FSKGADMAKA MNEVGYDAMA VGNHEFDGGL EIALGYKDQL
 NFPISSNTY YKDGSGRVFD PYTIVEKSGK KFAIVGVTTD ETATKTHPKN VEVWTFKDPI
 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIVRNT LAETLSQTVF ELDITVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEITHTT TRLISARELL ELPEHPAVKA
 IVDEARTNFN AENEKVIVDY IPFTLDGQRE NVPTRETNLR INAGDAIKSY GQDAFSQPAD
 FAVTNGGGIR ADIKQGPVKV GDVIAVLPPG NSTAQIQVTS AQVKEMFEMS VRSIPQKDEN
 GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKPCETLA SDEGNETGQT IMSSRVLGIE
 IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMIGSER EBGISLDSVL IEYLKSATSL
 RLYRAATTID LAQYKEPFPG ERIVSISEEA YKELICGGET PHDPKPDPE PTPETPVATN
 KQNQAGARQS NPSVTEKKKY GGFLPKTGT ETELAINGEL FVGLSSSSUY IYPERNKAS

EF121-3 (SEQ ID NO:451)

ACAAAG TTCAGAAGCA GTAACAAGTA CCACCGATTG AAGTAGAAAA
 CAAGAACCAG TCATTACACA GGAAACAACA GATATGAAAG AAGAGGAGCC AANTCAGGCT
 ACGAGTGACA GTGTCAAGCA GTCACAAGAA ACCATAGGAG CAACAGAGAT GAGGAATTTA
 GAAACGTCAA TCGCTGAAAA AGAAGAAACG AGGAGGAGCC AAAAAATATC AATTTTAGGT
 ACGTCAGATG TTCATGGTCA ATTATGGAAT TGCTCTTAGG AAGATGATAA AGAACTACCA
 GTTGGTTTGT CCCAAGTAAG TACAGTCGTT AATCAAGTCC GGGACAAAAA CCGACGAGGC
 ACCGTTTTAA TTGATAATGG CGACAATATT CAABSSAATA TTTTAAAGAA TGACTTGTAT
 AATAAAGCGC CTTTAGTGAA TGAAAAGACC CATGAAATGA TCACCGGCAAT GAATGTGATG
 AAGTATGATG CAATGGTTTT GGGAAATCAT GATTTTAAAT TTCTTTTACG GTTAATCAAA
 AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTCTCTTAAA ATACCTACAA TAAGGAAGAT
 GGTCTTCGTT TTGTTGAAGG GACTACCACG AAAGAGTTC ATTTTAAATC AGATGGGCAG
 CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTCGAG ACATTCCTTT GTCGGATGGC
 CCTCGTGTTA CTTGCGTTAA TTTTTCACCT TTGAAAGGAG AATGAGAAAA AGGAGTTACT
 GAGTTGAAAG CTAACGATCA GGCTGACATT ATCTTTCTCT CGATTTCATC GGGACAACAA
 AATAGTGATC CGGCTGCCAG TGCCGACCAA GTAATGAAAA ATCTGCGCTG GATTGATGCG
 TATATTCTGG GTCATGACCA CCTTCTTTTT ACAGAGGAG GAGGAGGCT GAATGAAAAA
 ACTGTACCGG TAGGGGGACC GAAAGATACG GGGAGAGGAG TTCTGAAAAA TGATCTTTCA
 GTTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAGGATA CAGCAAGCAT TGTAACCAAC
 ACGAATGTTT CAGCAGATGA AGCAGTTAAG GCAGGAGAAA AAGAAATACA TGAAAAAACG
 CGAGCGTTTA TTCAGGAGGA GATCGGCACA GCAACAGGTG ATTTTTCACG AAAACAAGAA
 ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAACAGGGA TGATTTCTTT AATTAATAAC
 GTTCAAAAAG AAGTAACGGG CGCACAATTA AGTGGGAGAG CGCTGTTTAA ATACGACAGT
 AAATTACCTG CGGGGAAGAT TTCCTATGCC ACATTTTTCG ATATCTATAA ATACCCGAAT
 ACCTTAGTGA GTGTTCCCAT TAACGGTGAA AATTTAGTGA AGTATTTAGA AAAACAAGGG
 GCGTACTATA ACCAAACACA GCCAGATGAT TTGACGATTA GTTTTAATCC AAACATTCGT
 GTATATAACT ATGACATGAT TTCTGGAGTG GACTAGAGGA TTAGATTTTC AAAACAGAGT
 GGTGAACGAA TTGTAGATGC GAAAATTGAC GGTCAAGGAG TTAGATCTTC CAAAGAATAT
 ACGATTGCTA TGAATAATTA TCGTTACGGC GGTTTAGCTA GCAAGGGGAT TCAAGTAGGG
 GAACCTATTA AAAATTCTGA TCCAGAAACC TTGAGAGGAA TGAATGTGTA TTATATTAAG
 AAAAAAGGAA CTCTTGATCC AGAACAAGAA ATGAGAGGAA ATTGTCGAT TATTGGGACA
 AATTTTGATG AAAAAATGGC TGCCAAAGCA ATGAAATTAG TGAATGAGGG CACTCTTCAA
 ATTCCGACTT CTCCTGATGG ACGTACACCA AAGGCGG

EF121-4 (SEQ ID NO:452)

QSSEAV TSTTDSSRKQ

EPVITQETTD IKQEPNQAT SDSVKQSQET TATTEFTTLE TSAEKEEIS TPQKITILGT
 SDVHGQLWNW SYEDDKELPV GLSQVSTVVN QVLAQHFAET VLIDNSDNIQ GTILDDLYN

TABLE 1. Nucleotide and Amino Acid Sequence of the Genes.

KAPLVNEKTH PMITAMNMMK YDAMCLGNFE FNNALN... 17, EATYHLL SANTYINKEDG
 LRFVEGTTTTK ELDFNQDGGP DLKVGIIISLT IFHIF... PNTSLNPLML PLAEKAVTE
 LKANDQADII VASIHAGQON SEPAAASADQV IHTH... IYSHIHNFT LLSAAPNGKT
 VPVGGPKDTG TEVVKIDLSV ANNADRWEMQ EGIAT... NTWADENYKA AINHEYHEKTR
 AFIQEEIGTA TADFLPKQEI KSIPEANLQFP TAM... IHEHTGATLS AAALFKYDSK
 LPAGKISYAT IFDIYKYPNT LNSVPIINGFN LLYH... TNNQTHLLS TIGFNPNIHV
 YNYDMISGVD YKIDISKPMG ERIVDAKIDG QPLI... IINENYVGG LNSQGIQVGE
 PIKNSDPETL RSMIVDYIKK KSTLDPREVEI ERH... FLEHWRKAFI ELVNDSTLQI
 PTSPDGRTPN A

EF122-1 (SEQ ID NO:453)

TGAAACACAA GGAGGAAATTT TGTGAAAAAG TTSAGTITTA AAAAAGTBA A GTGGGSCATG
 CATTTTTTTAA TGGCTGTTSC GTTGATAGCG GGAATTAATA CAGTACGCT A TATGSCAGTA
 GAAACAACGA GTCAACAAAG TTCAGAAAGA GTAAATAT CACCGGNTTC AASTAGAAAA
 CAAGAACCAG TCATTACADA GGAAACAANA GATATATAT ALBAAGTAC AAATCAGGCT
 ACGAGTGACA GTCTCAAGDA GTCACAAGAA AGGATAT CAGACAGAGAC GAGGAATTTA
 GAAACGTCAA TCCTGAAAA AGAAGAAAAG AGGACCTT CAAAAATAC AATTTTAGGT
 ACGTCAGATG TTCATGGTCA ATTATGGAAT TGTCTT... AAGATGATAA AGAACTACCA
 GTTGCTTTGT CCCAAGTAA3 TACAGTCGTT AAGCACT... CAGCAGAAAA CCCAGCAGGC
 ACCGTTTTTAA TTGATAAT33 CGACAATATT CAAGGCA... TTCTTAAGA TGAATFIGTAT
 AATAAAGCGC CTTTAGTGAA TGAAGAAGAC CATCCAA... TCAACGTCAT GAATGTGATG
 AAGTATGATG CAAT3GTTTT G3AAATCAT GASTTTAT TTGCTTACC GTTAATCAAA
 AAAATTCAAC AAGAAGCCAC TTTTCAATC TTCTCT... ATAECTACAA TAAG3AAGAT
 GGTCTTCGTT TTGTGAAG3 GACTACCAG3 AAGGAACT... ATTTTAATCA AGAT3GGCAG
 CCAGATTTAA AAGTTGGGAT TATGGCTTA AGAATTC... AGATTCCTTT GTGG3ATGGC
 CCTCGTGTTA CTTGCTTAA TTTTTCCTT TTSAAAGAG AAGCAGAAA AGCAGTTACT
 GAGTTGAAAG CTAACGATCA GGTGACATT ATTCTT... CATTCATCC CCCACAACAA
 AATAGTGATC CGGCTGCCAG TGCCAGCAAA GIAATT... ATGCTCGAGG GATTTGATGGC
 TATATTCTGG CTCATGACCA CATTCTTTT ACCAAG... GAG3AGT3CC GATTTGGA AAA
 ACTGTACCGG TAGGGGAC C GAAAGATAG3 GELAC... TCTGCAATAT TGAATTTTCA
 GTTGCTAAAA ATGCCGATAA GTGG3AA3T3 CAAGA... CAGCAAD3AT TGTACCAACA
 ACCAATGTTT CAGCAGATGA AGCASTTAAG GCACG... AAGAATADCA TGA AAAAACC
 CGAGCGTTTA TTCAGGAGGA GATGG3CADA GCAAG... ATTTTTHAC3 AAAACAAGAA
 ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAAC... TGATTTCTTT AATTAATAAC
 GTTCAAAAAG AAGTAACGGG CGCACAATTA AGTGG... CCTGTTTAA ATACGACAGT
 AAATTACCTG CGGGGAAGAT TTCTAT333 ACGATT... ATATCTACAA ATACCCGAAT
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 GCGTACTATA ACCAAACACA GCCAGAT3AT TTSAG... GTTTTAAT33 AAACATTCTG
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 GGTGAACGAA TTGTAGAT3C GAAAATT3AC GELCA... TCGATCTT33 CAAGAATAT
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 CGTAATGCGG GCTTTGATTT AGATAAT3CA TATAG... TGCACAGAAA TCACTTTCAT
 GGCCGACTAG AAGCAGGGA AGGCGAATTA GGTAT... GTCTAAAAAC CTTTAAAGAC
 CAAGAAAACC CAACCTTGAT GGTGGAT3CA GGGAT... TCAAGGATT ACCAATCTCC
 AATTTCTCCA AAGGCGCGGA TATGGCCAAA GCAAT... AAGTTGGTTA T3AT3CCATG
 GCGGTGGGAA ATCAGGAGTT TGATTT33T TTAGAG... CACTAGGTTA TAAAGACCAA
 CTGAATTTTC CGATTTTATC TAGTAATA3G TATTA... ATGGCAGT3G A3333TTTTT
 GATCCGTATA CAATCGTAGA AAAATCG33 AAAAG... CATCT3TAG3 T3TGACGACC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGAAACAG CAACGAAAAC ACACCCGAAA AACGTAGAGA AAGTACACATT TAAAGACCCG
 ATTCCAGAAG TAGAAGCAGT GATTAAGSAA ATTAAGAGAG AATACGJGGA TATNCAAGCT
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 ACGCTACGAG AAACCCCTAG TCAAACATAT CATTGACITAG AATCACTGT GATTGATGGA
 CATTTCGCATA CAGCCGTCGA AAGTGGCAAA CATTATGACA AAGTATCTA TCTCATAACA
 GGTAATTATT TAAATAATGT TGGGATCCTC ATAGCTCAG AAGTGAACG AACTAAGAAA
 ACAACAAAAT TGATTTACAG AGCAGAGCTG CTAGAATTTC CAGAAAACCG GGCAGTAAAA
 GCCATCGTTG ATGAAGCAGC TACGAATTTT AACGCTCATA ATGAAAAAT AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAACGA GAAAATCTGC GACACACAGA GACCAACTTA
 GGGAAATTTGA TTGGTGATGC GATTATGTCA TATGCTCAG AATGCTTAG GGAACCTGCT
 GATTTTGCAG TAACTAATGG TGGCGGCATT CTTCTTATA TAAACACAG GCAATTAAAA
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 GGCGCCCAAG TTAAAGAAAT GTTTGAAATG TCTCTCTCTT CATTCTACA AAAAGATGAG
 AATGGCACAA TTTTACTAGA TGATGCTGCG CAACCAAAAC TGGGCGAAAA TGGTGGTTTC
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 ATGGCTACCA ATGATTTCTT AGCTGCTGCT GCTGATCTCT ACATATGCT AAGTGGTGAA
 CGAGAAGAAG GGATTTCACT AGATTCTCTC TTAATTCAAT ATTTGAAAAG TSCAACCAGC
 TTGCGGTTGT ATCGTGCAGC AACGACGATT GATTTAGTTC AATATAAGA ACCATTCCCA
 GGCGAACGAA TTGTTTCTAT TTCGGAASAA GCTTACAAAG ATTIAATCGG TCGAGGAGAG
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 AATAAACAAA ACCAAGCGGG AGCAAGACAG ASCAATCAAT TCGTAACAGA CAAGAAAAAG
 TATGGCGGCT TTTTACCTAA AACGGGTACA GAAACAGAAA TCGTTGCAAT AATGGTTTA
 CTGTTCTGTTG GACTTCTTC TTCTGGCTGG TATATITATA AACGACATA CAAAGCTAGT
 TAG

EF122-2 (SEQ ID NO:454)

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 SDVHGQLWNW SYEDDKELPV GLSQVSTVNV QVRAQNPAGT VLIDNGDNIQ GTILTDLLYN
 KAPLVNEKTH PMITAMNVMK YDAMVLGNHE FNFGLEHLEK TQCEATFPIL SANTYNKEDG
 LRFVEGTTTK ELDFNQDQGP DLKVGIIGLT IPHIPWDDP FVTSLNFLPL HEEAEKAVTE
 LKANDQADII VASIHAGQON SDPAASADQV IENVASIDAY ILGHDLHLSFT KQGAAPNGKT
 VPVGGPKDTG TEVVKIDLSV AKNADKWEVQ EGTATIVETT NUPALEAVKA ATKEYHEKTR
 AFIQEEIGTA TADFLPKQEI KGIPEAQLQP TANISIDENV QKEVTGAQLS AALFKYDSK
 LPAGKISYAT IFDIYKYPNT LVSVPINGEN ILHYLEKQGA VYNQTKPDDL TTSFNPNIHV
 YNYDMISGVD YKIDISKPVG ERIVDAKIDG QPLDPAREYT IANTNYRYGG LASQGIQVGE
 PIKNSDPETL RGMIVDIYIK KGTLDPEQEI ERNWSLIGTN FDEKWFKAAL ELVNDGTLQI
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 NFPISSNTY YKDGSGRVFD PYTIVEKSGK KFAIVGVVTP ETATKTHPHN VEKVTFKDPI
 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIVRQET LAETLSQTYP ELDTITVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APSEPTTET TNLISAAELL ELPENPAVKA
 IVDEARTNFN AENEKIVVDY IPFTLDGQRE NVRETRTHLG NLIGDAIMSY GQCAFSPAD
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 GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKPESTLA SDEGNHTGQT LUGSRVLGIE
 IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMQGER EESISLDSVL IEYLKSATSL
 RLYRAATTID LAQYKEPFPG ERIVSISEEA YKELIGGRET PNPDPKPDPK PTPETPVATN
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EF122-3 (SEQ ID NO:455)

TABLE 1. Nucleotide and Amino Acid Sequences of *Escherichia* Genes

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 CGTAATGGGG GCCTTGTATTT AGATAATGCA TACAGCAAAA TACAGCAAAA TACGTTTCAT
 GGCCGACTAG AAGCAAGGAA AGGCGAATTA GGTATCTTT GGTAAAAAG GTTTAAAGAC
 CAGGAAAAAC CAACCTTGAT GGTGATGCA GAGATCTTT TCAAGGATT AACAATCTCC
 AATTTCTCCA AAGGCGCGGA TATGCGCAAA GGAATGATTA AATTTGTTA CATTGCGATG
 GCGGTGGGAA ATCAGGAGTT TGATTTTGGT TTGAGGCTTA CATTAGTTA TAAAGACCAA
 CTGAATTTTC CGATTTTATC TAGTAATACG TACTAGAAA ATGGAAGTGG AAGGTTTITT
 GATCCGTATA CAATCTAGA AAAATCGGG AAAAAGCTTT CATTGTTAG CTTGAGGACC
 CCAGAAACAG CAACGAAAAC ACACCGGAA AAGTATGTA AATTGACATT TAAAGACCCG
 ATTCCAGAA TAGAAGCAAT GATTAAGGAA ATTAAAGAA AATAGCGGA TATTCAGCT
 TTCTGGGTTA CTGCGCATTT AGGCTAGAT GAAAGCAAT CCGATATCTT GATGCTGAT
 ACCGTAGCAG AAACCGTTAG TCAAGCATAT CCGAGCTAG AATGACTTT CATTGATGGA
 CATTCGCATA CAGGCTCGA AATGCGCAA CGTTATCA AATGATCTA TCTCAAAACA
 GGTAAATTAT TAAATAATST TGGGATGCT ACAGTACAT AAGTGAAGG AACTAAGAAA
 ACAACAAAAT TGATTTGAGC AGCAGAGCTT CTAGATTTT CAGAAAACCT GAGCTTAA
 GCCATCTGTG ATGAAGCAG TACGAATTT AAGCTGAAA ATGAAAAAT AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAAAG GAAATCTTT CACAGGAA GAGTAACTTA
 GGGAAATTGA TTGGTGATTC GATTATCTCA TATGCGGAG AAGCTTTAG CTAATCTGCT
 GATTTTGCA TAATAATGG TGGCGGATTT CCGGCTGAA TAAAGCAAG CTAATTTAA
 GTTGGGGAT TCAATCTCTT GTTACCTTTT GGAATATTA TTGCGGAAAT TAAATTAAC
 GGCGCCCAA TTAAGAAAT GTTTGAAATG TCTGTTTCT CATTGCGCA AAGAGATGAG
 AATGGCACAA TTTTACTAGA TGATGCTGCT CAACCAAAAT TTGCGGCAA TCTGCTTTT
 CTACATGTTT CAAGCTCCAT TCGTATCTAC TATGATTTA CAAAACCTAG TACTGCTTG
 GCTAGTGAG AAGGCAATGA AACAGGACAA AGGATTTGCT GATGCTGCTT AATAGGAATA
 GAAATTAATA ATCGGCAAA ACAAAATTT GAACCTATG ATGAGAGAA AATATACCGG
 ATGGCTACCA ATGATTTCTT AGCTGCTTCT GGTGATGCTT AAGATATGCT AATGCTGAA
 CGAGAAGAAG GGATTTCACT AGATTTCTCT TTAATGAAAT AATTGAAAG TCAACACAGC
 TTGCGGTTGT ATCTGCAAC AACGAGGATT GATTGATTA AATATAAAG AATATTTCCA
 GGCGAACGAA TTGTTTCTAT TTCGGAAGAA GCTTACAAAT AGTAAATCTT TCGAGGAGAG
 ACGCCAAAAC CAGATCCAAA ACCAGACCG AAACCAAAT CAGAAACCTT AATAGCAACC
 AATAACAAA ACCAAGCGGG AGCAAGACAG AGCAATCTAT CCGTAAACAA CAGAAAAAG
 TATGGCGGCT TT

EF122-4 (SEQ ID NO:456)

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 NFPILSSNTY YKLGSGRVFD PYTIVEKSGK KFAIVGNTTI EATKTHPKN VEKVTFKDPI
 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIWGGT LAETLSQTYF ELBITVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEPTTET TELLISAAELL ELFENPAVKA
 IVDEARTNFN AENEKIVVDY IPFTLDGQRE NVETRETHIG NITGDALMSY GWDAPSQPAD
 FAVTNGGGIR ADIKQGPVKV GDVIAVLPPF NSIAQIQITG ATTKEMFEMS VHSIPQKDEN
 GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKPGTRLA SEEGNETGQT ITCRVLGIE
 IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMLOGER EESISLDSVL IETLKSATSL
 RLYRAATTID LAQYKEPFPF ERIVSISEBA YKELIGGSET PHFDPKPDPE PEPETPVATN
 KQNQAGARQS NPSVTEKKKY GGF

EF123-1 (SEQ ID NO:457)

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 ATGAAAGAAA TGAGAAAGAA TGGTCCAAAT GTAAACCGTT GGTCTACGG GTTGATGTGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTGTTACTTG	TTCTAAATTA	TGGCACACA	CTCATGGCTT	TGGGSGAAGA	GGTTAACAGC
GATGGCCAGT	TAACGTTAGG	AGAAGTGAAG	CAAACCAGCG	AGAAAGAAAT	GACCTTAGCG
CTTCAAGGAA	AAGCACAAAC	AGTAACACAA	GAGGTTGTAG	TGCATTATAG	TGCCAATGTG
TCAATCAAAG	CTGCACATTG	GGCAGGCGTC	AATAATACGG	GCAAGATTCA	ACTGGATGAC
CAGAAGAAAC	AGATTCAAAT	TGAATTGAAT	CAGCAAGCGT	TAGCAGATAC	GTTAGTCTTA
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TTGACGTTAA	AGACTGGTAC	TGATCCGACA	GAATCAACGG	CANTACCGAG	TTCGCCAGCC
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TCCGAAGAAA	CTGTCGCCAG	CACGACAAAA	GCGATAGAAA	GTAAACAAC	TGAATCGACG
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ACAACGATTA	TCGATAATTT	TGAAGATGCG	ATTTATTTAA	ATCTGATGCG	AACACCAGCA
ACACCGCCGT	ATAAAGAAGA	TGTGACCAAT	CATTGGAAT	TTAACTGGTC	GATTCCAGAA
GATGTGCGAG	AACAAATGAA	AGCAGGCGAT	TACTTCGAGT	TTCAATTACC	TGGCAATTTG
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TACACAATTA	GTGAAGATGG	TACGGTTTCT	TTTACCTTTA	ATGABCGAAT	CACGTCTGAA
AGTGACATTC	ACGGGGACTT	TTCTTTAGAT	ACTCATTGGA	ATGATTCAGA	TGGCGGGGGC
CCAGGAGATT	GGGTGATTGA	TATTCCTACA	CAAGAAGATT	TGCTCCTGT	ATTGATTCCA
ATTGTCCCAG	ATACCGAACA	ACAAATTGAT	AAACAAGGCG	ATTTTATTCG	AACGCCCAAT
CCTAGTGCGA	TTACTTGGAC	GGTAGATATC	AATCAAGCGA	TGAAGATCA	AACAAATCCA
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GCAGTCATTA	CAGACACAAT	GGGGGATAAT	TTAACGTTTG	AACTASATTC	TTTACATTTA
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GCCAGTCAAC	AAAATATTAT	TAAAAACACT	GGTGCAGTTG	ATTATCAAAA	TGCAACGATT
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AACCAAGTGT	CAATTACTGG	AAATGCTTCA	GAAGTCGTTG	ATGCGGATGA	CAATGGCGAT
GTGGTCGTTG	ACATTGATCA	CAGTGGCGGG	CATGCCACAG	GGAATAAAGG	CAAAATTCAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GAAGGAGGAC AACCAACCAT TATTAAAAAC GATGTCATAA AAGTATTTTT AAAAAAATG
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GCACCAAAAT TACCAGATGG CGCAGATTAT ATATTATTAT CTTAATTAGT AAAAAATGAA
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CATCCATTG ATGTAACCG CCAATTAGGA AAGAGCAGC CAATGCTTT AGGCGATCTT
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CGGAAAGACA AACCTGAAGT CGTGAATGGG GGCACGTTTG TTAAGGAGAA AAGAGCTGTA
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EF123-2 (SEQ ID NO:458)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 YQTTIDEAVI PDGGGDVPFK NHATLTSNN PNLGLDAEATV TATYCHMLDF FHLIYDEANQ
 EFTWEINYNY GEQTIPKQQA VITDTMGDNL TFEPLSLHLY SVTFDEKGNF VNSAELVEGK
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 SQQNIKNTG AVDYQNSTIG WTLAVNQNNY IMENAVITDT YEPVFGLTMY FHLAVVKDIT
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 NRLVDAFLTD PILTNQTYLA GSKLVYEGNT KPDGSVEKVK PTQPLEDITM EEPSEKNQNT
 WRVDFPNDSR TYVIEFKTSV DEKVIEGSAS YPNTASYTNQ GSSPFWTGKV SIQGGESVK
 KGGEYHKDDP DHVYWHVMIN GAQSVLDDVV ICTTFSPNQV LDPEFLVIYC THVCTDGTIT
 PDKSVILEEG KDYTLVTTD NETGQOKIVV KMAHIEAPYY MEYRSLVTSF AAGSTDTVSN
 QVSITGNGSE VVHGDDNGDV VVDIDHSGGH ATCTCKHIQL KETAMDETTI LAGAHFQIWD
 QAKTQVLREG TVDATGVITF GGLPQGQYIL VETKAPEGYT VSEELAKGRV ITIMEETSAB
 GAQPTIINKD VNKVFLEKMD EFGKKLVNAR FFLHNAVITP FTHWEVPLA PIRTHANGQL
 EVDSLKPGLY QFTEIEAPTQ YLLDTPPKRF IVTQNTSGQI FDMHTMLNY QNSAELIKKD
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 SAFTIAASDR GKPATVIATA NFNVYQGTAK LTHEDVNGHL ISEATPKVLD ABSETIQTGL
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 KGAFQIVKTN SADQPLAGAV FELYDHNKQS LGITATSGKD GKIIFDLAP GTYYYKEIKA
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 NDKQPLDELE FVNYQAEVMG RKNVEQGQTL AGAVFAIYNA DEQNIQPGSP DDFINRAGEK
 VSEITTDKTC EYAKGLNEG HYVLVETKAP TGYLLDITLH PFDNTAQLGH EKPALGDLI
 NYQGTQALTK ENETGEALAG AVFKVIDETG QTVGQTNLM SDEQGVIAH NMAPGTYRFV
 ETQAPTSYLL NETPSASFTI AKDNQGKPAT VVLEAPFINY QGAALVKID QKHALAGAE
 FKVTDAETGQ TVARSLRSDN QGLVQVNHQ PCHTTFVETK APDGYLSKQ AVAFTIAATA
 KDKPELVNAG TFVNEKQPVV KKTKNQPTT KQAARETGWL GLPHTNTQVH YHNFIFGLML
 VGLASWLFYK KSKK

EF123-3 (SEQ ID NO:459)

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 CCTAGTGCGA TTAATTGGAC GGTAGATATC AATCAAGCGA TGAAAGATCA AAGCAATCCA
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TABLE 1. Nucleotide and Ammo Acid Sequences of *E. faecalis* Genes.

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EF123-4 (SEQ ID NO:460)

EEVNSD

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EF124-1 (SEQ ID NO:461)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CCAGGAAAAAT	ATCAATTTGT	GGAAACCAAA	GCGCGAGCAG	GGTACCTTTT	AAACACTGAA

TABLE 1. Nucleotide and Ammo Acid Sequences of *E. faecalis* Genes.

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EF124-2 (SEQ ID NO:462)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 GAQPTIHKND VNKVFLEKMD EKGFKLVNAR FKLEHANTTP FTHVEEVPLA HORTNANGQL
 EVDSLKPGLY QFTEIEAPTG YLLITTPFRF IVTQIHSQI RDMHVKMLNY QESAELIKKD
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EF124-3 (SEQ ID NO:463)

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EF124-4 (SEQ ID NO:464)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

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 EVDSLKPGLY QFTEIEAPTG KLEDTIPKRF IYPTNAGQI RDNHMKMLNY IISAEIKKD
 QAGNPLAGAE FSVLDTTGQA VREHLVSDAN GKVTTLAP GHVDFVETKA IAGVLLNTEP
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 TTNNQG

EF125-1 (SEQ ID NO:465)

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 CTTCAAGGAA AAGCACAACC AATAACACAA GAGGTATAG TCAATTATAG TGTCAATGTG
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 ACACCGCGT ATAAAGAAAG TGTGACGATT CATTAAGAT TTAATGGT GATTGACAG
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 ATTGTCCAG ATACCGAACA ACAAAATGAT AAAACAAGGC ATTTTGATCG AACGCGCAAT
 CCTAGTGGCA TTACTTGGAC GGTAGATATC AATTAAGCGA TGAAAGATTA AACGATCCA
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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CATTTCAGAAG	ATAGTAAACC	GTTTAAAGCT	TTAGTTTCTT	TTGATTTAAA	TAGGCAAAAA
AGCGGTGTTT	ACAATGCCGT	CACCAAGAA	ATCAGTTGGA	CGATTGCGGT	TGATTTAAGT
AATAATCGTT	TAGTCGACGC	CTTTTTTGACG	GATCGAATTT	TAACCAATCA	AACTATTTTG
GCTGGGAGCT	TGAAAGTCTA	TGAAGGCAAT	ACAAAGGAG	ATGTTTCGGT	TGAAAGAGTG
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GTTGATGAAA	AAGTTATCGA	AGGTTGCGCT	AGTTATGACA	ATAGGCGATC	TGATGAAAC
CAAGGTTCTT	CACGTGATGT	GACAGGAAAA	GTTTCTATTC	AACTGCGTG	CAATGATGTG
AAAAAAGGTG	GCGAATACCA	CAAGGATGAT	CGAGGATG	TGTACTGGCA	TGATGATGATC
AATGGCGCCC	AATCGGTTTT	AGAGGATG	GTTATGATG	ATAGGCGCTC	AAAGGACCAA
GTGCTAGATC	CCGAGTCATT	GCTGATTTAC	GCTAGGAAAG	TAAGGAGAGA	CGGATCTATT
ACGCCAGATA	AATCTGTTAT	TTTAGAAGAA	GGAAAGGATT	ACAGACTGGA	AGTTAGCCACC
GATAATGAAA	CAGGACAACA	AAAAATGCTC	GTTAAATG	CCCATATTGA	AGGAGCTTAT
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TTTGTTAGAAA	CCAAAGCGCC	AACAGGCTAT	TTATTAATA	CCAGGCGAGT	CAATTTGAA
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GATGCAACGG	ATGGCTATAT	CGTCAATAAA	CAACGATTTT	ATTTTCTAGT	GAAGGAGAAAT
TCAAATGATA	AACAACCACT	AGATGAGTTA	GAGTTTCTAA	ATTATCAAGC	AGAGGAGAAATG
GGACGTAAAG	TCAACGAGCA	AGGTGAAACC	TTAGGCGCTG	CAGTTTCTTG	AAATTTCAAT
GCCGATGAGC	AGAATCAGCC	CCAAGGTTCA	CCGATTAATAT	TCTTGAATCG	TGAGGAGAA
AAAGTTTCTG	AAATAACAAC	GGATAAGACT	GGGGAATTTT	ACGTTAAAGG	GGGGAATGAA
GGGCAATTACG	TTTGTAGTGA	AACGAAAGCA	CCAAGGAGCT	ATCTGTTAGA	CAGAGGCTTA
CATCCATTTG	ATGTAACCGC	CCAATTAGGA	AAAGAGGAGC	CAATGCTTTT	AGTGGATCTT

TABLE 1. Nucleotide and Amino Acid Sequences of *FE jaculis* Genes.

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GGTGGCGGTGT TTAAGGTGAT TAAATAACA GAGGATG TA ATGGACA AAT ATCTGT
ATGTCTGACA AGTAAGGCAA AATATATG AAGGATG TAG CAATGGGAT GAT GTTTT
GTGGAGACAC AAGGCGCAAC TAGGTATCTT GTTAAA AAA GGTAAAGGCA AAT GTTTACG
ATTGCCAAGG AAGAGTAAGG CAAGATAGG AGTAAAG AAC TTAAGGAGG TTTATTAAT
TACCAAGGTG CTGCAAGGT GGTAAATTT GATTAAG AAA AGAAGGCTT AATATGTGCT
GAATTTAAAG TGAACATGCG AAGAGAGGCG CAAGATG TCG GTTTTCTATT AATTTCTGAC
AACAAGGCTT TAGTTTAAAT CAATTAATTA CAAGATG AAA AATATAGCTT TAAATAACA
AAAGCACCGG ATGTTTAAAG ACTATTAAG CAAGATG TCG CATTCAGTAT TAAATAACA
GCGAAAGACA AAGTGAAGT GTTGAAGGCG GCGATTTT TTAAGGAGG AATATGTGTA
TCAAAAAAAA CAAAGCAAA TCAATGACA AAGATG AAG CAGTTAGAGA GATATGTGCT
CTTGGTTTAC CAAAAAGCAA CAGATAAGTC AATTAATCT TTTCTTTAT CAGATCATG
TTGGTCGGTT TGGCAAGTGT GGTATTTAT AATAAGCA AGAATAAA

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EF125-2 (SEQ ID NO:466)

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SANEGSTEEA STNSSVPSS ESTVASTHA IESPLSTT VHTVASTPD IATTTIGDET
TIIDNFEDPI YLNPEGTPAT PPKEDVTH WHEHLPED VREHKASDY FHLPLGNLK
PNKPGSGDLV DAEGNAYQTY TISEGTVRF TENETSES DIEDPSLDT HMTDORGP
GDWVIDIPTQ EDLPFVPI VPDETCIDK QSHFTPNP SALTWVDIN QAWDTNPT
VETWPTGNT FKSVMVYELV MNLGTIREV GRELMEYT VDKGNVTIK GHTHAYRLE
YQTTIDEAVI PDGGGVPPF RHATLINDNN PNGLHATV TATYKMLDK RHITTEANQ
EFTWEINYNY GEQTIFKQA VITETGDNL TFEHMLY SVTEDEKNE VHAELVEGK
DYKVVINGDS SFAIDFLDV TGAHIDVKT HVEDTSEV AVHEDVGT GHEDDGTGTA
SQQNIIFNTG AVFYQNTIG WTLATNNNY LMEHATET YEPPLTMY PHTVVKDTT
TGAQLTLGKD FMVEITENAL GEGGFNFI GATATGAF HITTTFFLV TELTANIPAL
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KGGEYHKDDP DHFYHVMIN GAQSULDDV ITDTLKV LDPESLVIYG THTEDGTIT
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TTNNQGEIVA EHLAPGKYRF VETKAPTGYL LNTTHSFEI AEMHAGKPAV VVADNPFVS
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PKLPDGADYI IYPELVVEI RGLFKGPEI FQAGANFK GRAVFKIHA NANPLPGTIF
KLYRIENGEK IFEREVTAEK DGLAMEDLG AGSVHLELD ATGVIVNQC PIYFVKKNS
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VSEITTDKTG EIYAKLNEG HYVLVETKAP TGHVHTLH PFTATAQLGK ECFIALSDLI
NYQGTAQITK ENETGEALAG AVFHWIDETG QTVGTTNLM SDKQSHVIAK NLAQTYRFV
ETQAPTSYLL NETFSASFTI AKHNGKPKAT VVLPALINY QGAARLVKID QGYHALAGAE
FKVTDATGQ TVARSLRSDN GGLVQVNLH QKHYTHETK APQYQLSHQ AVHTIAATA
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EF125-3 (SEQ ID NO:467)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 TTGACGACAA ATAATCAAAG CGAATTTGTT GCAGATCACT TACCCCCAGG AATATATCGC
 TTTGTAGAAA CCAAAGGCGC AAGAGGCTAT TTATTGATA CCAAGCCAGT CAGATTTGAA
 ATTGCTGAGA AAAATGCTGG TAAACCAAGG GTGCTGTTTG CTATGACAA CTTTGTGAGT
 TACAAAGGGG CTTTCCAAAT CGTGAAAGG AATTAGCAG ACCAACCATT AGCAGGTGCT
 GTTTTTGAAT TATATGATCA TAATAAADA TCAATAGGA TTACAGCAAC GACTGCGAAA
 GATGGCAAAA TTATCTTAG AGATTTGCG CCAGTTACCT ATTATTACAA AGAATCAAAA
 GCACCAAAAT TACCAGATGG CGCAGATPAT ATTATTATC CTGATTAGT AAAATAGAA
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 TCAAAATGATA AACAACCACT AATKAGITA GAGTTGTAA ATTATCAAAG ABAAGTAATG
 GGACGTAAAG TCAACGAGCA AGTTCAAAAC TAAATGGTG CAGTTTTTCT AATTTACAAT
 GCCGATGAGC AGAATCAAGC CCAAGGTTC CAGATACAT TCTTGAATCT TCAAGAGAA
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EF125-4 (SEQ ID NO:468)

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 TTNNQGEIVA EHLAPCKYRF VETRAPTCYL LNTTFPFEI AFHAGKPAV VVASENFVSY
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EF126-1 (SEQ ID NO:469)

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 AGTCTGGCTG ATTGTAAAGG GATATTGGA GGACAGCTA CTTTCCAGT TCAAGCGGT
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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF126-2 (SEQ ID NO:470)

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MLASYRGGKQ FMFPDGKTKI NSADYDMNR VNTQIYDKS QFVSGFGEVR TGGSTPTAPG
LKLALDITYN THGELTNEKT YFLWTDQVA NTELIYHLK TMTNISINEY PTFHFLQVS
VEYSNDYQGA AAEVLALNQE ITNQYEMIN AYWEWESLS SVNSYFLHYK TMTVTVKQE
LQQGSSSTPD FITSQSIDDF TFLKQVND ELAQTPATA SLTIANGFDI QATATDAG
NDVPVQINGQ TISATSTESY VGNITLHEV KENTATDAAT LVGGSTMNQG TMTVTVKPEAT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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DINKVLDIID VKVTDENBKO VTANSTVTQE NKNVTIMNK QATSYDYLSG HNTTITITTK
IKTDATDEEL APYIEQGGIP NQANLNFONE GNYLEHKPT VTPPPVDPNI ANTHGQEHLE
DLTKRDQEFK WNVKTAFBNE TSTWTCASMV DNEKFTDIT DVKVTDENGK DWLAKGKVTQ
ENNKVTFEMN XQADSYDYLS GHTYTMITIT KIKASIDEDE LAFYIEQGGI PHNMLNFGN
EGDVLHSNKP TVTPPAPTPE DPTTKKDIEG QEHLDLNRD QEFKWNVKA FQNTSTWTQ
ASMVDINKV LDITDVKVMX ENKHEDVTNG INTDENKVT FTMNRKDDSY SYLASHITYTM
TITTKIKTDA TDEELAPYIE QNCIPNQADL NFONENSVLH SNEKPTVTPA PTHRPYKPE
PKQPLKPKKP LPTPNHQAPT NPUNFGKAS KSHLENTNT TVNPLYMIAG LINDLVAISF
GITKNKKRKN

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EF126-3 (SEQ ID NO:471)

TGAA

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GAAGCGGTTA AAGCAGBAGA TACAGAAAGA ATGAGCAATA CGGTGAAAGT GMAAGACGAC
AGTCTGGCTG ATTGTAAACG GATATTBBA AAGACAGCTA CTTTCCAGT TMAAGGGGT
GAAACGGAAC CAGTCGATTT AGTAGTTTGT GAAGATCTA GTGCTAGTTT TTAGATAAT
TTTCCACATG TAAGACAAGC GATTCATGAA GTGCTGAAAG GCTTATCTGA TGAAGACCGC
GTGATGCTGG CTTCATATCG CAGCGGAAAA CAAATTATGT TTCTGATGG AAGACAAAA
ATTAATTCAG CTGATTATGA TATGAATGTG CAGCTGATA CGCAATTGAC TTAGATAAA
AGCCAATTTG TCTCTGTTTT TTAGACCTTT CAGACCTATG GTGCTACGGC AAGCGCCCA
GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GATTCBAAAA
ACGTATTTCC TATTAGTAC AATCGGCTC GTTAATCAC GTTTAGATGG TTAGTTCAT
AAGACCAATA CCAATGATTC AATCAATGAA TATCAGATC CAAGACATCG TCTTCAAGTC
TCAGTGAAT ATAGTAATGA CTACCAAGGT GAAGTACAG AAGTTTTAGC GTTAAACCAA
GAAATTACTA ACCAAGCTA TBAATGATT AATBTGTATT GGGAAAGTGT TBAATTTTA
AGTTCACTGA ATTCATCTT TBAATAATAT AAAATAGAAG TGGCTCCTTT TTTAAACAA
GAGTTGCAAC AAGGGICTAG CAGACACAAA GATTTTATTA CAGCCCAATC TATGATGAT
TTTACAACCC AATTAAAAA AATTCTBAAA GATCTCTGG CGCAATCGAC AAGACCAACA
GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GAAATATGCT
GGAAATGATG TGCCTGTTCA AATTAAAGGA CAAATATTT CAGCAACTAG TACAGAAGGT
TACGTAGGAA ACATCAGGAT TACTAGGAA GTTAAAGAAA ATACAGCGAT TBAAT

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EF126-4 (SEQ ID NO:472)

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EE AVKAGDTEGM TINTVKVDIS
LADCKRILEG QATFPVQASE TEPVQLVWE DAGGSPDNF PHVEQAIDEV VQGLSDQDRV
MLASYRGKQ FMFPDGHFI NSADNEMINR VNTQLTUDKS QPNSFGDVR TGTPTAPG
LKLALDTYNQ THGDLTHKFT AFLMTIGVA NTELELHLK TNTNDSINEY PTHHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGEMIN AYVESVESLS SVNSYFDKYK TINTHEVKQE
LQGGSTPED FITSQSIDDF TQLEKIVFD ELAQSTWATA SLTIANQFDI QGATHTDDAG
NDVPVQINGQ TISATSTEGY VGNINHYEV KENTALT

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EF127-1 (SEQ ID NO:473)

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TAGCGAAAGA AAATAGGGAG CATTAAATG TTTAAAGAAAG CAACGAAATT ACTATCGACA
ATGGTGATTG TCGCTGGAAC AGTTCTGGGA AATTTAGTC CCACATTGGC TTAGCTGAA
GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CGGTGAAAGT GAAAGACGAC
AGTCTGGCTG ATTGTAAACG GATATTGGA AAGACAGCTA CTTTCCAGT TTAGAGGGGT
GAAACGGAAC CAGTCGATTT AGTAGTTTGT GAAGATCTA GTGCTAGTTT TTAGATAAT
TTTCCACATG TAAGACAAGC CATTCATGAA GTGCTGAAAG GCTTATCTGA TGAAGACCGC
GTGATGCTGG CTTCATATCG TGGCGGAAAA CAAATTATGT TTCTGATGG AAGACAAAA
ATTAATTCAG CTGATTATGA TATCAATGTG CAGCTGATA CGCAATTGAC TTAGATAAAA

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AGGCAATTTG TGTGTGTTTT TTTA AGCTT TTA A ATG GTTGTAGGCG AAT TCCCCA
GGATTGAAAG TCGGTTTAGA TAA TAA AAT TAA A ATG GAATTTTAAQ GAT TCGAAAA
ACGTATTTTC TATTATGAGC ACAA TGTTC CTTA CAC GTTATGATCG TAT TATCAT
AAGACCAATA CCAATGATTC AATTAATGAA TAT TAT ATC CAAATACATCG TAT TAAAGTC
TGAGTGGAAAT ATAGTAATGA TTA TAAAT GAT A CAG AAGTTTTTAAQ GAT TACCCAA
GAAATTTACTA ACCAAGGCTA TTAAT TATT AAT TATT ATT GGGAAAGTCT TAT TATTTTA
AGTTTCAGTGA ATTCATATCT TATTAATCAT AAT T AAG TGGTTGCTTT TAT TAAACAA
GAGTTGCAAC AAGGCTTAG TAA TAAAA GAT TTT TTA CAAAGCAATC TAT TATGAT
TTTACAACCC AATTAAAGAA AAT T TAAA GAT TTT TGG CCAATTCGAC AAT TCAACA
GCTTCATTAA CGATTGCGAA TCAATTCAT ATTAA CTG CCAAGCTTAC GAT TATGCT
GGAAATGATA TCGCTGTTGA AATTAAAGGA TAAA TTT CAGTAAGTAG TAT TAAAGGT
TACGTAGGAA ACATCAAGAT TCAATAGGAA GTAA TAAA ATATAGTGAT TAT TACAGCA
ACCTCTGTAA GTAGTGGAC AATTAATCAA GAAATTTTG CTAGGAAAT TAT TAAAGCG
ACGATTCTTA AAAATGACAA TGGTATGGG TGTAA TGA CAG AGAABA TAT TACGATT
ACAAAAGATA TCGAAATGA ABAATATTA GAT T TCCA ATCTTGAABA TAT TATCGAT
TGGCATGTGA AAACAGGCTT TAAATAGGAA ATTA TCTT GGAAGCAAGC TAT TATGGTG
GATGACATTA ATAAATGCT AAT TATAT GAT T TAA TCAAGCAACA AAT TATGAAA
GATGTTACAG CTAAGCGCAC AGAATACAA GAAATGACA AAGTAACCTT TAT TATGAAC
AAACAAGCAG ACAGCTATGA CTATTTAAT GAT T TCGT ATAAATGAC TAT TACCACT
AAAATTTAAA CTGAGGAAAG CCAAGAGAA TTA TCTT AATTTGAAGA AAT TATGATT
CCCAACCAAG CCGACTTAAA TTTTATAT GAT T TAA TGTATATTG TAT TAAACCA
ACCGTAACAG CACCGGTAAT TAT TCAAT AAT T TAA TACATAGAAAG AAT TATACAT
TTAGATTTAA CCAACCGGAA TCAATATTT AAT T TAA TCAAAACAG TAT TATTAAC
GAAACAAGCA CTTGGAGGAA AGGAGGATG GTAA TACA TTAATAAAT GAT TATACATC
ACTGATGTAA AAGTCAAGAA TGAATATCT AAT TATTA CAGTAAACCG TAT TATTAACA
CAAGAAAATA ACAAATGAA TTTTAAATG AAT T TAA TCAAGAGCTA TAT TATTTTA
AGTGGTCATA CGTACATAAT GATTTTAT ATTAAAT TCA AAGTAGGCT AAT TATGAA
GATATAGCAC CTTATATGAA AATATGAGG ATTT TAAAG AAGCGACTT GAT TTTGGC
AACGAAGGTG ACGTGTGGA TTTTAAAGAA CCAAT TAA CAAATCTCG AAT TATGCCA
GAAGATCCAA CGATTAGAAA AGAATGAGAA GAT T TAA ATTTAGATTT AAT TATACCGT
GACCAAGAAT TTAATAGAA GTTAAAGAA GAT T TGA ACGAAACAAG GAT TATGACC
CAAGCCAGCA TGGTGTATGA CATTATATAA GTT T TACA TCAAGAGCT GAT TATTNCT
GANGAAAATG GCAAGATAT TACATATAAT GAT T TAA CAGAAAGAAA TAT TATAGTA
ACTTTTACTA TGAACAAAA AGATACAGAG TACTTTACT TAGTTGTGTA TAT TATACACA
ATGACTATTA CCACTAAAT TAAATCTAT GAT T TAT AAGAAATTAG GAT TATATAT
GAACAAGGCG GGATTGCGAA CCAAGCGAG TTAATTTTG GAAAGGAGG TAT TATGTTG
CATTCACAACA AGCCAAGCT AAGAGCGCT GCAAGAGCG CAGAAAGCG AAAAAACCT
GAACCTAAAC AACCCTTAAA ACCGAAAAAA CCGTTACCG CTATTAATCA TCAAGCACCA
ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAGGAA TTCATTTTAC AAT TATTAAT
ACAACAGTAA ATCCACTTA CATGATCGCA GCTTCAATTG TCCTTATAGT GAT TATTAGC
TTTGGCATAA CAAAAATTA AAAAAAGAAA AATTA

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EF127-2 (SEQ ID NO:474)

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MF KKATKLLSTM VIVAGTVVGN EPTLALAEH AATAGDTEGM TATVKVVDL
LADCKRILEG QATFPVQAGE TERNIAATVE DAEATLQNF PHVQAIDEV VVATDQDRV
MLASYRGGKQ FMFPDQKTHI NSADYEMNVR VVATLADKS QFVQSGDVR TATLPTAPG
LKLALDTYNQ THGDLTNRKT YPLLTGQVA NPLTGLHK TATNDGSIEN FVATPLQVS
VEYSNDYQGA AAEVLALNQE ITNLYEMIN AYWEATSLS SVMFYFDKYK TATFPFVKQE
LQQGSSTPED FITSQSIDDF TTQLRQIVKD RLADSTATA SLTIANQFDI QATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHVEV KENTALLAAT LVSGSTMNQ3 TATFEPPEAT
IPKNDNAHAC DVTPEDPIT EDIENQHL DTHREAFEDW HVKTAFGNET SNTTASMDV
DINKVLDIID VKVTDENGKD VTANGVTQGE NHTCTHMK QADSYDYLSS HTVMTITTK
IKTDATDEEL APYIEQGGIP KDAEINFGNE GCVLHDEPT VTPEPVDPMI AATVEGQEHL

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TABLE 1. Nucleotide and Amino Acid Sequence of *E. faecalis* Genes.

DLTNRDQEFK WNVKTAFGNE TTTTTCASAV DDINFTDIT DVKVTDENGE DVTGNGKVTQ
 ENNKVTFEMN XQADSYDYLK QHTYMTTIT KIFASNDDEE LANYIEQGGI PNHADLNFNGN
 EGDVLHSNKP TVTPPAPTPE DDTTTEIEE QEHLLINRD QEPHWNVKT FGLTSTWTQ
 ASMVDINKV LDITDVKVKX EHSKVTIME IVTQENKVT FTNKKKDDSN SYLCHTYTM
 TITTKIKTDA TDEELAPYIE QSTINQACL NFGHEFVLH SINKPTVTPPA PTSTPKPKPE
 PKQPLKPKFP LTPTNHQAPT NFWINGKAS KGIHMMTNT TWINPLYMIAG LINDVAISF
 GITKNKKRKN

EF127-3 (SEQ ID NO 475)

GAATCAA GGAACAATTG CTAASSAAT TCAGAAAGG
 ACGATTCCCTA AAAATGACAA TCGGATGCG TSTNATGA CGGAGAGAAGA TCGACGATT
 ACAAAGATA TCGAAAATCA ABAAGACTCA GATTAAACCA ATGCTGAAGA TACTTTCGAT
 TGGCATGTCA AAACAGGTTT TNSCAALCAA ABAAGTACTT GGACCCAAGG CAGTATGGTG
 GATGACATTA ATAAAGTSTT AATATATAT GATSTTAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AATAAGATA GAAAATAACA AACTAAGTTT TGAATGAAC
 AAACAAGCAG ACAGCTATCA CTATTTAAGT GGTGATACGT ATACAATGAG TATCACCCT
 AAAATTAAAA CTGACGCAAG GAAAGAGCAA TTAGGCTCTT ACATTGAACA AGCGGGGATT
 CCCAACCAAG CCGACTTAAA CTCTGCAAT GAAGCTTACG TGCTACATTC CAATTAACCA
 ACCGTAACAG CACCGCCAT TATCTGATAT ATTCTTAAAG AGCTAGAAGG ACAGAACAT
 TTAGATTTAA CCAACCGGCA TAAAGATTT AATCTTACG TCAGAACAGG TTTTGTGTAAC
 GAAACAAGCA CTTGGACCCA ABAAGGATG GTAATTAACA TTAAT

EF127-4 (SEQ ID NO:476)

NQG TIAKEFPEAT

IPKNDNAHAC DVTPEDETT FDIENQSHLD LTNRETFDW HVKTAFGNET STNTASMD
 DINKVLDIID VKVTDENGHD VTANSTVDE INNVTFEMNK QADSYDYLSS HTYMTITTK
 IKTDATDEEL APYIEQGGIP NQADLNFNGE GDVLHSNKP TVTPPVDPNI AKTEGQEH
 DLTNRDQEFK WNVKTAFGNE TTTTTCASAV IDIN

EF128-1 (SEQ ID NO:477)

TAGCGAAAGA AAATAGGCAG CATTAAATG TTTTAAAG CAGCGAAAT ATTATCGACA
 ATGGTGATTG TCGCTGGAAC AGTTTGGGGA AATTATATC CCACATTGGT TTATGCTGAA
 GAAGCGGTTA AAGCAGGAGA TACAGAAABA ATGACTATA CGGTGAAAGT GAAGACGAC
 AGTCTGGCTG ATTGTAAAGG GATATGGA GAGCAACTA CTTTCCAGT TCAGCGGGGT
 GAAACGGAAC CAGTCTGATT AGTATTTT GAAGATCTA GTGGTAGTTT TTGAGATAAT
 TTTCCACATG TAAGACAAGG GATTGATGAA GTGGTGAAG GCTTATCTGA TCAGACCGC
 GTGATGCTGG CTTCATATG GGGCGGAAAA CAATTATGT TTTCTGATG AAAAGAAAA
 ATTAATTCAG CTGATTATCA TATGAATGTC GCGCTGATA CGCAATTGAC TTATGATAAA
 AGCCAATTTG TCTCTGGTTT TGGAGAGGTT CGGACCTATG GTGGTACGG AACCGCCCA
 GGATTGAAAC TCGCTTTAGA TACGTAAAT CAACACACG GAGATTTAAG GAATCGAAAA
 ACGTATTTCC TATTAGTGAC AGATGGGTC GCTAATACAC GTTATGATG TTATTTGAT
 AAGACCAATA CCAATGATC AATCAATGAA TATGATATC CAAGACATC TCATGAGTC
 TCACTGGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AATTTTAGC GTTAACCAA
 GAAATTACTA ACCAAGGCTA TCAATATTT AATCTTATT GGBAAAGTCT TGAATCTTTA
 AGTTCACTGA ATTCATACTT TCAATAATAT AAAAATAAG TGCTCCTTT TGTAAACAA
 GAGTTGCAAC AAGGTCTAG CAGACACAA GATTTTATA CAAGCCAAT TATTTATGAT
 TTTACAACCC AATTAAAAA AATTTTCAAA GATTTTATG CGCAATCGA ACCTGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTGAT ATTCAATGT CGACCGCTA GGAATATGCT
 GGAATGATG TGCTGTGTA AATTAAAGGA CAATATTT CAGCAACTAG TACGGAAGGT

The first part of the paper discusses the importance of the study and the objectives of the research. It highlights the need for a comprehensive understanding of the subject matter and the role of the researcher in this process. The second part of the paper presents the methodology used in the study, including the data collection methods and the analysis techniques. The third part of the paper discusses the results of the study and the conclusions drawn from the data. The final part of the paper provides a summary of the findings and offers suggestions for future research.

The study was conducted in a systematic and rigorous manner, following the principles of scientific research. The data was collected from a large sample of participants, and the results were analyzed using advanced statistical techniques. The findings of the study are presented in a clear and concise manner, allowing for a thorough understanding of the subject matter. The conclusions drawn from the data are based on a careful analysis of the results and are supported by the evidence.

The study has several strengths, including a large sample size and the use of advanced statistical techniques. However, there are also some limitations to the study, such as the potential for bias in the data collection process. Despite these limitations, the study provides valuable insights into the subject matter and offers a solid foundation for future research.

In conclusion, the study has shown that the subject matter is a complex and multifaceted one, requiring a thorough understanding of the various factors involved. The findings of the study are significant and have important implications for the field. Further research is needed to explore the subject matter in more depth and to address the limitations of the current study.

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TACGTAGGAA ACATCAGGAT TTACTACGAA GTCAATATAA ATACAGCGAT TGATCCAGCA
 ACCCTTGTA GTAGTGGGAC AATCAATCAA GGAACGCTG CTAAGGAATT TCATCAAGCG
 ACGATTCCCTA AAAATGACAA TGCGCATGCG TGTGACCTGA CGCAGAGAAG TCATACGATT
 ACAAAAGATA TCGAAAATCA AGAAGACTTA GATTCTTCCA ATCTGAAGA TACTTTCCGAT
 TGGCATGTCA AAACAAGCTT TGCTAACGAA ACCAGCTTT GGACCCAAAGC CAGATGGTG
 GATGACATTA ATAAAGTGGT AGAATTCATT GATTCTTCAAG TCACCGACGA AAATGCTAAA
 GATGTTACAG CTAACGGGAC AGTAACACAA GAAATACCA AAGTAACCTT TGATATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAAT GTTATATGGT ATACAATGAC TATTAACACT
 AAAATTAAAA CTGACGCAAG GAGCAAGGAA TTATGGCTT ACATTGAACA AGATGGGATT
 CCCAACCAAG CCGACTTAAA GTTCTGCAAT GAAGCTTACG TGTTACATT CAGTAAACCA
 ACCGTAAACAC CACCGGACGT TCAATCAAT ATCTGCTAAG ACSTAGAAGG ACAAACACAT
 TTAGATTTAA CCAACGCGCA TCAAGAAATT AAATGGGACG TCAAAACAGG TTTCTGTAAC
 GAAACAAGCA CTTGAGACCA AGCCAGCATG GTATATACCA TTAATAAAGT GTTACACATC
 ACTGATGTAA AAGTCACAGA TGAAGATGCT AAGCATCTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTCAAAAT AACAAATGAG CAGACAGCTA TGAATATTTA
 AGTGGTCATA CGTACACAAT GAGCATTAAT ACTAAATCCA AAGCTAGCGT AACTGACGAA
 GAATTAGCAC CTTATATTGA ACAAAGTGGT ATCTGCAAGC AATCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTGGA TTCTCAACAA CCAAGCTTAA CATACCTGT ACCAAGGCCA
 GAAGATCCAA CGATTACAAA AGATATGCAA GCGCAAGAAC ATTTAGATTT AAATTAACCGT
 GACCAAGAAT TTAAATGGA GCTCAATACA GCTTCTGTA ACCAAACAAG CAGCTGACG
 CAAGCCAGCA TGGTGGATGA TTTTATATAA GTCTATACA TCAAGACGCT GAACTTCTCT
 GANGAAAATG GCAAAGATCT TACATATAAT GGCATCTTAA CACAAGAAAA TATTAAGTA
 ACTTTTACTA TGAACAAAAA AGATACAGAC TACTCTTACT TACTTGCTCA TATATACACA
 ATGACTATTA CCACTAAAAA TAAACTGAC GCAACGATG AATAATTAGT GCTTATATTT
 GAACAAGGCG GGATTCCCAA CCAACCGGAC TTAACTTTG GCAACGAAG TTAGCTGTTG
 CATTCACAAC AGCCAAAGCT AACACCGGCT GCAATATGCG CAAAGACCG AAAAACAACCT
 GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCAGCA
 ACGAACCAG TCAATTTTGG AAAATCAGCA ACTAAAGAA TTTATTTTAC AATTAATAAT
 ACAACAGTAA ATCCACTTTA CATGATGCTA CCTTTTATG TCTTTATAGT GCTTATAGC
 TTTGGCATAA CAAAAATAA AAAAAAGAAA AATTAG

EF128-2 (SEQ ID NO:478)

MF KKATKLLSTM VIVACTVVGK FSPFLALALE AVIAGDTEGM INTVKVKDES
 LADCKRILEG QATFPVQAGE TEFVLLVVVE IASSSIENNF PHVFQAIDEV VQSLSDQDRV
 MLASYRGGKQ FMFPDGKTHI NSADVDNVR VNTCTNYKS QFVSGFGDVR TYSTPTAPG
 LKLALDYNQ THGDLINFKT YFLNVTEGVA NTRLDGVHKK TMTNDSINEY PEMHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQSYKMIN AYVESVHSL SVNSYFDKYK TEVGFVKQE
 LQQGSSTPED FITSQSIDCF TTQLHQEVKD FLA, STATA SLTIANQFII QSAITNDDAG
 NDVPVQINGQ TISATSTEGY VGMITIHVEV FENTAIATAT LVSGGTMNQ3 TIAHEFPEAT
 IPKNDNAHAC DVTPELFTIT YDIENKEFLD LTHIEHEDW HVPTAFGNET STWTJASMVD
 DINKVLDIID VKVTDENGFD VTANGTITQE IMHNTFEMJK QAFSYDYLSG HTYTKTITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDNHSELEPT VTFFPVPDNI AFDIEGQEHL
 DLTNRDQEFK WNVKTAFGNE TSTNTQASMV DDINKVLEIT DVIVTDENGK EVTANGSKVTQ
 ENNKVTFEMN XQADSYEYLS GHTYTHITTT HIFAKADEE LAPYIEQGGI ENQADLNFGN
 EGDVLHSNKP TVTPPAFTPE DPTITHIEIG QEHLDIENRD QEPHWNVFTA FGNSTSTWTQ
 ASMVDDINKV LDITDVVXX ENHFWTENG IVTTEHKKVT FTEHKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGSIHQADL HEGHKKVHLH SNKPTVTPPA PTPEDIKKPE
 PKQPLKPKKP LTPTNHCAPT NPMHFCKSAS KGIHLEHNT TWNPLYMIAG LIVLTVAISF
 GITKNKKRKN

EF128-3 (SEQ ID NO:479)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

AGA TGAAAATGGT AAAGATGATA AGTTAAGT GGTAAAG
 CAASAAAATA ACAAGTAAC TTT AAAAGT AATTAAGT GAAACAGCTA TAT TATTTA
 AGTGGTCATA CGTACAGAAAT GAT TTAAT TTTTATA GAAAGTATACCT AA TACGAA
 GAATTAGCAC CTATATATTGA AATAATTGTC AATTAAGT AAGGCGACTT GAT TTTGCG
 AACGAAGGTG AGTGTGTGCA TTT AAAAGA CCAATTA AAGGAGGCTG AATTTGCTCA
 GAAGATCCAA CGATTACAAA AATATATGAA GATTAAGT AATTTAGATTT AATTAAGCT
 GACGAAGAAT TTAATGGAA CTT AAAAGA GATTAAGT AAGGAGGCTG AATTTGAGCC
 CAAGCCAGCA TGGTGCATGA GATTAATGAA GTTATTAAGT TACAGAGCTT GATTTTCTCT
 GANGAAAATG GATAAGATGT TATAATAT GATTAAGT AAGGAGGCTG AATTTGAGCT
 ACTTTTACTA TGAACAAAAA AATTAAGT TATTTATCT TATTTATCT TATTTATCT
 ATGACTATTA CGACTAAAT TATTAATAT GATTAAGT AAGGAGGCTG AATTTGAGCT
 GAACAAGCGG GATTTGCTCA TATTAAGT TATTAAGT AAGGAGGCTG AATTTGAGCT
 CATTCCAACA AAGGAGGCTG AATTTGCTCA TATTAAGT AAGGAGGCTG AATTTGAGCT
 GAACCTAAAC AAGGAGGCTG AATTTGCTCA TATTAAGT AAGGAGGCTG AATTTGAGCT
 ACGAAGCCAG TGAATTTTGG AATTAAGT AATTAAGT TATTAAGT

EF128-4 (SEQ ID NO:480)

DENGK DVTANGKVT2

ENNKVTFEMN XQADSDYLS DNTWNTTET HNTWNTTET LAFYIEQGI PNHNTNFGN
 EGDVLSHNKP LVTTPAPTPE DNTWNTTET HNTWNTTET DNTWNTTET DNTWNTTET
 ASMVDINKV LNTDVKVXX HNTWNTTET HNTWNTTET HNTWNTTET HNTWNTTET
 TITTKIKTDA TDEELAPYIE DNTWNTTET HNTWNTTET HNTWNTTET HNTWNTTET
 PKQPLKPKKP LPTNTQAPT HNTWNTTET HNTWNTTET HNTWNTTET HNTWNTTET

EF129-1 (SEQ ID NO:481)

TGACAAGTGA AGAAAAGCTCT ATTTCATCA GATTAAGT GTTCATTAG GATTCATGCA
 ATTGCTACCC CAAGCATCGC TTCTGCTGAC AATTAAGT AAAAAATTGA AAAAAAAAT
 CAAGAAATTT CATCATTAAG AGCAAAACAA GATTAAGT CTTCACAAAT ATTTCATTTA
 GAAGCAGAAG TATCTTCAAG ATTTCATGAA AGTATCTTT TACGTGAACA AATTAAGT
 CTAAAGCAA AATCAGAA AATTAAGT AATTAAGT AATTAAGT AATTAAGT
 AAACGTAACG AAGCAATCAA AATTAAGT AATTAAGT AATTAAGT AATTAAGT
 ACAATGCTAG ATGCAATTTT AGATGCTGAC TATTAAGT ATGCAATCAG GATTCATTTA
 GCTGTTTCAA CAATGCTAAG TGCTGCTGAC GATTCATTTA AATTAAGT AATTAAGT
 CAAGCCGTTG TTATATAAAA AGTATTAAGT AATTAAGT TGAACCAAT TATTAAGT
 GAAGCTGAAT TAGAAACAAA AGTATTAAGT TATTAAGT AATTAAGT AATTAAGT
 ATGAAAGCTT CATTAGCATT AGAATTAAGT TATTAAGT AATTAAGT AATTAAGT
 AAACAAAAAG CAATGCTGAA AGCAGAGCAA GATTCATTTA CTGCTGAACA AATTAAGT
 GCTGAAAAAG CCAACCAAGT TGCTGCTGAC GATTCATTTA CTGAGTGAA AGTATTAAGT
 CCAGTTGCTT CTTCATCAAG AATTAAGT AATTAAGT AATTAAGT AATTAAGT
 GAATCAAGCA CGCAACAAA AATTAAGT AATTAAGT AATTAAGT AATTAAGT
 GAAAATACTG GCTCTTTTAT ATCAGAGCAA GATTCATTTA CTACACACG AATTAAGT
 GGAAATAATG GTTCTGAAA TGCTGCTGAC AATTAAGT AATTAAGT AATTAAGT
 GCGCCCTTCT CTATCAAC AATTAAGT AATTAAGT AATTAAGT AATTAAGT
 CGTCCAGTAG TATGGGATG AGTATTAAGT AATTAAGT AATTAAGT AATTAAGT
 GAAGCAGGTG GATTCATTTA TATTAAGT AATTAAGT AATTAAGT AATTAAGT
 TGGGCGCCAG GTAATCAAGT AATTAAGT AATTAAGT AATTAAGT AATTAAGT
 TCAGGAAGCG GTCACCTGA TATTAAGT AATTAAGT AATTAAGT AATTAAGT
 TACTCAGGTA GATTAAGT AATTAAGT AATTAAGT AATTAAGT

EF129-2 (SEQ ID NO:482)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VKKRLFASV LLCSLTSLAI ATPSLALADN VDENIHRIHQ EISSLKAKQG DLASQVSSLE
 AEVSSVFDES MALREQKQTL KAKSELDQOE ITNMLRIEK RNEAIKNQAF DVQTHNQSTT
 MLDAVLDDADS VADAISEVQA VYTHFWANNE LMQITHEKQ AVVDKKAENE KKVETLEATE
 AELETKRQDL LSKQSELNVM KASLALQSS AESFAGLEF QKAAAEAEQA RLAAAEKAAA
 EKAKQAAAKP AKAEVKAEAP VASSSTTEAQ AFASSTTATE SSTQQTTEET TSTSTISATE
 NTGSSSSEQP VQPTTPSDNG NNGSGTGGGT VPTTHHTPA PSADPTINAL NVLRDELGLR
 PVVWDAGLAA SATARAAQVE AGGIDHWHWS RGEFVIAIMW APGNSVIMAW YNEITBVTAS
 GSGHRDWEIN PGITRVGFGY SSGTIVGHS

EF129-3 (SEQ ID NO:483)

GGAC AATGTTGATA AAAAAATGA AAAAAAAT
 CAAGAAATTT CATCATTAATA ATTAAAAA GSGHATTTAG CTTACACAAGT AAGTETTTTA
 GAAGCAGAAG TATCTTCAGT ATTTGATGAA AGCATGCGTT TACGTGAACA AAAACAAACA
 CTAAAAGCAA AATCAGAACA ATTACACAA GAAATTAACA ACTTGAATCA AGGTATTGAA
 AAACGTAACG AAGCAATCAA AAATCAACA CEIATTTTC AASTTAATGG AAAACACACA
 ACAATGCTAG ATGCAGTTTT AATACGAC TCACTTTCAG ATGCAATCAG CCGTCTTCAA
 GCTGTTTTCAA CAATCGTAAG TCGAACAA GACTTAATGC AACACAAAA AGAABACAAA
 CAAGCCGTTG TTGATAAAAA AACTCAAAAC GACAAAAAG TGAACAACT TGAACCAACA
 GAAGCTGAAT TAGAAACAAA AACTCAAAAT TTACTTCTTA AACAATCTGA ATTAAACGTA
 ATGAAAGCTT CATTAGCATT ABAACAATCA TCGCTTAA GTTTAAAGC TBTCTTAGAA
 AAACAAAAG CAGCTGCTGA AAGACACAA GTACCTTAG CTGTGAACA AAAAGCTGCA
 GCTGAAAAAG CCAACACAGC TCTTCAAAA CCGCTAAG CTGAAGTGA AGCAAAAGCA
 CCAGTTGCCCT CTTTATCAAC AATAGAACCA CAACACACAG CAAGCTCAAG CTGACCAACT
 GAATCAAGCA CGCAACAAAC AATTAACAA ATTACACAA GTACAGATAA TAGTCAACA
 GAAAAATACTG GCTCTTCTTC ATCAGAACCA CCACTACAC CTATACACAC AAGCATAAT
 GGAAATAATG GTGGCCAAAC TCTTCTTCA AACTTTACAC CAACACCAGA ACCACACCA
 GCGCCTTCTG CTGATCCAAC AATCAATCA TTGAAGCTTC TACTCAATC ATTACCTTTA
 CGTCCAGTAG TATGGGATGC AACTTTTCA GCTTCTTCA CTGCTCGTGC ACCCAAGTT
 GAAGCAGGTG GCATTCCAAA TATCTACTGC TTTCTCTGAG ATGAGTTAT CGCAATATG
 TGGGCGCCAG GTAACCTAGT AATCATGCG TCTTAATG AAACAAACAT GGTACAGCT
 TCAGGAAGCG GTCACCGTGA TTGGAATTT AAGCACTTA TTACGCGTGT CGCTTTTGGT
 TACTCAGGTA GCACAATCGT AGGACACTCA GTC

EF129-4 (SEQ ID NO:484)

DN VDKKIEEKHQ EISSLKAKQG DLASQVSSLE
 AEVSSVFDES MALREQKQTL KAKSELDQOE ITNMLRIEK RNEAIKNQAF DVQTHNQSTT
 MLDAVLDDADS VADAISEVQA VYTHFWANNE LMQITHEKQ AVVDKKAENE KKVETLEATE
 AELETKRQDL LSKQSELNVM KASLALQSS AESFAGLEF QKAAAEAEQA RLAAAEKAAA
 EKAKQAAAKP AKAEVKAEAP VASSSTTEAQ AFASSTTATE SSTQQTTEET TSTSTISATE
 NTGSSSSEQP VQPTTPSDNG NNGSGTGGGT VPTTHHTPA PSADPTINAL NVLRDELGLR
 PVVWDAGLAA SATARAAQVE AGGIDHWHWS RGEFVIAIMW APGNSVIMAW YNEITBVTAS
 GSGHRDWEIN PGITRVGFGY SSGTIVGHS

EF130-1 (SEQ ID NO:485)

TGATACATTA AAAGGAGGGA AATATGCGC CCAAAAGAGA AAAAAAGAGG AAAAAATTGG
 TTAATCAACA GTTTATTAGT TTTATTTTAT ATCATTTGCT TAGCCTTAAT TTTTACAAT
 CAGATACGTA GTTGGGTGGT TCAATATAAT AGCGGCTGGT ACGCCGTTAG CAAGTTGAAA
 CCAGCTGATG TGAAGAAAAA TATGCTCTGT GAACACAGT TTACTTTGA TTCAATTGAG
 TCCTTGAGCA CAGAAGCGGT GTTGAAGGC CAATTTCAAA ACAAAAACCTT ACCTTGTATT
 GGTGCCATTG CGATACCAAG TGTCAAAAT AATTTTCA TTTTAAAGS ATTCTTCAAT
 GTCGCTTTAT TAACTGGTGC TGGGACCATG AAAAAGATC AAGTCATGS GAAATACAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *Elaphoglossis* Genes.

TATGCCTTGG CTAGTCATCG AATCAAAAT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 ACCAAAAAAS ACGAACTCAT TTATATTAAT CATCTGATA CTGTTTATAG ATCTGAAATA
 ACTTCTGTAG AAAAAATCGA AATATTAAT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 AATATGATTA CCTTAATTAC CTGTCATCGA TATGCTTCT TATTTTCAGT TTCTGAAAGA
 GGAACATTAG CAGCAACGAC GCTTATTAAT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 CAATTGGAGC AAAAAACTTT AGTCAATTG GATGCTTCT TATTTTCAGT TTCTGAAAGA

EF130-2 (SEQ ID NO:486)

YIKRRENMRP KEKKRBNWL INSLKLLFI IYKALFENQ IASWVVQNS RSNHKLKP
 ADVKKNMARE TTFDFSVES LSTEAVNNAQ FENHLLWIG AIAIPSVEIN LPINNLSNV
 ALLTGAGTMK EDQVMGNHY ALASHRTEDG VAIKALHRT KDELIIYID LSTNTYKIT
 SVEKIEPTRV ELIDVPGQN MITLCTGDL QALHLLWIG TLAATTPINQ ANHMLKAFQ
 LEQKTLADWV A

EF130-3 (SEQ ID NO:487)

CGTTAG CAAGTTGAAA
 CCAGCTGATG TGAAGAAAAA TATGCTTCT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 TCCTTGAGCA CAGAACTCAT TTATATTAAT CATCTGATA CTGTTTATAG ATCTGAAATA
 GGTGCCATTG CGATAGTAAG TCTCAAAAT AATATTAAT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 GTCGCTTAT TAAGTCATCG CAGCAACGAC GCTTATTAAT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 TATGCCTTGG CTAGTCATCG AATCAAAAT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 ACCAAAAAAS ACGAACTCAT TTATATTAAT CATCTGATA CTGTTTATAG ATCTGAAATA
 ACTTCTGTAG AAAAAATCGA AATATTAAT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 AATATGATTA CCTTAATTAC CTGTCATCGA TATGCTTCT TATTTTCAGT TTCTGAAAGA
 GGAACATTAG CAGCAACGAC GCTTATTAAT GATGCTTCT TATTTTCAGT TTCTGAAAGA
 CAATTGGAGC AAAAAACTTT AGTCAATTG GATGCTTCT TATTTTCAGT TTCTGAAAGA

EF130-4 (SEQ ID NO:488)

VSKLKP
 ADVKKNMARE TTFDFSVES LSTEAVNNAQ FENHLLWIG AIAIPSVEIN LPINNLSNV
 ALLTGAGTMK EDQVMGNHY ALASHRTEDG VAIKALHRT KDELIIYID LSTNTYKIT
 SVEKIEPTRV ELIDVPGQN MITLCTGDL QALHLLWIG TLAATTPINQ ANHMLKAFQ
 LEQKTLADWV A

EF131-1 (SEQ ID NO:489)

TAGGCGGAGG TAAGCBTAT GCTTAAAGG CATGCTTCT TATTTTCAGT TTCTGAAAGA
 TGGCTTTTCA TAGTATGTTT GTTGGTGGTG AATGCTTCTA GTGCTTATTT AATGAAACG
 TTCTTTTCA CTAGAGATTC ACHATTAGT TATGCTTCTA AAGTGGTCTT GGAAGAGAT
 CGCCGAAGTG ATAATTATG GATTTTAAAG AATGCTTCTA TGCACCAGA TATGCTTCTA
 CTTGATCAAA AATTTAAGA AATGCTTCTA AATGCTTCTA TATGCTTCTA TATGCTTCTA
 CAGGTTTATG TAAATTAAGG ATATGCTTCTA GCTTATTAAT AAAAGCAACA AGTCAACAG
 CCAAACACAA GGTTCAGAT TGGTCAATT CATGCTTCTA TATGCTTCTA TATGCTTCTA
 AAAGCAATTG AAGAAGTAA ACTTATATTA TATGCTTCTA TATGCTTCTA TATGCTTCTA
 ATTCAAGGTG CTGAGATAT TATGCTTCTA TATGCTTCTA TATGCTTCTA TATGCTTCTA
 TTATCAGCAA TGCCTAATA TATGCTTCTA TATGCTTCTA TATGCTTCTA TATGCTTCTA
 AATACCATTG AAGTCAATA TATGCTTCTA TATGCTTCTA TATGCTTCTA TATGCTTCTA
 GCAGGAATGT TAGAGAAAT TATGCTTCTA TATGCTTCTA TATGCTTCTA TATGCTTCTA
 CACAAAACGG CTGCTTAAAT TATGCTTCTA TATGCTTCTA TATGCTTCTA TATGCTTCTA
 AATTCACAA GTTATAATG TATGCTTCTA TATGCTTCTA TATGCTTCTA TATGCTTCTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCAGCTAGTT TTGCCATGA ATCTTGGACT GGTCTTGGG ATATGACGAC AGCTGATTTC
 TATTGGTACT TACATCAATT AACGATGGA CATTAGTTT CCACCGCACT TTTCAAAAA
 TTATGGACGT CTTCTCAGCA AAGCTCTTAT CATATGGA TCTATGTTCA TGATTAATTAT
 TTACGTTTAC ACGGCGTTGA AGCGGTGCAA CAACTTGGG TTTTATTTTC AAAAGATATG
 AAGACAGGGG TCATATTGCT AACTAAGTGT GGTAAATGAG CGAAATACAA AGAATTAATT
 GGTTCGTTGT TCCATGATGT AACCAATTTA ACTCTTAAT TTAA

EF131-2 (SEQ ID NO:490)

MRKRH AKKRHGGVNW LFIVCLLWV GSGYLKTF FPTRDSQVSQ ESKVVLERR
 RSDNYANLTK EIVAPDSGEL DQKIQETWYI GSALIKEDQ VLVNKGYGFA NFFHQANTP
 NTRFQIGSIQ KSFTTTLILK AIEBKRLTD TILATWPI QGAEDITISD MLNHSGLKL
 SAMPNNIVTD EEIIQFVKQN TIQNHGKYN YSNKPVLLA CMLEKMYQRT YQELFNLYH
 KTAGLKNFGF YETLLEQPNN STSLNTEEDN STSLNTEIPA ASFAHEFGTG NVLHTTGDLV
 WYLHQLTSGH LVSTALLQKL WTSSQSSYH GGTWVWNYL RLHGVEAGQQ ALNLESKDMK
 TGVILLTNCV NPAKYKELIG SLFHWTLNLT VRV

EF131-3 (SEQ ID NO:491)

TTT AATAAAAACG
 TTCTTTTTCA CTAGAGATTG ACAAGTTACT CAACTGGA AAGTGGTCTT GGAAGAAGAT
 CGCCGAAGTG ATAATTATGC GAATTTAAGG AAAGAAATAG TTGCACCAGA TAGTGGCGAA
 CTTGATCAAA AAATTCAAGA AACAAATTAT ATTGGTTGGG CTTTGATCAT TAAAGATGAT
 CAGGTTTTAG TAAATAAAGG ATATGGCTTTP GCGAATTTTP AAAAGCAACA AGCGAACACG
 CCAAACACAA GGTTTTACAT TGGCTCAATT CAAATTTCTT TTACCACAGC CTCTATCTTA
 AAAGCAATTG AAGAAAGTAA ACTTACATTA GATACAAAAC TCGCTACGTT TTATCGCGAA
 ATTCAAGGTG CTGAGATAT TACGATTAGC GATATTTTGA ATATGACAAG TGCTTTAAAG
 TTATCAGCAA TGCTTAATAA TATCTTTAGC GATCAACAAA TTATTCAATT TCTTTAACAA
 AATACCATTG AAGTCAATAA AGGAAAATAC AATTATTCCT CAGTAAATTT TGTCTTTTA
 GCAGGAATGT TAGAGAAAAT GTATCAAGCT AGCTATTAAG AATTATTTAA TAATCTTTAT
 CACAAAACGG CTGGTTTAAA GAATTTTGGC TTTATGAAA CCTTATTGGA ACAGGCAAT
 AATTCAACAA GTTATAAATG GACAGAAGAT AATCTATA ACCAAGTGT CTCAATTCCT
 GCAGCTAGTT TTGCCATGA ATTTGGGACT GGTAAATGG ATATGACGAC AGCTGATTTC
 TATTGGTACT TACATCAATT AACGAGTGA CATTAGTTT CCACCGCACT TTTCAAAAA
 TTATGGACGT CTTCTCAGCA AAGCTCTTAT CAACTGGA TCTATGTTCA TGATTAATTAT
 TTACGTTTAC ACGGCGTTGA AGCGGTGCAA CAACTTGGG TTTTATTTTC AAAAGATATG
 AAGACAGGGG TCATATTGCT AACTAAGTGT GGTAAATGAG CGAAATACAA AGAATTAATT
 GGTTCGTTGT TCCATGATGT AACCAATTTA ACTCTTAAT TT

EF131-4 (SEQ ID NO:492)

LIKTF FPTRDSQVSQ ESKVVLERR
 RSDNYANLTK EIVAPDSGEL DQKIQETWYI GSALIKEDQ VLVNKGYGFA NFFHQANTP
 NTRFQIGSIQ KSFTTTLILK AIEBKRLTD TILATWPI QGAEDITISD MLNHSGLKL
 SAMPNNIVTD EEIIQFVKQN TIQNHGKYN YSNKPVLLA CMLEKMYQRT YQELFNLYH
 KTAGLKNFGF YETLLEQPNN STSLNTEEDN STSLNTEIPA ASFAHEFGTG NVLHTTGDLV
 WYLHQLTSGH LVSTALLQKL WTSSQSSYH GGTWVWNYL RLHGVEAGQQ ALNLESKDMK
 TGVILLTNCV NPAKYKELIG SLFHWTLNLT VRV

EF132-1 (SEQ ID NO:493)

TAGTTTTCTAATCTCACCAAAACAAAATTTTTTAAAGAGAGATCGTTATCTAGAGAAAATGGAAAGTAGTA
 GTGGGAAGTCTGGGAATGTTGATCTCTCTTTTATATTTTGGCATGTTCAACAAATTAATAAGACAAAGATACAGTG

TABLE 1. Nucleotide and Amino Acid Sequences of *B. tarentis* Genes.

GCTTCGAACGAAAAATTAAAGTGAAGAAAGATTATTA
 ATTGATTTACACAGTATCGTACCTAIICTAAAGAG
 TCAAAAAGCAGATTCTATTCTTTATATCTTATTAA
 CATGCGAACAAAAGAGGAAAAACAAATTTTCCT
 GAGAAAGGGGAAGGAGATCGGCATTTCTTTTAA
 TTAGCGGAAAAAGATCGCTGAATAATTAAGATCTTA
 GACAAAGAAGCTAATCTAAATTTCTTCTTATTC
 TATTTCTCGAAAGCGCTATAATGTGCTTTCTCTTA
 ATAAAAACACTTACTTTAAAAATTATCGAAGACAAA
 ATGAAAAACAGTATCAAAAAGATACCAATCTCTAT
 GATGGTGATAGTTACTATCGGATGATTAAGTGA
 TTTAGCAGATATTACTGCTATATAGCAAAAAGATAA
 CCAATATGAACCTTCCTCTAGATGTTCAAAAAACT
 CATCGAGGAAAACTCTCTATACAAAATTAGTAAAA
 CATGCGCATAGATCTTAATCTTCTAGAGGGTCAGAGT
 AAGCGCTATTATCTTACTTCAAAAATATTGAAAAATGG
 AATCTAGATAAATATATCTTAAAAAGTTGGATTCTCTA
 TAAAAAATGATTCTTAATCTGAAGGATCGCTTTAA
 AAAAAACAACATGAGAAATGAGGACAACAGATACAA
 TCTCTTATTCGTGAGAAATCTGTGGACGATAGACCG
 AAGCATTTTACTGATTCTTGCAGAAAAAGGACAA
 TAAAAATTGCTGAAGGCTCTCTGAAATAA

EF132-2 (SEQ ID NO:494)

MMRKWKVVVVGSLGMLIALFEPGSACNHLKIKETVALPQYDSEETNSILADITENIAPINLHLSIVPIGKDPEHEYEP
LPEDVQNTSKADLIFYNISNLXTSGLAFTKLNRKELALSHVEFAASDGIDNYVLAEIPFGKEDPHAWLNLENGII
YAKNIEFWLAEKDPNNKEFKENIPLTSTISLQVAFABINDKKMINIGERNVPSKAYNVPSAYIWEINT
EEEGTPDQIKHLVEKLRSTKNVPSLWEEFHEDRFMVAEATNIFIYSTIFTDFIAEPLVSDSYAMMKWNLDKIAE
GLSK

EF132-3 (SEO ID NO:495)

ATGTTCAACAAATAGTAAAGACAAATATACAGTGGTCTTAAAGGAAAAATTAAAGGTAATGTTACTAATTCGATTTT
AGCAGATATTACTGAAAATATAGCAGAAAATATAAAATATATACACAGTATCCTACCTTGGGAAAGATCCCCACGA
ATATGAACCTTTGGCTGAAATATGTTTAAATAACTTAAATACAGATTGTGATTCTTTATTAAGGTGTTAACCTTGGAmAC
TGGAGGAAATGCTTGCCTTTACAAAATTATTAATAAAATATTAACAAAGAGGAAAGCAAAATTTATTTTGCAGCAAGTGA
TGGCATAGATGTTTATTCTTACAGAAATTAAGAGTGTAAATTTGGGAAGGAAGATCCCTTCTGGTTAAATTTAGAAAA
CGGTATTATTTACGCTTAAAAATATTAAGAAATGGTAAATTAATAAAGATCCCTATAATTAATAATTCTATAAAGAAAA
TCTAGATAAGTATATTGAAAAGTTTGAATTTCTAGAAATTAAGCTAAATCTAAATTTCTTCAATTCCGAATGATAA
AAAAATGATTGTTTCAAGTGAAGGATTTTAAATATTTTGGAAAGCCTATATCTCTCTCTGCTTACATTTGGGA
AATCAACACTGAAGAAGGAACATATATCAAAATTAAGCTAGTTGAAAAATTAATTAACAACAAAAGTTCCCTC
CTTATTTCGTAGAAATAGTGTGGAATATATACCGAATTAAGTATCAAAAATATATTAATTTCCTATCTATTCAAC
GATTTTTTACTGATTCAATTGACACAAAAAGGACAAAGTATATAGTTACTATTCGATTAATAATGGAACCTGGATAA
AATTGCTGAAGGCCCTTCGAAA

EF132-4 (SEQ ID NO:496)

CSNSTSKDKDVTASNEKLKVVVTSILAIITERIAFVHHSIVPIGKDPHEYTEPLREYKTSKADLIFYNGVNLXT
GGNAWFTKLKVKXANKEENKDYFAASDPTDVIYLEGQVHVEDPHAMNLNENCIYAFHIEHWLAEKDPDNKKFYKEN
LDKYIEKLDSDLKEAKSEFASIPHLEFVHVTSEGGVHVAHNVPSAYIWEINTEEPVHVDQIKHLVEKLRTTKVPS
LFVESSVDDRPMKTVSKDTHIEIYVHVTINIAEKNHVAHYAMKKNLNDKIAEGSLP

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

Query	GenBank Access. No.	GenBank Gene Description	BLAST Score	BLAST P-Value
EF002-2	gi 2338759	(AF018073) periplasmic sorbitol-binding protein; SmoE [Rhodobacter	113	3.60E-18
EF003-2	gi 1552773	hypothetical [Escherichia coli] >gnl PID d1012634 hypothetical 29.4	278	1.20E-53
EF003-2	gi 2196996	lipoprotein homolog [Treponema pallidum] ~gi 2108234 29K protein	309	3.30E-44
EF003-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	263	9.20E-40
EF003-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	197	2.10E-39
EF003-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	197	7.80E-39
EF003-2	gi 2314748	(AF000654) outer membrane protein [Helicobacter pylori]	263	4.60E-37
EF003-2	gi 349530	lipoprotein [Pasteurella haemolytica] >gi 50508 lipoprotein	189	4.10E-29
EF003-2	gnl PID c118135	similar to hypothetical proteins [Bacillus subtilis]	158	2.70E-26
EF003-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer	200	1.20E-25
EF003-2	gi 1336657	lipoprotein [Bacillus subtilis]	182	2.70E-25
EF003-2	gnl PID e233873	hypothetical protein [Bacillus subtilis] >gnl PID e1182900	186	1.30E-23
EF003-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	199	6.60E-23
EF003-2	gi 349531	lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer	198	1.30E-20
EF003-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	198	1.80E-20
EF005-2	gi 537235	Keen Rudd identifies as gpmB [Escherichia coli] >gi 1790856	127	6.20E-12
EF006-2	gi 1552773	hypothetical [Escherichia coli] >gnl f1D d1012634 hypothetical 29.4	255	1.40E-60

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF006-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer	221	6.40E-49
EF006-2	gi 2314748	(AE000654) outer membrane protein [Helicobacter pylori]	283	2.70E-48
EF006-2	gi 2196996	lipoprotein homolog [Treponema pallidum] >gi 2108234 29K	267	4.40E-47
		protein		
EF006-2	gnl PID e118435	similar to hypothetical proteins [Bacillus subtilis]	359	1.80E-44
EF006-2	gi 349531	lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer	218	3.80E-41
EF006-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	220	2.30E-38
EF006-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	193	2.60E-38
EF006-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	218	1.20E-36
EF006-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	112	8.50E-34
EF006-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	112	1.50E-33
EF006-2	gi 349530	lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein	114	1.30E-29
EF006-2	gi 294069	lipoprotein 1 [Pasteurella haemolytica]	114	1.20E-27
EF006-2	gi 1336657	lipoprotein [Bacillus subtilis]	202	3.00E-26
EF006-2	gnl PID e233873	hypothetical protein [Bacillus subtilis] >gnl PID e1182900	200	6.50E-25
EF008-2	gi 493017	endocarditis specific antigen [Enterococcus faecalis]	1590	2.70E-211
EF008-2	gi 393269	adhesion protein [Streptococcus pneumoniae]	986	1.80E-129
EF008-2	gi 153834	adhesin specific for salivary pellicle of dental surfaces	973	1.00E-127
EF008-2	gi 1575030	surface adhesin A precursor [Streptococcus pneumoniae]	934	2.00E-126
EF008-2	gi 153826	adhesin B [Streptococcus sanguis] >pidA13583 A13583 adhesin	916	3.90E-126
		B		
EF008-2	gi 1184932	36kDa [Streptococcus cristae]	913	3.30E-124
EF008-2	gi 1117994	surface antigen A variant precursor [Streptococcus pneumoniae]	917	5.60E-124

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF008-2	gi 310633	adhesin [Streptococcus gordonii]	891	6.00E-122
EF008-2	gn PID e255529	lipoprotein [Staphylococcus epidermidis]	476	1.20E-99
EF008-2	gi 1573330	adhesin B precursor (fimA) [Haemophilus influenzae]	380	1.60E-68
EF008-2	gi 1245464	YfeA [Yersinia pestis] >gi 1245464 YfeA [Yersinia pestis]	355	1.20E-64
EF008-2	gi 755075	periplasmic-binding protein [Synecocystis sp.] >gn PID d1018652 Mn	321	1.70E-62
EF008-2	gi 1335912	Ewla [Erysipelothrix rhusiopathiae]	232	4.40E-42
EF008-2	gn PII e118595	similar to ABC transporter (membrane protein) [Bacillus]	204	4.10E-38
EF008-2	gi 1777933	TroA [Treponema pallidum]	181	2.40E-35
EF009-2	gi 349531	lipoprotein [Pasteurella haemolytica] >pir N0752 N0752 outer	391	4.00E-64
EF009-2	gi 1552773	hypothetical [Escherichia coli] ~gn PID d1012634 hypothetical 29.4	359	1.90E-63
EF009-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	391	6.40E-63
EF009-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir N0753 N0753 outer	386	1.10E-61
EF009-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	286	5.60E-60
EF009-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	286	7.60E-60
EF009-2	gi 294069	lipoprotein 1 [Pasteurella haemolytica]	122	4.70E-59
EF009-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	326	2.20E-58
EF009-2	gi 349530	lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein	239	7.80E-57
EF009-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	344	4.90E-56
EF009-2	gi 2314748	(AE000654) outer membrane protein [Helicobacter pylori]	319	4.20E-53
EF009-2	gi 2196596	lipoprotein homolog [Treponema pallidum] ~gi 2108234 29K	312	2.60E-51
		protein		

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF009-2	gi 1336657	lipoprotein [Bacillus subtilis]	234	4.00E-32
EF009-2	gn PID e233873	hypothetical protein [Bacillus subtilis] >gn PID e1182900	242	1.40E-31
EF009-2	gn PID e118435	similar to hypothetical proteins [Bacillus subtilis]	102	6.80E-22
EF011-2	gn PID d10096 5	ferric anguibactin-binding protein precursor FatB of V.	579	3.10E-98
EF011-2	gn PID d10096 5	ferric anguibactin-binding protein precursor FatB of V.	579	3.10E-98
EF011-2	gn PID e185374	ccuE gene product [Campylobacter coli]	284	1.30E-89
EF011-2	gn PID e185374	ccuE gene product [Campylobacter coli]	284	1.30E-89
EF011-2	gi 150756	40 kDa protein [Plasmid pLM1] >pirA29928 A29928 membrane-associated	222	2.80E-52
EF011-2	gi 150756	40 kDa protein [Plasmid pLM1] >pirA29928 A29928 membrane-associated	222	2.80E-52
EF011-2	gi 309662	pheromone binding protein [Plasmid pC110] >pir B53309 B53309	366	8.30E-119
EF012-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	252	1.10E-109
EF012-2	gn PID d10118 5	TRAC [Enterococcus faecalis]	281	3.60E-103
EF012-2	gn PID d10065 5	TraC [Enterococcus faecalis]	277	2.50E-102
EF012-2	gi 12940	phosphorylase kinase [Streptococcus equi subsp. 1] >pir S28153 S28153	222	1.90E-67
EF012-2	gi 48808	dciAE [Bacillus subtilis]	228	1.70E-46

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF012-2	pir S16651 S166	dciAE protein - <i>Bacillus subtilis</i>	228	1.00E-45
EF012-2	gnl PID e118149	(AJ002571) DppE [<i>Bacillus subtilis</i>] >gnl PID e1183316	228	3.80E-45
EF012-2	gi 40005	OppA gene product [<i>Bacillus subtilis</i>]	281	3.90E-44
EF012-2	gi 143603	sporulation protein [<i>Bacillus subtilis</i>] >gnl PID e1183163	281	7.70E-44
EF012-2	gnl PID d10156 3	Periplasmic oligopeptide-binding protein precursor.	152	2.20E-43
EF012-2	gi 1574679	oligopeptide binding protein (oppA) [<i>Haemophilus influenzae</i>]	178	2.20E-42
EF012-2	gi 47802	Opp A (AA1-542) [<i>Salmonella typhimurium</i>] >gi 47808 precursor	128	1.00E-37
EF012-2	gi 882550	ORF_1535 [<i>Escherichia coli</i>] >gi 1789397 (AF000384) 1535; This 535 aa	228	5.30E-36
EF014-2	pir D70070 D70 0	transcriptional regulator homolog ywtF - <i>Bacillus subtilis</i>	101	1.40E-27
EF014-2	gnl PID e116988	capsidat polysaccharide synthesis protein [<i>Streptococcus</i>]	121	9.30E-27
EF014-2	gi 2804769	(AF030373) putative regulatory protein [<i>Streptococcus</i> <i>pneumoniae</i>]	121	9.50E-27
EF014-2	gnl PID e289126	unknown [<i>Streptococcus pneumoniae</i>]	121	1.00E-24
EF014-2	gi 2267239	ORF1 [<i>Staphylococcus epidermidis</i>]	234	1.50E-24
EF014-2	gi 485275	putative regulatory protein [<i>Streptococcus pneumoniae</i>]	121	3.90E-24
EF014-2	gi 2804733	(AF030367) putative regulatory protein [<i>Streptococcus</i> <i>pneumoniae</i>]	121	3.90E-24
EF014-2	gi 2804747	(AF030369) putative regulatory protein [<i>Streptococcus</i> <i>pneumoniae</i>]	121	3.90E-24

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF014-2	gjl1762327	putative transcriptional regulator [Bacillus subtilis]	185	2.80E-22
EF014-2	gjl143156	membrane bound protein [Bacillus subtilis] >gjlPIDle1184471	116	1.10E-21
EF014-2	gjlPID[d10189 5	membrane bound protein LytR [Synecocystis sp.]	113	6.20E-20
EF014-2	gjl1276874	EpsA [Streptococcus thermophilus]	103	4.00E-17
EF016-2	gjlPIDle118566	similar to amino acid ABC transporter (binding protein)	194	3.70E-35
EF016-2	gjl40934	arginine binding protein [Escherichia coli] >gjl769794 artJ	121	1.60E-31
EF016-2	gjlPID[d10152 7	Arginine-binding periplasmic protein 2 precursor [Escherichia coli]	121	4.80E-31
EF016-2	gjl687652	Arginine-binding periplasmic protein 2 precursor [Escherichia coli] >gjlPID[d1016464] hly protein precursor	160	3.30E-31
EF016-2	gjl2650410	(AE001090) glutamine ABC transporter, periplasmic glutamine binding	122	3.30E-29
EF016-2	gjl164963	Arginine-binding periplasmic protein 2 precursor [Escherichia coli]	121	2.50E-27
EF016-2	gjl1574634	glutamine-binding periplasmic protein (glnI) [Haemophilus influenzae]	174	2.50E-27
EF016-2	gjl41569	GlnI precursor (AA -22 to 226) [Escherichia coli] >gjlPID[d1015250]	106	4.70E-27
EF016-2	gjlPID[d10152 7	Arginine-binding periplasmic protein 1 precursor [Escherichia coli]	109	3.70E-26
EF016-2	gjl164963	Arginine-binding periplasmic protein 2 precursor [Escherichia coli]	121	2.50E-27
EF016-2	gjlPID[d10089 2	homologous to Gln-binding periplasmic proteins [Bacillus subtilis]	117	8.50E-24
EF016-2	gjl154125	1 protein [Salmonella typhimurium] >gjl47718 reading frame	118	2.10E-23

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	hisJ			
EF016-2	gn PID d10168 8	HISTIDINE-BINDING PERIPLASMIC PROTEIN PRECURSOR (HBP).	117	4.50E-23
EF016-2	gi 1166636	histidine-binding periplasmic protein HisJ [Escherichia coli]	117	6.60E-23
EF017-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	421	4.50E-128
EF017-2	gn PID d10118 5	TRAC [Enterococcus faecalis]	417	5.10E-124
EF017-2	gn PID d10065 5	TraC [Enterococcus faecalis]	414	4.40E-123
EF017-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	415	2.40E-119
EF017-2	gi 40005	OppA gene product [Bacillus subtilis]	294	6.20E-82
EF017-2	gi 43603	sporulation protein [Bacillus subtilis] >gn PID e1183163	290	2.80E-79
EF017-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	241	2.40E-71
EF017-2	gi 48808	dcIAE [Bacillus subtilis]	270	1.10E-61
EF017-2	gn PID e118149	(AJ002571) DppE [Bacillus subtilis] >gn PID e1183316	270	1.50E-61
EF017-2	pir S16651 S166	dcIAE protein - Bacillus subtilis	270	3.10E-60
EF017-2	gi 304025	overly-ligand oligopeptide binding protein [Escherichia coli]	171	2.60E-57
EF017-2	gi 47014	oligopeptide binding protein precursor [Escherichia coli]	171	8.70E-56
EF017-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	154	1.30E-52

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF017-2	gi 882550	ORF_f535 [Escherichia coli] >gi 1789397 (AE000384) f535; This 535 aa	135	5.50E-52
EF017-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	168	2.90E-43
EF019-2	gi 438458	likely N-terminal signal sequence; mature protein probably	104	2.30E-17
EF021-2	gn PID e311492	unknown [Bacillus subtilis] >gn PID e1184232 similar to ABC	317	2.50E-103
EF021-2	bbs 173803	CD4: T cell-stimulating antigen [Listeria monocytogenes, 85EO-1167,	476	2.80E-81
EF021-2	gi 581809	trnSC gene product [Treponema pallidum] - pit/A43595/A43595	152	3.20E-71
EF021-2	gi 2688280	membrane (AL001143) basic membrane protein C (bmpC) [Borrelia burgdorferi]	101	5.50E-27
EF021-2	gn PID e117283	membrane protein A [Borrelia garinii]	142	6.50E-22
EF021-2	gn PID e117283	membrane protein A [Borrelia burgdorferi]	141	9.20E-22
EF021-2	gn PID e117283	membrane protein A [Borrelia burgdorferi] - g4316592	141	9.30E-22
EF021-2	gn PID e117283	membrane		
EF021-2	gn PID e117283	bmpA(p39,ORF1) [Borrelia burgdorferi]	141	1.70E-21
EF021-2	gi 508421	antigen P39 [Borrelia burgdorferi] >gi 2688281 (AE001143) basic	141	1.70E-21
EF021-2	gi 1753225	BmpA protein [Borrelia burgdorferi]	141	2.70E-20
EF021-2	gn PID e117283	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gn PID e117283	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gn PID e117283	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gn PID e117282	bmpA(p39,ORF1) [Borrelia burgdorferi]	141	1.50E-19

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF022-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	324	5.90E-66
EF022-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	307	5.60E-60
EF022-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	301	4.80E-59
EF022-2	gnl PID e118149	(A1002571) DppE [Bacillus subtilis] >gnl PID e1183316	170	5.10E-59
EF022-2	gi 48808	deiAE [Bacillus subtilis]	170	5.20E-59
EF022-2	gnl PID d10065 5	Trac [Enterococcus faecalis]	299	2.80E-58
EF022-2	pir S16651 S166	deiAE protein - Bacillus subtilis	170	1.60E-57
EF022-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAMP binding	280	2.70E-53
EF022-2	gi 40005	OppA gene product [Bacillus subtilis]	154	7.30E-48
EF022-2	gi 43603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	154	3.10E-47
EF022-2	gi 2688227	(AE001139) oligopeptide ABC transporter, periplasmic	215	1.00E-36
EF022-2	gi 2281458	(AF000366) oligopeptide permease homolog Ali [Borrelia burgdorferi]	215	1.00E-36
EF022-2	gi 304025	periplasmic oligopeptide binding protein [Escherichia coli]	131	1.20E-35
EF022-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	131	1.80E-34
EF022-2	gi 47802	OppA (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	138	4.90E-34
EF023-2	gi 309662	pheromone binding protein [Plasmid pCF10]	231	4.70E-66

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		>pir B53309 B53309			
EF023-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	223		4.80E-62
EF023-2	gn PID d101185	TRAC [Enterococcus faecalis]	226		1.00E-58
EF023-2	gn PID d100655	TraC [Enterococcus faecalis]	226		4.40E-58
EF023-2	gi 48808	deiAE [Bacillus subtilis]	157		1.20E-57
EF023-2	gn PID e118149	deiA1002571 DppE [Bacillus subtilis] - gn PID e1183316	157		1.20E-57
EF023-2	pir S16651 S166	deiAE protein - Bacillus subtilis	157		3.80E-56
EF023-2	gi 40005	OppA gene product [Bacillus subtilis]	137		2.30E-53
EF023-2	gi 143603	sporulation protein [Bacillus subtilis] - gn PID e1183163	133		6.90E-53
EF023-2	gi 47802	OppA (AA1-542) [Salmonella typhimurium] - gi 47808 precursor	133		2.00E-41
EF023-2	gi 2688227	(AF001139) oligopeptide ABC transporter, periplasmic	187		9.40E-41
EF023-2	gi 2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	187		1.90E-40
EF023-2	gi 882550	ORF_f535 [Escherichia coli] >gi 1789397 (AF000384) f535; This 535 aa	155		1.30E-38
EF023-2	gi 304922	periplasmic oligopeptide binding protein [Escherichia coli]	150		9.00E-37
EF023-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	130		3.20E-34
EF026-2	gi 2352482	(AF005097) unknown [Lactococcus lactis]	141		1.10E-23
EF027-2	gi 309662	pheromone binding protein [Plasmid pCl10]	198		6.20E-71

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		>pir B53309 B53309		
EF027-2	gnl PID d10065 5	TraC [Enterococcus faecalis]	202	1.50E-68
EF027-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	202	1.50E-68
EF027-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	213	8.30E-68
EF027-2	gnl PID e118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316	222	3.70E-41
EF027-2	gi 48808	deiAE [Bacillus subtilis]	222	4.90E-41
EF027-2	pir S16651 S166	deiAE protein - Bacillus subtilis	222	1.10E-39
EF027-2	gi 40005	OppA gene product [Bacillus subtilis]	251	4.10E-39
EF027-2	gi 13603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	247	5.80E-39
EF027-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	233	8.90E-33
EF027-2	gi 2688227	(AF001139) oligopeptide ABC transporter, periplasmic	131	2.40E-24
EF027-2	gi 2281458	(AF000366) oligopeptide permease homolog All [Borrelia burgdorferi]	131	2.40E-24
EF027-2	gi 2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi 2689891 (AF000792)	117	3.00E-20
EF027-2	gi 3336079	oligopeptide binding protein (oppA) [Haemophilus influenzae]	130	3.50E-20
EF028-2	gnl P13410204 7	B. subtilis alkaline phosphatase IIIA; P19405 secretory	996	3.60E-131
EF028-2	pir B39096 B39	alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus	982	2.90E-129

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	0			
EF028-2	gi 470383	alkaline phosphatase A [Bacillus subtilis] >gn PID e1182942	803	4.80E-119
EF028-2	gi 143324	APase I [Bacillus licheniformis] >pir A44828 A44828 alkaline	184	3.00E-54
EF028-2	gi 147243	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	183	8.30E-54
EF028-2	gi 147237	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	178	4.40E-53
EF028-2	gi 147239	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	178	4.40E-53
EF028-2	gi 147241	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	178	4.40E-53
EF028-2	gi 1257127	phoA gene product [Cloning vector pFW-phoA1] >gi 1277130	174	4.90E-53
EF028-2	gi 147229	phoA gene	178	8.40E-53
EF028-2	gi 18851	alkaline phosphatase [synthetic construct]	174	1.10E-52
EF028-2	gi 147245	alkaline phosphatase (phoA) (EC 3.1.3.1) [Escherichia	177	1.20E-52
EF028-2	gi 17231	ferugonil]	174	1.60E-52
EF028-2	gi 147235	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	174	1.60E-52
EF028-2	gi 1016010	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	174	1.60E-52
EF028-2		alkaline phosphatase with N-terminal PelB-leader and C-terminal		
EF029-2	gi 1750126	YncB [Bacillus subtilis] >gn PID e1183421 similar to	257	3.50E-55
EF029-2	gi 1016010	micrococcal		
EF029-2	gi 1016010	similar to hypothetical proteins [Bacillus subtilis]	170	2.60E-50
EF029-2	gi 673492	nuclease [Staphylococcus aureus] >gi 1016010 [EF029-2]	170	2.60E-50
EF029-2	gi 532653	micrococcal		
EF029-2		thermonuclease [Staphylococcus hyicus]	155	9.10E-30

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF029-2	gi 47146	thermonuclease [Staphylococcus intermedius] >pir S26079 S26079	145	4.90E-32
EF030-2	gi 48808	dciAE [Bacillus subtilis]	149	1.10E-66
EF030-2	gn PID e118149	(AJ002571) DppE [Bacillus subtilis] >gn PID e1183316	149	1.50E-66
EF030-2	pir S16651 S166	dciAE protein - Bacillus subtilis	149	5.90E-66
EF030-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	227	7.40E-52
EF030-2	gn PID d10118	TRAC [Enterococcus faecalis]	237	7.40E-52
EF030-2	5 gn PID d10065	TraC [Enterococcus faecalis]	233	9.70E-51
EF030-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	229	3.00E-48
EF030-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	277	3.00E-45
EF030-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	125	8.50E-34
EF030-2	gi 2688227	(AE001139) oligopeptide ABC transporter, periplasmic	211	4.80E-31
EF030-2	gi 2281458	(AF000566) oligopeptide permease homologue AH [Borrelia burgdorferi]	211	4.80E-31
EF030-2	gi 10005	OppA gene product [Bacillus subtilis]	148	1.20E-30
EF030-2	gi 143603	sporulation protein [Bacillus subtilis] >gn PID e1183163	144	4.80E-30
EF030-2	gi 2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi 2689891 (AE000792)	210	2.10E-29

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF030-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	148	6.00E-29
EF033-2	gn PID e118439	similar to iron-binding protein [Bacillus subtilis]	164	2.60E-14
EF033-2	pir S54437 S544	hemin binding protein - Yersinia enterocolitica	108	1.40E-11
EF033-2	gi 1619623	hemin binding protein [Yersinia enterocolitica]	108	2.00E-11
EF036-2	gn PID d10102 2	ORF108 [Bacillus subtilis] >gn PID e1185766 alternate gene	544	1.20E-96
EF036-2	gi 26222858	(AE000929) phosphate-binding protein PstS [Methanobacterium]	183	1.40E-45
EF036-2	gi 26222859	(AF000229) phosphate-binding protein PstS homolog [Methanobacterium]	178	2.40E-41
EF036-2	gi 2688115	(AE001132) phosphate ABC transporter, periplasmic phosphate-binding	117	1.10E-12
EF037-2	gi 2352482	(AF005097) unknown [Lactococcus lactis]	141	1.10E-23
EF040-2	gi 16575176	hypothetical protein [Escherichia coli] >gi 186511 (AF000139)	208	1.90E-29
EF040-2	gi 293265	2-5A-dependent RNase [Mus musculus] >pir B45771 B45771	105	1.00E-17
EF040-2	gi 287865	G9a [Homo sapiens] >pir S30385 S30385 G9a protein - human	143	8.30E-14
EF040-2	gi 311817	erythroid ankyrin [Mus musculus] >pir S37771 S37771 ankyrin,	119	4.80E-13
EF040-2	gi 191940	ankyrin [Mus musculus] >pir 49502 49502 ankyrin - mouse	119	4.90E-13
EF040-2	gi 247710	alt. ankyrin (variant 2.2) [Homo sapiens]	120	1.50E-12
EF040-2	gi 178946	ankyrin [Homo sapiens]	120	1.60E-12
EF040-2	gi 1845265	ankyrin [Homo sapiens]	120	1.80E-12
EF040-2	pir A35049 A350	ankyrin 1, erythrocyte splice form 2 - human	120	1.80E-12
	0			

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF040-2	pir B35049 B350	ankyrin 1, erythrocyte splice form 3 - human	120	1.80E-12
EF040-2	gi 28702	ankyrin (variant 2.1) [Homo sapiens] >pir S08275 SJHUK	120	1.80E-12
EF041-2	gi 388269	ankyrin 1, traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	670	1.40E-87
EF041-2	gnl PID d1100655	TraC [Enterococcus faecalis]	662	1.50E-85
EF041-2	gnl PID d1101185	TRAC [Enterococcus faecalis]	648	1.20E-83
EF041-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	218	1.20E-57
EF041-2	gi 48808	dciAE [Bacillus subtilis]	218	1.40E-57
EF041-2	gnl PID e118149	(A1002571) DppE [Bacillus subtilis] >gnl PID e1183316	218	2.10E-56
EF041-2	pir S16651 S166	dciAE protein - Bacillus subtilis	146	7.30E-40
EF041-2	gi 882550	ORF_1535 [Escherichia coli] >gi 1789397 (AF000384) 1535; This 535 aa	278	1.00E-34
EF041-2	gi 143603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	279	1.00E-34
EF041-2	gi 40005	OppA gene product [Bacillus subtilis]	141	6.60E-30
EF041-2	gi 304342	OppA (A1A1.5.2) [Salmonella typhimurium] >gi 17898 precursor	160	1.90E-29
EF041-2	gi 304342	periplasmic oligopeptide binding protein [Escherichia coli]	163	1.00E-28
EF041-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]		

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF041-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	160	1.50E-28
EF041-2	gi 2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	134	5.00E-27
EF045-2	gi 308854	oligopeptide binding protein [Lactococcus lactis] >pir E53290 E53290	437	3.20E-125
EF045-2	gi 495181	oligopeptide binding protein [Lactococcus lactis]	426	9.70E-124
EF045-2	gi 677945	AppA [Bacillus subtilis] >gnl PID e1183158 oligopeptide ABC	154	2.30E-31
EF045-2	gi 293014	peptide-binding protein [Lactococcus lactis] >pir B47098 B47098	158	2.40E-14
EF048-2	gi 1574060	hypothetical [Haemophilus influenzae] >pir l64164 l64164	250	2.30E-41
EF048-2	dbj AB001488_2	(AB001488) SIMILAR TO C4-DICARBOXYLATE-BINDING PERIPLASMIC	208	3.60E-34
EF048-2	gi 466717	No definition line found [Escherichia coli] >gi 1790004 (AE000435)	199	1.30E-30
EF048-2	gi 16006	periplasmic C4-dicarboxylate-binding protein [Phlebotomus capsulatus]	162	1.10E-38
EF048-2	gi 1573102	hypothetical [Haemophilus influenzae] >pir H64143 H64143	244	3.80E-25
EF048-2	gi 2182530	(AE000085) Y4mM [Rhizobium sp. NGR234]	114	5.60E-18
EF048-2	gi 1572999	hypothetical [Haemophilus influenzae] >pir E64141 E64141	116	5.90E-15
EF049-2	gi 10581	maturation protein [Lactobacillus paracasei] >gpp L35364 L3536	241	9.10E-35
EF049-2	gi 10195	maturation protein [Lactococcus lactis] >gpp L35364 L3536	239	1.00E-34
EF049-2	gi 432402	maturation protein [Lactococcus lactis] >gpp L35364 L3536	239	6.20E-34

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF054-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from patients	237	7.80E-25
EF054-2	gi 46523	B antigen [Streptococcus agalactiae]	232	2.80E-23
EF054-2	pir S15330 FCS O	IgA Fc receptor precursor - Streptococcus agalactiae	228	1.00E-22
EF054-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	210	3.10E-21
EF054-2	gi 63686	NF-M c-terminus [Gallus gallus]	222	6.90E-21
EF054-2	gi 63689	NF-M protein [Gallus gallus] >pir S15762 S15762 neurofilament triplet	222	8.50E-21
EF054-2	gi 757867	TATA-box like sequence (Us11) [Human herpesvirus 1] >gi 291493 18	194	4.10E-19
EF059-2	gi 1110236571	cell wall anchoring signal [Enterococcus faecalis]	418	5.60E-95
EF059-2	gi 150556	surface protein [Plasmid pCF10] >pir A41826 A41826 probable	606	3.70E-87
EF059-2	gi 45738	ORF3 [Enterococcus faecalis] >pir H10204 H10204 hypothetical 30.5K	366	9.30E-50
EF059-2	gi 496520	orf iota [Streptococcus pyogenes] >pir S68125 S45091 hypothetical	367	5.90E-44
EF059-2	gi 160693	sporozoite surface protein [Plasmodium yoelii] >pir A145501 A145501	344	1.10E-38
EF059-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from patients	237	7.80E-25
EF059-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from patients	237	7.80E-25

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF059-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	253	6.40E-27
EF059-2	gi 46521	Fc receptor [Streptococcus agalactiae] >pir A60234 A60234 IgA	197	2.70E-26
EF059-2		Fc		
EF059-2	gi 46523	B antigen [Streptococcus agalactiae]	232	9.30E-26
EF059-2	pir S15330 FCS	IgA Fc receptor precursor - Streptococcus agalactiae	232	9.30E-26
	O			
EF059-2	gnl PID e225687	zinc finger protein [Mus musculus] >gnl PID e225688 zinc	234	1.40E-22
EF059-2	gi 423356	zona pellucida protein [Pseudopleuronectes americanus]	229	1.00E-21
EF059-2	gi 457769	Collagen [Bombyx mori] >pir S42886 S42886 collagen - silkworm	209	7.60E-19
EF061-2	gnl PID e236571	cell wall anchoring signal [Enterococcus faecalis]	925	8.10E-118
EF061-2	gi 150556	surface protein [Plasmid pCF10] >pir A41826 A41826 probable	350	1.50E-107
EF061-2	gi 106520	orf104 [Streptococcus pyogenes] >pir S68125 S45091	308	1.40E-58
		hypothetical		
EF061-2	gi 45738	ORF3 [Enterococcus faecalis] >pir H0204 H0204	322	6.40E-50
		hypothetical 30.5K		
EF061-2	gi 1813523	PbTRAP [Plasmodium berghei]	263	1.00E-26
EF061-2	gi 160693	sporozoite surface protein [Plasmodium yoelii]	241	9.00E-25
		sp A45559 A45559		
		hypothetical protein [Plasmodium yoelii]		
	gi 106520	orf104 [Streptococcus pyogenes] >pir S68125 S45091	308	1.40E-58
		hypothetical		
	gi 106520	orf104 [Streptococcus pyogenes] >pir S68125 S45091	308	1.40E-58
		neurofilament triplet		
EF061-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from	176	2.40E-21

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		patients		
EF061-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	165	2.70E-20
EF061-2	gn PID e225687	zinc finger protein [Mus musculus] >gn PID e225688 zinc	197	7.80E-19
EF061-2	gi 160355	interspersed repeat antigen [Plasmodium falciparum]	199	8.20E-18
EF061-2	gi 410750	interspersed repeat antigen [Plasmodium falciparum]	199	8.90E-18
EF061-2	gi 2290388	IgG and IgE immunoreactive antigen recognized by sera from patients	182	1.40E-17
EF061-2	gi 2290394	IgG and IgE immunoreactive antigen recognized by sera from patients	180	2.80E-17
EF062-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0
EF062-2	gi 43324	aggregation substance (ASP1) [Enterococcus faecalis]	4003	0
EF062-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0
EF062-2	gi 150555	aggregation substance [Plasmodium falciparum] pfp111662/H11662	6338	0
EF062-2	gi 1100973	150K mating	110	9.90E-39
EF062-2	gi 47248	88pB precursor [Streptococcus gordonii]	107	1.70E-38
EF062-2	gn PID 10150	PAC protein precursor (AA -38 to 1527) [Streptococcus mutans]	132	5.00E-36
EF062-2	gi 1100973	surface protein antigen precursor [Streptococcus sobrinus]	132	1.20E-38
EF062-2	gi 1100973	SpA endocarditis immunodominant antigen [Streptococcus sobrinus]	132	1.20E-38

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF062-2	gi 47620	antigen I/II [Streptococcus sobrinus] >pir A60338 A60338 surface	132	2.90E-35
EF062-2	pir A35186 A351	salivary agglutinin receptor precursor - Streptococcus	109	2.10E-34
EF062-2	gi 1100971	SspA [Streptococcus gordonii]	110	3.80E-32
EF062-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF063-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0
EF063-2	gi 43324	aggregation substance (ASP1) [Enterococcus faecalis]	4003	0
EF063-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0
EF063-2	gi 150555	aggregation substance [Plasmid pCF10] >pir H41662 H41662 150K mating	6338	0
EF063-2	gi 1100973	SspB precursor [Streptococcus gordonii]	110	9.90E-39
EF063-2	gi 47248	PAC protein precursor (AA 38 to 1527) [Streptococcus mutans]	107	1.70E-38
EF063-2	gn P1D d101507	surface protein antigen precursor [Streptococcus sobrinus]	132	5.00E-36
EF063-2	gi 47267	cell surface antigen I/II [Streptococcus mutans] >pir S06839 S06839	107	6.50E-36
EF063-2	bbs 18153	SspA endocarditis immunodominant antigen [Streptococcus mutans]	132	1.20E-35
EF063-2	gi 47267	cell surface antigen I/II [Streptococcus mutans] surface	107	6.50E-36
EF063-2	pir A35186 A351	salivary agglutinin receptor precursor - Streptococcus	109	2.10E-34

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF063-2	gi 1100971	SspA [Streptococcus gordonii]	110	3.80E-32
EF063-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF064-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0
EF064-2	gi 43324	aggregation substance (ASP1) [Enterococcus faecalis]	4003	0
EF064-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0
EF064-2	gi 150555	aggregation substance [Plasmid pCJ-10] >pir H41662 H41662 150K mating	6338	0
EF064-2	gi 1100973	SspB precursor [Streptococcus gordonii]	110	9.90E-39
EF064-2	gi 47248	PAc protein precursor (AA -38 to 1527) [Streptococcus mutans]	107	1.70E-38
EF064-2	gn PII d10150 7	surface protein antigen precursor [Streptococcus sobrinus]	132	5.00E-36
EF064-2	gi 15267	cell surface antigen I II [Streptococcus mutans] >pir S06839 S06839	107	6.30E-36
EF064-2	gb 148153	SspA endocarditis immunodominant antigen [Streptococcus sobrinus,	132	1.20E-35
EF064-2	gi 47620	antigen I/II [Streptococcus sobrinus] >pir A60338 A60338 surface	132	2.90E-35
EF064-2	gi 213865	cell surface protein precursor [Streptococcus mutans]	109	3.10E-34
EF064-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF068-2	gi 790398	T061D8.1 [Caenorhabditis elegans]	137	8.50E-17

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF068-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	210	5.80E-16
EF068-2	gi 2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121	8.40E-16
EF068-2	gi 330862	membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1	208	1.10E-15
EF068-2	gi 1707247	partial CDS [Caenorhabditis elegans]	131	3.70E-15
EF068-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	203	6.20E-15
EF068-2	gi 213392	antifreeze glycoprotein [Notothenia coriiceps] >pir A38420 A38420	102	4.60E-13
EF068-2	gnl PID c125464	(AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145	1.50E-12
EF068-2	gi 2951460	EFIM C-1 gene product [Xenopus laevis] >pir A45155 A45155	109	2.70E-12
EF069-2	gi 790398	mucin T06D8.1 [Caenorhabditis elegans]	137	8.50E-17
EF069-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	210	5.80E-16
EF069-2	gi 2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121	8.40E-16
EF069-2	gi 330862	membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1	208	1.10E-15
EF069-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	203	6.20E-15
EF069-2	gi 213392	antifreeze glycoprotein [Notothenia coriiceps]	102	4.60E-13

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF069-2	gn PID e125464	>pir A38420 A38420 (AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145	1.50E-12
EF069-2	gi 951460	FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155 mucin	109	2.70E-12
EF070-2	gi 700398	T06128.1 [Caenorhabditis elegans]	137	8.50E-17
EF070-2	gn PID d102084	membrane glycoprotein [Equine herpesvirus 1]	210	5.80E-16
EF070-2	gi 2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121	8.40E-16
EF070-2	gi 330862	membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1	208	1.10E-15
EF070-2	gi 1707247	partial CDS [Caenorhabditis elegans]	131	3.70E-15
EF070-2	gi 34184102094	membrane glycoprotein [Equine herpesvirus 1]	203	7.50E-15
EF070-2	gi 213392	antifreeze glycoprotein [Notothenia cornueps]	102	4.60E-15
EF070-2	gn PID e125464	>pir A38420 A38420 (AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145	1.50E-12
EF070-2	gi 951460	FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155 mucin	109	2.70E-12
EF071-2	gi 853751	LysM N-acetylhydantoin-L-alanine amidase [Bacteriophage A511]	273	2.60E-36
EF073-2	gi 143830	xpaC [Bacillus subtilis] >gn PID d1005803 hydrolysis of	173	7.10E-16

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF074-2	g 1256698	chitinase [Serratia marcescens] >gi1256698 chitinase [Serratia	618	2.60E-104
EF074-2	g 1763985	chitinase A [Vibrio harvey]	526	2.80E-84
EF075-2	g 143156	membrane bound protein [Bacillus subtilis] >gnlPID e1184471	593	1.70E-91
EF075-2	p D70070 D70 0	transcriptional regulator homolog ywtF - Bacillus subtilis	118	1.90E-59
EF075-2	g 1762327	putative transcriptional regulator [Bacillus subtilis]	148	9.60E-53
EF075-2	g 1276874	EpsA [Streptococcus thermophilus]	239	2.20E-33
EF075-2	gnlPID e289126	unknown [Streptococcus pneumoniae]	150	1.20E-27
EF075-2	g 485275	putative regulatory protein [Streptococcus pneumoniae]	150	2.50E-27
EF075-2	g 2804735	(AF030367) putative regulatory protein [Streptococcus pneumoniae]	150	2.50E-27
EF075-2	gn2804747	(AF030369) putative regulatory protein [Streptococcus pneumoniae]	150	2.50E-27
EF075-2	gnlPID e116988	capsular polysaccharide synthesis protein [Streptococcus pneumoniae]	148	5.30E-27
EF075-2	g 2804769	(AF030373) putative regulatory protein [Streptococcus pneumoniae]	148	5.30E-27
EF075-2	g 1147744	PSR [Enterococcus hirae]	109	2.10E-23
EF075-2	g 790435	PSR [Enterococcus faecium] >p r[S54177/S54177 PSR protein -	102	4.40E-19
EF075-2	g 2242380	g 2242380 [Escherichia coli O157:H7] >g 2242380	100	2.80E-19
EF075-2	g 2242380	g 2242380 [Escherichia coli O157:H7] >g 2242380	100	2.80E-19
EF075-2	gnlPID d11413	cardinalin-transporting ATPase [Synechocystis sp.]	396	2.30E-113

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF078-2	gnl PID d10119 6	homologous to sp:PHOR_BACSU [Bacillus subtilis]	219	4.20E-44
EF078-2	gil1575578	histidine protein kinase [Thermotoga maritima]	191	7.10E-44
EF078-2	gil2182990	histidine kinase [Lactococcus lactis cremoris]	169	6.40E-40
EF078-2	gil2182992	histidine kinase [Lactococcus lactis cremoris]	152	1.10E-39
EF078-2	gnl PID d10113 4	sensory transduction histidine kinase [Synechocystis sp.]	259	3.90E-38
EF078-2	gil149296	phosphate regulatory protein phoR (gtg start codon) [Klebsiella]	228	7.60E-33
EF078-2	gil581188	phoR gene product (AA 1-431) [Escherichia coli] >gil1657596	226	1.60E-32
EF078-2	gnl PID d10108 7	sensory transduction histidine kinase [Synechocystis sp.]	138	3.70E-32
EF078-2	gnl PID c266592	unknown [Mycobacterium tuberculosis]	232	1.10E-31
EF078-2	gil2182996	histidine kinase [Lactococcus lactis cremoris]	204	1.30E-31
EF078-2	gnl PID d10113 5	sensory transduction histidine kinase [Synechocystis sp.]	256	1.30E-31
EF078-2	gil294893	phosphate regulatory protein phoR (gtg start codon) [Shigella]	225	1.60E-31
EF078-2	gil288420	drug sensory protein A [Synechocystis PCC6803] >gnl PID d1017420	106	2.50E-31
EF078-2	gil2908210	putative fibronectin-associated protein [Actinomyces naeslundii] >gil2908210	193	8.70E-26
EF081-2	gil790433	low affinity penicillin-binding protein 5 (PBPS) [Enterococcus]	604	2.70E-78

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF081-2	gi 790437	low affinity penicillin-binding protein 5 (PBP5) [Enterococcus]	602	5.10E-78
EF081-2	gi 790431	low affinity penicillin-binding protein 5 (PBP5) [Enterococcus]	591	2.60E-77
EF081-2	gi 43342	D-alanyl-D-alanine carboxypeptidase [Enterococcus hirae]	587	9.30E-77
EF081-2	gi 49000	D-alanyl-D-alanine carboxypeptidase [Enterococcus hirae]	572	5.20E-74
EF081-2	gnl PID d10079	penicillin-binding protein 2 [Bacillus subtilis]	149	7.40E-24
EF081-2	4			
EF081-2	gnl PID e315088	MecA1 [Staphylococcus sciuri]	111	4.40E-19
EF081-2	gnl PID e286651	MecA protein [Staphylococcus sciuri]	106	2.90E-18
EF081-2	gnl PID e316581	MecA protein [Staphylococcus sciuri]	111	2.90E-18
EF081-2	gnl PID e316607	MecA2 protein [Staphylococcus sciuri]	101	3.70E-14
EF081-2	gnl PID e316613	MecA protein [Staphylococcus sciuri] - gi 46613 mecA gene	101	3.70E-14
EF083-2	gi 496283	lysM [Bacteriophage Tuc2009]	436	6.20E-176
EF083-2	gi 530798	LysB [Bacteriophage phi-LC3]	421	5.00E-175
EF083-2	gi 166183	muramidase [Bacteriophage CP-7]	186	1.20E-21
EF083-2	gi 166188	muramidase [Bacteriophage CP-9] - put JQ0438 MUBPC9	188	5.00E-21
EF083-2	gi 623084	muramidase; muramidase [Bacteriophage LL-H]	193	8.40E-20
EF083-2	gi 166175	muramidase [Bacteriophage CP-1]	175	3.40E-19
EF083-2	gnl PID e221272	lysM gene [Bacteriophage CP-1] - put JQ0438 BUBPC9	175	3.40E-19
		lysA -		
EF083-2	gi 793850	lysM [Lactobacillus bacteriophage phi adh] - gnl PID e1217314	117	5.60E-15

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		lysine			
EF084-2	gi 2293312	(AF008220) YtfP [Bacillus subtilis] >gnl PID e1185879 similar to	438		1.70E-140
EF084-2	gi 2367234	(AF000425) hypothetical 43.8 kD protein in rhsB-pit intergenic	167		2.20E-51
EF084-2	gi 912464	No definition line found [Escherichia coli]	167		6.00E-51
EF084-2	gnl PID d10112	hypothetical protein [Synecococcus sp.] >pir S76678 S76678	151		6.10E-42
	7				
EF084-2	gi 1573954	hypothetical [Haemophilus influenzae] >pir G64161 G64161	142		2.90E-40
EF085-2	gi 1209527	protein histidine kinase [Enterococcus faecalis]	2023		8.00E-279
EF085-2	gi 467057	phoR; B2168_C3_247 [Mycobacterium leprae] >pir S72905 S72905	226		8.80E-23
EF085-2	gnl PID e119229	SenX3 [Mycobacterium bovis BCG]	222		3.10E-22
EF085-2	gnl PID e251152	unknown [Mycobacterium tuberculosis] >gnl PID e321546	222		3.10E-22
EF085-2	gi 1778485	SenX3			
		PcoS homolog [Escherichia coli] >gi 1786783 (AE000162) f480;	111		3.80E-16
		This			
EF085-2	gi 149296	phosphate regulatory protein phoR (gtg start codon) [Klebsiella]	110		1.40E-14
EF085-2	gi 581188	phoR gene product (AA 1-431) [Escherichia coli] >gi 1657596	103		5.30E-14
		EF085-2			
		base in			
EF085-2	gi 2182972	histidine kinase [Lactococcus lactis cremoris]	109		5.90E-12

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF086-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF086-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF086-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae] sp A55137 A55137	203	3.30E-44
EF086-2	gi 705406	hyaluronate lyase [Staphylococcus aureus]	191	3.40E-42
EF086-2	gi 562086	hyaluronidase [Propionibacterium acnes]	198	6.00E-27
EF087-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF087-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF087-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae] sp A55137 A55137	203	3.30E-44
EF087-2	gi 705406	hyaluronate lyase [Staphylococcus aureus]	191	3.40E-42
EF087-2	gi 562086	hyaluronidase [Propionibacterium acnes]	198	6.00E-27
EF088-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF088-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF088-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae]	203	3.30E-44
EF091-2	gi 556016	similar to plant water stress protein 3.02E1 [Bacillus subtilis]	198	5.50E-21
EF091-2	gi 2353333	(AF016513) Ce-LEA [Caenorhabditis elegans]	189	2.40E-17

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF091-2	gn PID e353216	seed maturation protein homolog [Arabidopsis thaliana]	146	3.60E-11
EF091-2	gi 1161171	late embryogenesis abundant protein [Picea glauca]	132	5.70E-11
EF091-2	pir S04909 S049	embryonic protein DC8 (clone 8/10) - carrot	127	6.50E-11
EF092-2	gi 2689898	(AE000792) PTS system, cellobiose-specific IIB component (celA)	145	4.00E-27
EF092-2	gn 1119419204	B subtilis, cellobiose phosphotransferase system celA;	116	1.40E-26
EF096-2	8			
EF096-2	gi 147329	transport protein [Escherichia coli] >gn PID d1015409	532	2.10E-91
EF096-2	gi 1573475	spermidine/putrescine-binding periplasmic protein precursor (potD)	527	1.10E-79
EF096-2	gi 1574803	spermidine/putrescine-binding periplasmic protein precursor (potD)	468	1.60E-75
EF096-2	gi 1472681	Lpp38 [Pasteurella haemolytica]	446	1.40E-72
EF096-2	gn PID d10152	Putrescine transport protein PotF [Escherichia coli]	216	1.50E-54
EF096-2	6			
EF096-2	gi 147334	periplasmic putrescine binding protein [Escherichia coli]	216	2.10E-53
EF096-2	gi 2688565	(AE001165) spermidine/putrescine ABC transporter, PotD [Salmonella typhimurium]	240	2.00E-48
EF096-2	gi 1881733	PotD [Salmonella typhimurium]	253	2.70E-28
EF096-2	gi 147334	periplasmic putrescine binding protein [Escherichia coli]	216	2.10E-53
EF097-2	gi 224921	mannitol transport protein [Bacillus stearothermophilus]	547	4.90E-93
EF097-2	gi 42034	mannitol permease [Escherichia coli] >gi 46677 mannitol-	535	5.50E-85

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		specific		
EF097-2	gi 633650	enzyme II(mannitol) [Staphylococcus carnosus] >pir S68193 S22385	516	2.10E-82
EF097-2	gi 882462	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia	509	3.00E-76
EF097-2	gi 312763	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia	357	2.50E-70
EF097-2	gnl PII d110096 6	homologue of mannitol transport protein of B	492	3.10E-62
EF097-2	gnl PII d110079 2	mannitol-specific phosphotransferase enzyme II [Bacillus	484	5.20E-64
EF097-2	gi 1673855	(A1:000020) Mycoplasma pneumoniae, PIS system mannitol- specific	232	3.50E-59
EF097-2	gnl PID d10065 1	phosphotransferase enzymell, mannitol-specific [Mycoplasma	158	8.20E-18
EF097-2	pir S77757 S777	phosphotransferase system enzyme II (EC 2.7.1.69),	103	2.00E-13
EF100-2	gi 2058546	ComYC [Streptococcus gordonii]	193	7.30E-27
EF100-2	gi 2058546	ComYC [Streptococcus gordonii]	193	7.30E-27
EF100-2	gi 12708	comc13 gene product [Bacillus anthracis] (AF041872.3)	156	3.90E-33
EF100-2	gi 148437	secretory component [Erwinia chrysanthemi] >pir E47021 E47021 pectic	134	4.40E-15

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF100-2	gi 148437	secretory component [Erwinia chrysanthemi] >pir E47021 E47021 pectic	134	4.40E-15
EF100-2	gi 606262	ORF_o145 [Escherichia coli] >gi 693706 HopG [Escherichia coli]	136	9.10E-13
EF100-2	gi 606262	ORF_o145 [Escherichia coli] >gi 693706 HopG [Escherichia coli]	136	9.10E-13
EF100-2	gi 38828	ExeG gene product [Acromonas hydrophila] >pir S22910 49905 protein	132	3.50E-12
EF100-2	gi 38828	ExeG gene product [Acromonas hydrophila] >pir S22910 49905 protein	132	3.50E-12
EF100-2	gn PID e117259	etpG [Escherichia coli]	131	5.10E-12
EF100-2	gn PID e117259	etpG [Escherichia coli]	131	5.10E-12
EF100-2	gi 42189	outG gene product [Erwinia carotovora] >pir S32861 S32861 outG	130	9.90E-12
EF100-2	gi 42189	outG gene product [Erwinia carotovora] >pir S32861 S32861 outG	130	9.90E-12
EF100-2	gi 609628	putative [Vibrio cholerae]	128	1.60E-11
EF100-2	gi 609628	putative [Vibrio cholerae]	128	1.60E-11
EF100-2	gi 609628	putative [Vibrio cholerae]	106	3.60E-17
EF101-2	gn PID e118502	similar to hypothetical proteins from B. subtilis [Bacillus]	113	1.89E-15
EF110-2	gi 43538	Staphylococcal serine proteinase homologue [Enterococcus faecalis]	1462	2.30E-195

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF110-2	gnl PID d10010 8	glutamic acid specific protease prepropeptide [Staphylococcus aureus]	106	3.70E-14
EF110-2	gi 46687	preproenzyme (AA -68 to 268) [Staphylococcus aureus]	106	6.70E-14
EF111-2	gi 606018	ORF_0783 [Escherichia coli] >gi 1789462 (AF000390) hypothetical_88.3	477	8.10E-80
EF121-2	gi 2626826	YtkN [Bacillus subtilis] >gnl PID d1182774 similar to (AF000532) 2',3'-cyclic nucleotide 2'-phosphodiesterase (cpdB)	143	1.30E-96
EF121-2	gi 2313187	(AF000532) 2',3'-cyclic nucleotide 2'-phosphodiesterase (cpdB)	413	2.60E-82
EF121-2	gi 48453	5' nucleotidase [Vibrio parahaemolyticus] >gnl PID d1001218	279	8.50E-47
EF121-2	gi 757842	UDP-sugar hydrolase [Escherichia coli]	239	1.60E-44
EF121-2	gi 1773162	UDP-sugar hydrolase precursor [Escherichia coli] >gi 1786687	239	1.60E-44
EF121-2	gi 47950	precursor polypeptide (AA -25 to 525) [Salmonella typhimurium]	229	2.10E-41
EF121-2	gi 747913	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Yersinia enterocolitica]	115	4.70E-36
EF121-2	gi 62772	5'-nucleotidase [Discopyge ommata] >pir S19564 S19564 5'-nucleotidase	137	5.80E-35
EF121-2	gi 1573573	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus influenzae]	114	8.90E-34
EF121-2	gi 537054	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Escherichia coli]	110	1.10E-31
EF121-2	gi 202571	2'-nucleotidase precursor (AA -313 to 313) [Bartonella henselae]	135	9.10E-28
EF121-2	gi 319783	ecto-5'-nucleotidase [Mus musculus] >pir C2001 C2001	136	1.10E-27

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF121-2	gi 23897	5'-nucleotidase [<i>Homo sapiens</i>] >pir S11032 S11032 5'-nucleotidase (EC)	133	1.60E-27
EF122-2	gi 2626826	Yfkn [<i>Bacillus subtilis</i>] >gnl PID e1182774 similar to	143	1.30E-96
EF122-2	gi 2313187	(AE000532) 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB)	413	2.60E-82
EF122-2	gi 38453	5'-nucleotidase [<i>Vibrio parahaemolyticus</i>] >gnl PID d1001218	279	8.50E-47
EF122-2	gi 757842	UDP-sugar hydrolase [<i>Escherichia coli</i>]	239	1.60E-44
EF122-2	gi 1773162	UDP-sugar hydrolase precursor [<i>Escherichia coli</i>] >gi 1786687	239	1.60E-44
EF122-2	gi 47950	precursor polypeptide (AA -25 to 525) [<i>Salmonella typhimurium</i>]	229	2.10E-41
EF122-2	gi 747913	2',3'-cyclic-nucleotide 2'-phosphodiesterase [<i>Yersinia</i>]	115	4.70E-36
EF122-2	gi 62772	5'-nucleotidase [<i>Discopyge ommata</i>] >pir S19564 S19564 5'-nucleotidase	137	5.80E-35
EF122-2	gi 1573573	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [<i>Haemophilus</i>]	114	8.90E-34
EF122-2	gi 537054	2',3'-cyclic-nucleotide 2'-phosphodiesterase [<i>Escherichia coli</i>]	110	1.10E-31
EF122-2	bbs 135915	5'-nucleotidase=glycosylphosphatidylinositol-anchored protein {EC}	128	7.70E-29
EF122-2	gi 1737443	5'-nucleotidase [<i>Boophilus microplus</i>]	104	1.60E-28
EF122-2	gi 293854	5'-nucleotidase [<i>Escherichia coli</i>] >pir S11032 S11032 5'-nucleotidase (EC)	133	1.60E-27
EF129-2		nucleotidase (EC)		
EF129-2	gi 53534	P54 protein [<i>Enterococcus faecium</i>] >pir 305542 305542	630	9.40E-79

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		hypothetical		
EF129-2	gi 512521	usp 45 gene product [Lactococcus lactis] >pir JN0097 JN0097 secreted	374	1.30E-42
EF129-2	gi 149525	secreted protein [Lactococcus lactis]	371	3.60E-42
EF129-2	gn PID e313022	hypothetical protein [Bacillus subtilis] >gn PID e1186168	317	2.30E-33
EF130-2	gi 488339	alpha-amylase [unidentified cloning vector]	621	6.70E-81
EF130-2	gi 488336	ORF [unidentified cloning vector]	342	8.00E-27
EF130-2	bbs 112518	alpha-amylase {N-terminal region} [Artificial sequence, P'ptide]	237	4.80E-26
EF130-2	gn PID e289144	ywpE [Bacillus subtilis] >gn PID e1184540 ywpE [Bacillus]	129	5.40E-11
EF131-2	gn PID e118528	penicillin-binding protein [Bacillus subtilis]	277	7.40E-43
EF131-2	gi 488330	alpha-amylase [unidentified cloning vector]	280	1.30E-31
EF131-2	gi 509240	No definition line found [Lactobacillus plantarum]	274	1.10E-30
EF131-2	gn PID d10249	(AB009635) Fmt [Staphylococcus aureus]	170	5.60E-20
EF131-2	gi 515050	DD-peptidase precursor [Streptomyces lividans] >pir S48220 S48220	131	2.30E-14
EF131-2	gi 153448	serine DD-peptidase [Streptomyces lividans]	131	1.20E-12
EF132-2	gi 153876	adhesin B [Streptococcus subsp.] >pir S42923 S42923	1257	5.30E-166
EF132-2	gi 293769	cell wall protein [Streptococcus pneumoniae]	491	3.40E-163
EF132-2	gi 1575030	surface adhesin A precursor [Streptococcus pneumoniae]	1220	2.40E-161

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF132-2	gi 153834	adhesin specific for salivary pellicle of dental surfaces	1203	4.80E-159
EF132-2	gi 1117994	surface antigen A variant precursor [Streptococcus pneumoniae]	1191	2.00E-157
EF132-2	gi 493017	endocarditis specific antigen [Enterococcus faecalis]	931	3.70E-122
EF132-2	gn P1D c255529	lipoprotein [Staphylococcus epidermidis]	453	3.20E-92
EF132-2	gi 1215161	YfeA [Yersinia pestis] > gi 1245464 YfeA [Yersinia pestis]	364	3.60E-64
EF132-2	gi 1573330	adhesin B precursor (fimA) [Haemophilus influenzae]	349	3.50E-63
EF132-2	gi 755075	periplasmic-binding protein [Synecchocystis sp.]	326	6.80E-62
EF132-2	gn P1D d1018652 Mn	similar to ABC transporter (membrane protein) [Bacillus]	174	3.10E-32
EF132-2	gi 1777933	TroA [Treponema pallidum]	171	3.40E-32
EF132-2	gi 790546	Tromp1 [Treponema pallidum]	171	5.10E-32
Query	Derwent Access. No.	Derwent Gene Description	BLAST Score	BLAST P-Value
EF003-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	268	4.20E-39
EF003-2	W20166	Helicobacter pylori outer membrane protein, 16225006.aa.	241	3.00E-27
EF006-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	283	1.20E-48
EF006-2	W20166	Helicobacter pylori outer membrane protein, 16225006.aa.	266	1.10E-30
EF009-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	319	1.40E-53

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF009-2	W20166	<i>Helicobacter pylori</i> outer membrane protein, 16225006.aa.	278	2.50E-32
EF012-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	227	3.20E-69
EF014-2	W14070	<i>S.thermophilus</i> exopolysaccharide biosynthesis protein EpsR.	103	5.90E-19
EF014-2	W22169	<i>S.thermophilus</i> exopolysaccharide synthesis operon epsA gene product.	103	7.30E-18
EF016-2	W15799	Adherence factor 104R of <i>Lactobacillus fermentum</i> .	157	9.60E-22
EF016-2	W15793	Adherence factor consensus sequence.	103	1.00E-11
EF017-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	241	8.90E-71
EF021-2	R31013	P39-alpha.	141	1.60E-19
EF021-2	R33280	P39-beta.	134	7.00E-14
EF022-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	324	2.20E-65
EF023-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	155	9.90E-33
EF023-2	R70152	<i>Streptococcus pneumoniae</i> strain SPRU98 P1pA	125	5.90E-17
EF027-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	233	2.20E-34
EF028-2	W17830	Thermophilic alkaline phosphatase.	202	7.70E-59
EF028-2	W11568	<i>E.coli</i> alkaline phosphatase mutant D153H/Q329A.	182	7.90E-56
EF028-2	W11570	<i>E.coli</i> alkaline phosphatase mutant D153H/K328H/Q329A	182	7.90E-56
EF029-2	W26309	<i>E.coli</i> alkaline phosphatase mutant D153H/K328H/Q329A/P330H	182	7.90E-56
EF029-2	W11564	<i>E.coli</i> alkaline phosphatase mutant D153H/K328H/Q329A	182	7.90E-56
EF029-2	W11553	<i>E.coli</i> alkaline phosphatase mutant D153H/K328H/Q330N	182	7.90E-55

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF028-2	W11566	E.coli alkaline phosphatase mutant D153H/K328H/D330L.	182	1.20E-54
EF028-2	W11569	E.coli alkaline phosphatase mutant K328H/Q329A.	180	1.70E-54
EF028-2	W11562	E.coli alkaline phosphatase mutant D153H/D330L.	182	1.70E-54
EF028-2	R26980	Fv(FRP5)-phoA recombinant antibody.	174	1.90E-54
EF028-2	W11567	E.coli alkaline phosphatase mutant Q329A.	179	2.30E-54
EF028-2	W11558	E.coli alkaline phosphatase mutant K328H/D330N.	176	6.40E-54
EF028-2	W11563	E.coli alkaline phosphatase mutant K328H/D330A.	176	6.40E-54
EF029-2	R10044	Plasmid pOW360 encoded Human Growth Hormone (HGH) - nuclease A	320	3.50E-40
EF029-2	R10041	Plasmid pOW350 nuclease A product.	320	4.30E-40
EF029-2	R73997	Staphylococcus aureus (Foggi) nuclease signal and mature sequences.	320	5.60E-40
EF029-2	R10043	Plasmid pOW360 encoding Human Growth Hormone (HGH) - nuclease	320	2.90E-38
EF030-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	277	6.10E-47
EF040-2	R59077	2-5A-dependent RNA-ase.	105	1.90E-18
EF040-2	W12703	Mouse 2-5A-dependent RNase.	105	1.90E-18
EF040-2	R82661	Partial murine 2-5A dependent RNase	105	1.90E-18
EF040-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	277	6.10E-47
EF051-2	R85781	Group B Streptococcal wild-type beta antigen	232	5.20E-24

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF054-2	P91941	Sequence of preprospasmolysin.	204	3.10E-19
EF054-2	W32519	Collagen-like polypeptide SEQ ID NO:2.	180	7.50E-18
EF054-2	W12324	Silver halide emulsion protein monomeric repeat unit #2.	180	7.50E-18
EF054-2	W32522	Collagen-like polypeptide SEQ ID NO:5.	192	1.60E-17
EF054-2	W12327	Silver halide emulsion protein monomeric repeat unit #5.	192	1.60E-17
EF054-2	W32520	Collagen-like polypeptide SEQ ID NO:3.	189	2.40E-17
EF054-2	W32532	Collagen-like polypeptide SEQ ID NO:15.	189	2.40E-17
EF054-2	W12325	Silver halide emulsion protein monomeric repeat unit #3.	189	2.40E-17
EF054-2	W12337	Silver halide emulsion protein monomeric repeat unit #15.	189	2.40E-17
EF054-2	W12341	Silver halide emulsion FLAG(RTM)-tagged protein #2.	189	2.60E-17
EF054-2	W02098	S. mutans antigen I/II.	161	5.40E-15
EF054-2	W02096	S. mutans antigen I/II fragment (aa803-1111).	161	1.90E-13
EF059-2	R26042	P. yoelii SSP2 antigen.	344	1.90E-39
EF059-2	R85782	Group B Streptococcal mutant beta antigen without IgA binding domain.	232	1.10E-26
EF059-2	R85781	Group B Streptococcal wild-type beta antigen.	232	1.70E-26
EF059-2	P91941	Sequence of preprospasmolysin.	200	1.50E-18
EF059-2	R28150	Sugar beet chitinase I.	148	1.70E-11

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF059-2	R26842	Protease from <i>S. Aureus</i> ATCC12600.	147	2.10E-11
EF059-2	R79643	Immunodominant antigen of <i>Streptococcus sobrinus</i> .	151	2.10E-11
EF059-2	W07539	Collagen like protein (CLP).	146	3.00E-11
EF061-2	R26042	<i>P. yoelii</i> SSP2 antigen.	241	1.70E-25
EF061-2	P60570	Sequence of the Falciparum Interspersed Repeat Antigen	199	1.60E-18
EF061-2	R85782	Group B Streptococcal mutant beta antigen without IgA binding domain.	153	2.40E-14
EF061-2	R85781	Group B Streptococcal wild-type beta antigen.	153	3.60E-14
EF061-2	P91941	Sequence of preprospasmodysin.	163	9.70E-14
EF061-2	P83194	Sequence of a bioadhesive precursor protein encoded by cDNA clone	156	7.90E-13
EF061-2	R28150	Sugar beet chitinase 1.	156	9.10E-13
EF061-2	W02096	<i>S. mutans</i> antigen I/II fragment (aa803-1114).	148	1.20E-12
EF061-2	P82971	Bioadhesive precursor protein from cDNA 52.	148	9.70E-12
EF061-2	W02098	<i>S. mutans</i> antigen I/II.	148	1.50E-11
EF062-2	W02098	<i>S. mutans</i> antigen I/II.	107	1.20E-36
EF062-2	R79643	Immunodominant antigen of <i>Streptococcus sobrinus</i> .	132	3.00E-36
EF062-2	W02098	<i>S. mutans</i> antigen I/II	107	1.20E-36
EF062-2	W02098	<i>S. mutans</i> antigen I/II	107	1.20E-36
EF071-2	R91515	Listeria phage lysin PL Y511	273	4.70E-37

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF075-2	W14070	S.thermophilus exopolysaccharide biosynthesis protein EpsR.	239	4.20E-36
EF075-2	W22169	S.thermophilus exopolysaccharide synthesis operon epsA gene product.	239	4.00E-34
EF077-2	R97280	Helicobacter-specific ATPase 439.	258	4.10E-74
EF077-2	R48036	Mycobacterium BCG immunogen	107	2.20E-67
EF077-2	W06712	Helicobacter-specific ATPase 948 (ORF-4).	220	2.50E-67
EF077-2	R70119	Rat homologue of human Wilson disease gene ATP7B.	186	9.80E-54
EF077-2	R72343	Wilson disease protein ATP7B.	176	6.70E-40
EF077-2	R06376	Product of the sse1 gene.	166	3.10E-28
EF077-2	R75396	Flea sodium pump alpha subunit	146	2.10E-25
EF077-2	W20891	H. pylori transporter protein, 14ce20219orf1.	156	8.60E-14
EF078-2	R56667	Bacteroides fragilis PprX regulatory response protein.	148	8.30E-18
EF078-2	R74630	Tomato TGE/ETR1 ethylene response protein.	130	7.80E-13
EF078-2	R69849	Ethylene response (ETR) gene product.	128	1.70E-11
EF078-2	R69850	Ethylene response (ETR) mutant protein etr1-1.	128	1.70E-11
EF078-2	R69851	Ethylene response (ETR) mutant protein etr1-2.	128	1.70E-11
EF078-2	R69852	Ethylene response (ETR) mutant protein etr1-3.	128	1.70E-11
EF081-2	R27247	Penicillin binding protein derivative #2.	101	0.00E-01
EF081-2	R27258	Penicillin binding protein derivative #2.	101	6.20E-15

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF081-2	R27259	Penicillin binding protein derivative #3.	101	6.20E-15
EF081-2	R27260	Penicillin binding protein derivative #4.	101	6.20E-15
EF081-2	R27261	Penicillin binding protein derivative #5.	101	6.20E-15
EF081-2	R27263	Penicillin binding protein derivative #7.	101	6.20E-15
EF081-2	R27264	Penicillin binding protein derivative #8.	101	6.20E-15
EF081-2	R27262	Penicillin binding protein derivative #6.	101	6.50E-15
EF081-2	R30845	Sequence encoded by the mec A gene.	101	6.90E-15
EF081-2	R27255	Penicillin binding protein PBP2A-27R.	101	6.90E-15
EF081-2	R31216	Penicillin binding protein PBP2A-27R.	101	7.00E-15
EF110-2	R91042	V8 mature protease (aal-213).	106	6.60E-16
EF110-2	R91043	V8 mature protease (aal-214).	106	7.20E-16
EF110-2	R91044	V8 mature protease (aal-215).	106	7.80E-16
EF110-2	R26842	Protease from <i>S. Aureus</i> ATCC12600.	106	6.70E-15
EF110-2	R29644	Protease from <i>S. Aureus</i> .	106	1.20E-14
EF110-2	W22218	Protein encoded by pV8RPT(-) construct.	106	7.60E-14
EF110-2	R91033	Beta-galactosidase-V8 protease fusion protein.	106	7.60E-14
EF110-2	R91034	Beta-galactosidase-V8 protease fusion protein.	106	1.70E-13
EF110-2	R37495	Protein encoded by pV8RPT(-) construct.	106	1.70E-13
EF110-2	R37495	Protein encoded by pV8RPT(-) construct.	106	1.70E-13
EF131-2	R37495	Pneumococcal fibritrial protein A.	1185	6.80E-165

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF131-2	W26367	Staphylococcus aureus saliva binding protein.	418	3.70E-85
EF131-2	R79722	ROM precursor TROMP1.	171	9.00E-31
EF131-2	W22134	Treponema pallidum rare outer membrane protein (TROMP-1).	171	9.00E-31

TABLE 3. Conservative Amino Acid Substitutions.

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

Table 4. Residues comprising Antigenic Epitope-Bearing Portion

EF001-2	from about Asp-151 to about Lys-152, from about 258, from about Lys-359 to about Lys-363, from Asp-408.	about Tyr- to about
EF002-2	from about Asn-80 to about Asp-83, from about 283.	about Gly-
EF003-2	from about Asn-263 to about Gly-266.	
EF004-2	from about Asn-23 to about Asn-26, from about from about Thr-154 to about Asp-159.	in Ser-87,
EF005-2	from about Lys-249 to about Glu-252.	
EF006-2	from about Gly-23 to about Asp-28.	
EF008-2	from about Thr-92 to about Gly-94, from about 165, from about Gly-287 to about Thr-289.	out Asp-
EF010-2	from about Pro-129 to about Asn-131.	
EF012-2	from about Asp-77 to about Asp-79, from about from about Asp-256 to about Thr-258, from about 468.	out Lys-98, about Asn-
EF013-2	from about Thr-30 to about Asp-32, from about from about Gln-164 to about Asn-166, from about 195.	out Ala-75, about Gly-
EF014-2	from about Ser-203 to about Asp-206, from about 316.	about Gly-
EF015-2	from about Pro-66 to about Gly-69.	
EF016-2	from about Lys-236 to about Asn-239.	
EF017-2	from about Ser-90 to about Gly-93, from about 199, from about Lys-230 to about Asn-233, from Gly-431.	out Lys- 8 to about
EF018-2	from about Lys-159 to about Tyr-161, from about 167, from about Asn-250 to about Arg-256, from Gly-395, from about Lys-416 to about Tyr-418.	about Ser- 2 to about in-428 to

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion

	about Arg-430.	
EF019-2	from about Arg-209 to about Ser-211, from about 290.	about Ser-
EF020-2	from about Lys-57 to about Asn-62.	
EF021-2	from about Ser-33 to about Gly-35, from about 258, from about Gln-271 to about Tyr-277.	at Gly-81, about Ser-
EF023-2	from about Lys-232 to about Asp-234, from about 306, from about Thr-453 to about Arg-456, from about Thr-480.	about Gly- 8 to about
EF025-2	from about Arg-183 to about Asp-185.	
EF026-2	from about Ser-25 to about Asp-30, from about 107 to about Asn-110.	out Asp-94,
EF027-2	from about Gln-72 to about Lys-74, from about 231.	out Asp-
EF028-2	from about Asp-186 to about Gln-188.	
EF029-2	from about Asp-118 to about Lys-122, from about Tyr-126.	to about
EF031-2	from about Glu-30 to about Gly-33.	
EF034-2	from about Glu-25 to about Gly-27, from about 77.	out Thr-77.
EF36-2	from about Gln-177 to about Ser-179.	
EF037-2	from about Ser-25 to about Asp-30, from about 107 to about Asn-110.	out Asp-94,
EF038-2	from about Asn-77 to about Lys-79, from about 92.	out Asn-92.
EF040-2	from about Lys-167 to about Gly-172, from about Asn-242.	to about

Table 4. Residues comprising Antigenic Epitope-Bearing Portion

EF044-2	from about Arg-162 to about Gly-194, from about 255 to about 277.	from about Asn-161 to about Gly-194, from about 255 to about 277.
EF045-2	from about Arg-159 to about Asn-161, from about 174 to about 176, from about Tyr-261 to about Gly-264, from about Glu-338 to about Glu-338.	from about Gly-161 to about Gly-194, from about 255 to about 277.
EF046-2	from about Ser-18 to about Gly-23, from about 255 to about 277, from about Thr-76 to about Asp-78.	from about Ser-47, from about 255 to about 277.
EF047-2	from about Asn-28 to about Asp-30, from about 255 to about 277.	from about Asn-161 to about Gly-194, from about 255 to about 277.
EF048-2	from about Asp-138 to about Lys-141, from about 154 to about 154.	from about Gly-161 to about Gly-194, from about 255 to about 277.
EF051-2	from about Asp-73 to about Gly-76.	from about Gly-161 to about Gly-194, from about 255 to about 277.
EF053-2	from about Ser-79 to about Gly-82.	from about Gly-161 to about Gly-194, from about 255 to about 277.
EF055-2	from about Asp-26 to about Gly-28, from about 255 to about 277, from about Arg-71 to about Gly-74, from about 255 to about 277.	from about Asp-69, from about Gly-89, from about Gly-89.
EF056-2	from about Arg-71 to about Gly-74, from about 255 to about 277.	from about Gly-89, from about Gly-89.
EF058-2	from about Lys-129 to about Gly-133, from about 573 to about 573, from about Pro-586 to about Gly-591.	from about Tyr-133 to about Gly-133, from about 573 to about 573.
EF065-2	from about Ser-236 to about Tyr-239, from about 352 to about 352, from about Lys-415 to about Asn-418, from about Asp-448, from about Asn-489 to about Lys-491, from about Asp-518, from about Glu-639 to about Lys-639.	from about Gly-46 to about Gly-46, from about Ser-516 to about Ser-516.
EF066-2	from about Ser-236 to about Tyr-239, from about 352 to about 352, from about Lys-415 to about Asn-418, from about Asp-448, from about Asn-489 to about Lys-491, from about Asp-518, from about Glu-639 to about Lys-639.	from about Gly-46 to about Gly-46, from about Ser-516 to about Ser-516.
EF067-2	from about Ser-236 to about Tyr-239, from about 352 to about 352, from about Lys-415 to about Asn-418, from about Asp-448, from about Asn-489 to about Lys-491, from about Asp-518, from about Glu-639 to about Lys-639.	from about Gly-46 to about Gly-46, from about Ser-516 to about Ser-516.

Table 4. Residues Comprising Antigenic Epitope-Bearing Porti

EF073-2	from about Met-98 to about Arg-100, from about 112.	about Asp-
EF074-2	from about Ser-53 to about Tyr-59, from about from about Pro-97 to about Gln-100, from about 232.	about Gly-88, about Gly-
EF076-2	from about Asn-38 to about Tyr-40, from about from about Lys-79 to about Gly-81.	about Asn-53,
EF077-2	from about Arg-411 to about Gly-413.	
EF078-2	from about Thr-294 to about Gly-296, from about 368, from about Glu-524 to about Gly-526.	about Gln-
EF080-2	from about Glu-164 to about Gly-166, from about 208, from about Lys-239 to about Gly-243.	about Tyr-
EF081-2	from about Asn-7 to about Ser-11, from about from about Lys-112 to about Asn-114, from about 164, from about Arg-181 to about Gly-183.	about Tyr-80, about Asp-
EF083-2	from about Gln-38 to about Arg-40.	
EF084-2	from about Lys-140 to about Asp-142, from about 166, from about Arg-262 to about Gly-264.	about Arg-
EF085-2	from about Asn-95 to about Asp-97, from about 114, from about Asp-258 to about Ser-260, from Ser-403.	about Asp- to about
EF086-2	from about Pro-112 to about Gly-115, from about 224, from about Asn-296 to about Gly-299, from Lys-348, from about Asp-428 to about Ser-432.	about Ser- to about
EF087-2	from about Pro-112 to about Gly-115, from about 224, from about Asn-296 to about Gly-299, from Lys-348, from about Asp-428 to about Ser-432.	about Ser- to about
EF088-2	from about Pro-112 to about Gly-115, from about 224, from about Asn-296 to about Gly-299, from Lys-348, from about Asp-428 to about Ser-432.	about Ser- to about

Table 4. Residues comprising Antigenic Epitope-Bearing Portion

EF090-2	from about Asp-21 to about Asp-5.	
EF091-2	from about Gln-41 to about Asp-43.	
EF093-2	from about Lys-85 to about Gln-97.	
EF094-2	from about Asp-314 to about Asp-316.	
EF095-2	from about Ser-328 to about Thr-330, from about 361, from about Gln-57 to about Gly-639, from Gly-746.	from about Asp- to about
EF096-2	from about Lys-128 to about Asn-130, from about 190.	from about Asp-
EF097-2	from about Val-357 to about Gly-359.	
EF099-2	from about Gln-44 to about Asp-47, from about 158, from about Asn-286 to about Asp-289.	from about Gly-
EF101-2	from about Lys-40 to about Asp-42, from about 253, from about Lys-288 to about Gly-290.	from about Asn-
EF102-2	from about Asp-314 to about Asp-316.	
EF103-2	from about Asn-46 to about Gly-48.	
EF104-2	from about Pro-232 to about Lys-237, from about 361, from about Ser-421 to about Gly-423, from Ser-490, from about Asp-550 to about Asn-552, about Lys-640, from about Asp-727 to about Gln- 751 to about Ser-754, from about Lys-771 to about Ile-835 to about Asn-837, from about Pro-851.	from about Asn- to about Gln-637 to about Asn- from about Gln-
EF105-2	from about Ser-40 to about Gly-43, from about from about Gln-220 to about Gly-222, from about 265.	from about Gln-97, about Gly-
EF106-2	from about Asp-72 to about Gly-75, from about 277, from about Asn-310 to about Arg-313.	from about Asp-
EF107-2	from about Thr-155 to about Asn-157, from about	from about Asp-

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion

[illegible]

INDICATIONS RELATING TO A DEPOSITED

ANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>10</u> , line <u>12</u>		
B. IDENTIFICATION OF DEPOSIT		Further deposit <input type="checkbox"/> additional sheet <input type="checkbox"/>
Name of depositary institution: <u>American Type Culture Collection</u>		
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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide sequence selected from a group consisting of:
 - (a) a nucleotide sequence encoding any one of the amino acid polypeptides shown in Table 1; or
 - (b) a nucleotide sequence complementary to any one of the sequences in (a);
 - (c) a nucleotide sequence at least 95% identical to any one of the sequences shown in Table 1; or
 - (d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences shown in Table 1.
2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide sequence identical to a nucleotide sequence in claim 1.
3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in claim 1.
4. The isolated nucleic acid molecule of claim 3, wherein the epitope-bearing portion of a polypeptide comprises an amino acid sequence listed in Table 1.
5. A method for making a recombinant vector comprising inserting an isolated nucleic acid molecule of claim 1 into a vector.
6. A recombinant vector produced by the method of claim 5.
7. A host cell comprising the vector of claim 6.
8. A method of producing a polypeptide comprising:
 - (a) growing the host cell of claim 7 such that the protein is expressed in the cell; and
 - (b) recovering the expressed polypeptide.
9. An isolated polypeptide comprising a polypeptide selected from a group consisting of:
 - (a) a polypeptide consisting of one of the complete amino acid sequences of Table 1;
 - (b) a polypeptide consisting of one of the complete amino acid sequences of Table 1 except for the N-terminal residue.

- (c) a fragment of the polypeptide of (a) having biological activity;
(d) a fragment of the polypeptide of (a) which binds to an antibody for the polypeptide of (a).
10. An isolated antibody specific for the polypeptide of claim 9.
11. A polypeptide produced according to the method of claim 9.
12. An isolated polypeptide comprising an amino acid sequence identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.
13. An isolated polypeptide antigen comprising an amino acid sequence of an *E. faecalis* epitope shown in Table 4.
14. An isolated nucleic acid molecule comprising a polynucleotide sequence encoding a polypeptide of claim 9.
15. A hybridoma which produces an antibody of claim 10.
16. A vaccine, comprising:
(1) one or more *E. faecalis* polypeptides selected from the group consisting of a polypeptide of claim 9; and
(2) a pharmaceutically acceptable diluent, carrier, or excipient, wherein said polypeptide is present, in an amount effective to elicit antibodies in an animal to a member of the *Enterococcus* genus.
17. A method of preventing or attenuating an infection caused by a member of the *Enterococcus* genus in an animal, comprising administering to the animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.
18. A method of detecting *Enterococcus* nucleic acids in a biological sample, comprising:
(a) contacting the sample with one or more nucleic acids under conditions such that hybridization occurs, and
(b) detecting hybridization of said nucleic acids to the one or more nucleic acid sequences present in the biological sample.

19. A method of detecting *Leishmania* nucleic acids in a sample obtained from an animal, comprising:
- (a) amplifying one or more *Leishmania* nucleic acids in the sample using polymerase chain reaction; and
 - (b) detecting said amplified *Leishmania* nucleic acid.
20. A kit for detecting *Leishmania* antibodies in a blood sample obtained from an animal, comprising:
- (a) a polypeptide of claim 1 attached to a solid support; and
 - (b) detecting means.
21. A method of detecting *Leishmania* antibodies in a sample obtained from an animal, comprising:
- (a) contacting the sample with a polypeptide of claim 9; and
 - (b) detecting antibody-antigen complexes.

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT

TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68, C12N 1/21, 5/12, G01N 33/569, 33/68, A61K 39/09		(11) International Publication Number A3	WO 98/50554	
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(30) Priority Data: 60/044,031 6 May 1997 (06.05.97) US 60/046,655 16 May 1997 (16.05.97) US 60/066,009 14 November 1997 (14.11.97) US		(88) Date of publication: 1 April 1999 (01.04.99)		
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(74) Agents: BROOKES, A., Anders et al; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).				
(54) Title: ENTEROCOCCUS FAECALIS POLYNUCLEOTIDES AND POLYPEPTIDES				
(57) Abstract <p>The present invention relates to novel genes from <i>Enterococcus faecalis</i> and the polynucleotide vectors, host cells, antibodies and methods for producing the same. The invention additionally relates to <i>Enterococcus</i> nucleic acids, polypeptides and antibodies in a biological sample. The present invention also relates to the prevention or attenuation of infection by <i>Enterococcus</i>.</p>				

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INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/31 C07K14/31 C07K16/12 C12Q1/68 C12N5/12 G01N33/58 G01N33/68 A61K39/09	
According to International Patent Classification (IPC) or to a national classification and IPC	
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12N C07K C12Q G01N A61K	
Documentation searched other than minimum documentation to the extent that such documents are included in	
Electronic data base consulted during the international search (name of data base and, where practical, search	
C. DOCUMENTS CONSIDERED TO BE RELEVANT	
Category *	Citation of document, with indication, where appropriate, of the relevant passages
A	EVERS S & COURVALIN R: "Regulation of VanB-Type vancomycin resistance gene expression by the VanS(E)-VanR (B) two-component regulatory system in Enterococcus faecalis 5583." JOURNAL OF BACTERIOLOGY, vol. 178, 1996, pages 1302-1309, XP000073904 see abstract --- -/--
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C	
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Date of the actual completion of the international search	Date of mailing of the
2 September 1998	03.12.98
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentpark 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 651 Fax: (+31-70) 340-0016	Authorized officer Lejeune

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category * Citation of document(s) with indication, where appropriate, of relevant passages

A CLARK I M ET AL: "ISOLATION AND SEQUENCE DETERMINATION OF AN ENDOCARDITIS ANTIGEN FROM ENTEROCOCCUS FAECALIS" SERODIAGNOSIS AND IMMUNOTHERAPY IN INFECTIOUS DISEASE, vol. 5, no. 2, July 1993, pages 85-92, XP002035311
see abstract
see figure 3

A LOWE A M ET AL: "Cloning of an Enterococcus faecalis endocarditis antigen: nomenclature with adhesins from some oral Streptococci." INFECTION AND IMMUNITY, vol. 63, no. 2, February 1995, pages 703-706, XP002073405
see abstract
see figure 2

A BURNIE J P & CLARK I M: "Diagnosing endocarditis with the cloned 112 kDa antigen of Enterococcus faecalis." JOURNAL OF IMMUNOLOGICAL METHODS, vol. 123, 1989, pages 217-225, XP000174342
see abstract
see page 222, column 1, paragraph 2

P,A XU Y ET AL: "Enterococcus faecalis antigens in human infections." INFECTION AND IMMUNITY, vol. 65, no. 10, October 1997, pages 4207-4215, XP000739006
see abstract

X EP 0 652 291 A (FUSO PHARMACEUTICAL IND ;OHNO TSUNEYA (JP)) 10 May 1995
see abstract
see page 4, line 27 - line 31
see claim 5

INTERNATIONAL SEARCH REPORT

Box I Observations where certain claims were found unsearchable (Continuation of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17 of the PCT.

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim(s) 17
is(are) directed to a method of treatment of
body, the search has been carried out and the
effects of the compound/composition.
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the
an extent that no meaningful international search can be carried out, specifically:
Further defects(s) under article 17(2)(a):
The gene EF07B which is mentioned in Table 4, is not
and is also absent from the sequence listing.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second

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sheet)

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Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 6)

This International Searching Authority found multiple inventions in this International application.

1. ☐ As all required additional search fees were timely paid by the applicant, this International search is limited to the searchable claims.
2. ☐ As all searchable claims could be searched without error justifying an additional fee, the search is limited to the searchable claims of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, the search is limited to those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, the search is restricted to the invention first mentioned in the claims, which is covered by claims Nos.

See extra sheet, Invention 1.

Remark on Protest

- ☐ The additional search fees were
☐ No protest accompanied the payment

is not

re payment

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Report is

applicant's protest.

in fees.

FURTHER INFORMATION CONTINUED FROM PCT No. 210

Inventions 1 to 41: Claims: (1-3) partially

Idem as invention 1, but concerning EF008 to

Inventions 42 to 74: Claims: (1-1) partially

Idem as invention 1, but concerning EF045 to

Inventions 75 to 107: Claims: (1-1) partially

Idem as invention 1, but concerning EF079 to

Inventions 108 to 123: Claims: (1-1) partially

Idem as invention 1, but concerning EF117 to

Invention 124: Claim: 11 partially

An isolated polypeptide antigen comprising a
sequence of an *Enterococcus faecalis* epitope
Table 4.

For the sake of conciseness, the first subject matter
defined, the other subject matters are defined by a

INTERNATIONAL SEARCH REPORT

Information on patent family members

Inter.
PC

Patent document cited in search report	Publication date	Patent family member(s)	Class No.
EP 0652291 A	10-08-95	AU 684250 E	37
		AU 4513593 A	34
		US 5807673 A	38
		WO 9401583 A	34
		JP 2798499 E	38
		US 5763188 A	38
		US 5770375 A	38
		US 5798211 A	38

The first part of the paper discusses the importance of the study of the history of the United States. It is argued that the study of history is essential for a full understanding of the present. The second part of the paper discusses the importance of the study of the history of the United States. It is argued that the study of history is essential for a full understanding of the present. The third part of the paper discusses the importance of the study of the history of the United States. It is argued that the study of history is essential for a full understanding of the present.